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Copyright (c) 1993 - 2000 Compugen Ltd.
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-I. WISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN FOR THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

-I. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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SEQUENCE FROM N.A.

MEDILINE-87315205; PubMed=3306373;

del Portillo H.A., Nussenzweig R.S., Enea V.;

del Portillo H.A., Nussenzweig R.S., Enea V.;

del Portillo H.A., Nussenzweig R.S., Enea V.;

Thailand.":

Mol. Biochem. Parasitol. 24:289-294(1987)

-1. FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNDOMINANT

-1. FUNCTION: THE CIRCUMSPOROZOITE FROM THE MOSQUITO TO THE

MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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Malaria; Sporozoite; Repeat; Signal.

SIGNAL 17 424 CIRCUMSPOROZOITE PROTEIN.

CHAIN 123 300 45 X 4 AA. TANDEM REPEATS OF N-A-N-P.
41 X 4 AA TANDEM REPEATS OF P-N-A-N. 
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101-3NN-1990 (Rel. 13, Created)
101-3NN-1990 (Rel. 13, Last sequence update)
101-3NN-1990 (Rel. 40, Last annotation update)
101-3NN-1990 (Rel. 40, Last annotation)
101-3
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100.0%; Pred. No. 5.7e-09;
iive 0; Mismatches 0;
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PIR, A54533; A54533.
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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412 AA; 44420 MW;
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BEDILRUE-SA150215: PubMed-6204383;

Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,

Hochmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,

Banders G.S., Reddy E.P., Diggs C.L., Miller L.H.;

Standers G. The gene encoding the immunodominant surface antigen on

Structure of the human malaria parasite Plasmodium falciparum.";

Science 225:593-599(1984)

I. FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT

SURFACE ANTIGER ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE

MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE

VERTEBRATE HOST).
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-:- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      CIRCUMSPOROZOITE PROTEIN.

A 3 A AA TANDEM REPEATS OF N-A-N-P.
A -> ANDNANDNA (IN REF. 4).

9E81146F59EBCEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                          Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 109; DB 1; 100.0%; Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-NG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 412 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                           Malaria; Sporozoite; Repeat; Signal.
SIGNAL 1 16 PROBABLE.
     EMBL; M83886; AAA29521.1; --
EMBL; M22987; AAA2927.1; --
PIR; A4557; A4557;
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR003067; Cromsprzoite.
Pram; PR00309; XEP.1; 1.
PRNTS; PR01307; CRCMSPRZOITE.
SMART; SM00209; TSP1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 DIEKKICKMEKCSSVFNVVNS 383
                                                                                                                                                                                                                                                                                                                         42646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K02194; AAA29524.1; -.
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
                                                                                                                                                                                                                                                                      101
194
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSP_PLAFA P02893;
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                         SEQUENCE
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us-09-763-397a-7.rsp

Mon Feb

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malaria parasite Plasmodium falciparum.";
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P06915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSP_PLABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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    A PART OF THE PRINT OF THE PRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                             Lockyer M.J., Schwarz R.T.; "Strain variation in the circumsporozoite protein gene of Plasmodium
                                                                                                                                                                                                                                                                                                                               MOI. Biochem. Parasitol. 22:101-108(1987).
--I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIRCUMSPOROZOITE PROTEIN.
47 X 4 AA TANDEM REPEATS OF N-A-N-P.; BD57A9A152B85E03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-91201303; PubMed-2016283;
Lal A.A. Goldman I.F.;
"Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 442;
                                                                                                                                  Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 109; DB 1;
100.0%; Pred. No. 6.1e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 23, Last sequence update) (Rel. 40, Last annotation update)
                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
    442 AA.
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CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                           CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; Sporozoite; Repeat; Signal.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M15505; AAA29554.1; -.
PIR; A54529, A44529.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                               MEDLINE-87115616; PubMed-3543671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.
Matches 21; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium reichenowi.
                                                                                                                                                                                                                                                                                                                                                                                                                      VERTEBRATE HOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 AA;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                             NCBI_TaxID=5848;
                                                                                                                                                                                                                                                                                                             falciparum."
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CSP_PLAFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408
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                                                                                                                                VERTEBRATE HOST).

MISCELLANGOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURRACE ANTIGEN OF THE ORGANISM.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATE HOST).

MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87089740; PubMed-2432395; Echinger D.J., Arnot D.E., Tam J.P., Nussenzweig V., Enea V.; Circumsporozoite protein of Plasmodium berghei: gene cloning and identification of the immunodominant epitopes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Cell. Biol. 6:3965-3972(1986).
-!- FUNCTION: THE CIRCUMSPORZOTTE PROTEIN IS THE IMMUNODOMINANT
SURENCE ANTIGEN ON THE SPORZOTTE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
J. Biol. Chem. 266:6686-6689(1991).
-!- FUNCTION: THE CIRCUMSPORZOTTE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPORCZOTTE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIRCUMSPOROZOITE PROTEIN.
62 X 4 AA TANDEM REPEATS OF N-A-N-P.
C031EEFBE2E35604 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 1; Length 38 Pred. No. 1.1e-08; .: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003067; Crcmsprzoite. InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M60972; AAA29561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.2
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A39756; A39756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE

Best Loca Matches

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RESULT 7

DOMAIN CHAIN

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15 X 6 AA TANDEM REPEATS OF Q-G-P-G-A-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- MISCELLANDOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDIANE SEQUENCE FROM N.A. MEDLINE-87137555; PubMed=3102479; Lal A.A., de la Cruz V.F., Welsh J.A., Charoenvit Y., Maloy W.L., McCutchan T.F., Structure of the gene encoding the circumsporozoite protein of Plasmodium yoelii. A rodent model for examining antimalarial sporozoite vaccines. "J. Blol. Chem. 262:2937-2940(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 malarias.";
Mol. Blochem. Parasitol. 28:31-38(1988).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNDDOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium berghei yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-140 AND 260-367 FROM N.A. MEDLINES-88237798; PUDMed-2287155, de la Cruz V.F., Lal A.A., MCCutchan T.F.; Variation among circumsporozoite protein genes from rodent
                                                                                                                                                                                                    Length 347;
                                                                                                                                                                                                    76.1%; Score 83; DB 1; Length 347
61.9%; Pred. No. 3.3e-05;
live 7; Mismatches 1; Indels
POTENTIAL.
CIRCUMSPOROZOITE PROTEIN.
13 X 8 AR REPEATS.
17 X 2 AR REPEATS OF P-Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
20-NG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sporozoite; Repeat; Signal.
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EMBL; M18821; AAA29559.1; -.
EMBL; M22698; AAA29560.1; -.
EMBL; AZ6271; OZZQM:
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                     313 DIDTEICKMDKCSSIFNIVSN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                   37776 MW;
                                                                                                                                                                                                                                                                                                                     1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSP_PLAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malaria;
                                                                                                                   SEQUENCE
                                                                                                                                                                                                          Query Match
                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
                                                                                          DOMAIN
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
CIRCUMSPOROZOITE PROTEIN.
13 X 8 AA TANDEM REPEATS.
16 X 2 AA TANDEM REPEATS OF P-Q.
FE8068A6D11D9551B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium berghei (strain Anka).

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBL_TaxID=5823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 76.1%; Score 83; DB 1; I
l Similarity 61.9%; Pred. No. 3.2e-05;
13; Conservative 7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 347 AA
                                                                                                   EMBL; M14135; AAAZ9577.1; --
PIR; A55083; OZZQMB.
InterPro; IPRO03067; Crcmsprzoite.
InterPro; IPRO03064; TSP1.
PRANTS; PRO0309; LSP1.1.
PRINTS; PRO1303; CRCMSPRZOITE.
SMART; SM00209; TSP1, 1.
MALAria; Sporozoite; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S07873; OZZQBK.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                     24 339 CI
93 196 13
206 238 16
339 AA; 37138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 DIDTEICKMDKCSSIFNIVSN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pram; PP00090; LSP_1; 1.
PRINTS: PR01030; CRMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X17606; CAA35608.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSP_PLABA
P23093;
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CSP_PLABR

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                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                       MEDLINE-89040027; PubMed-3054537;
Lal A.A., la Cruz V.F., Campbell G.H., Procell P.M., Collins W.E.,
Lal A.A., la cruz V.F., Campbell G.H., Procell P.M., Collins W.E.,
McCutchan T.E.;
"Structure of the circumsporozoite gene of Plasmodium malariae.";
Mol. Blochem. Parasitol. 30:291-294(1988).
-: FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURRACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium cynomolgi (strain Berok).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; Score 77; DB 1; Length 429; 57.1%; Pred. No. 0.0003; 2; Indels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIRCUMSPOROZOITE PROTEIN.
4 AA TANDEM REPEATS.
3629D641D1C0BB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 AA.
    429 AA
                                                                            20-AUG-2001 (Rel. 40, Last annotation u. CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malaria; Sporozoite; Repeat; Signal SIGNAL 15 PROBAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P04002; 1WFA.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE-87102878; Pubmed-3802196;
                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 DLETEICSLDKCSSIFNVSN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRMSPRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 314 4
429 AA; 41596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J03992; AAA29557.1; -. PIR; A54504; A54504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATE HOST)
                                                                                                                  Plasmodium malariae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                       NCBI_TaxID=5858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSP_PLACB
P08672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATE HOST).

-I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
MEDLINE-88186854; PubMed-3128542;
Lal A.A., la Cruz V.F., Collins W.E., Campbell G.H., Procell P.M.,
McCutchan T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Circumsporozoite protein gene from Plasmodium brasilianum. Animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 8 x 4 AA TANDEM REPEATS OF Q-Q-P-P. 38888 MW; 1EA56AFF7FFCB5E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 393;
                                                                            Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.6%; Score 77; DB 1; Length 393
57.1%; Pred. No. 0.00028;
Live 7; Mismatches 2; Indels
                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANDEM REPEATS OF G-N-A-A.
B32944419BC600AA CRC64;
                                                                        76.1%; Score 83; DB 1; I 61.9%; Pred. No. 3.5e-05; Live 7; Mismatches 1;
                                                                                                                                                                                                                                                                                                                      71737-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT)
                                                                                                                                                                                                                                                                                         393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                              7;
                                                                                                                                                                         333 DIDTEICKMDKCSSIFNIVSN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 DLETEICSLDKCSSIFNVSN 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35372 MW;
                                                                                                                                                     1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P04002; IWFA.
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Repeat; Sporozoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03203; AAA29553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.11
Matches 12; Conservative
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium brasilianum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278
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229 2
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 AA;
                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5824;
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P14593;
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  DOMAIN
SEQUENCE
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Gaps

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CSP_PLAMA

Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,

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--- MISCELLARROUS THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURPACE ANTICEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 X 11 AA TANDEM REPEATS OF G-N-Q-A-G-G-Q-A-G-A-G.
                 THE REPEAT SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRÓBABLE.
CIRCUMSPOROZOITE PROTEIN.
18 X 6 AA TANDEM REPEATS OF D-G-A-R-A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W., Nussenzweig R.S., Enea V.; "The circumsporozoite gene of the Plasmodium cynomolgi complex."; cell 48:311-319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium cynomolgi (strain Ceylon).
Eukaryota: Alveolata: Apicomplexa: Haemosporida; Plasmodium.
NCBL_TAXID=5819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8295A913C36420C5 CRC64;
        ANCHORING THE PROTEIN TO THE CELL MEMBRANE. TI WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71; DB 1;
Pred. No. 0.0021;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-TAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPORGITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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SEQUENCE FROM N.A.
MEDLINE-87102878; PubMed=3802196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [EA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRUCUCE.; InterPro; Pram; PR00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SWART; SM00209; TSP1; 1.
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344 DLETEVCTMDKCAGIFNVVSN 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M15101; AAA29537.1; -. PIR; A26255; OZZQAL.
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ilarity 47.6%;
Conservative
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es 10; Conserv
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Best Local Si
Matches 10;
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P08673;
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CSP_PLOC 13

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-1- MISCELLANBOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                            VERTEBRATE HOST).
MISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SUBRACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 1; Length 378; Pred. No. 0.0021; 3; Indels 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIRCUMSPOROZOITE PROTEIN.
10.5 x 9 AA REPEATS.
3 x 16 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36286 MW; 779BA081C140793F CRC64;
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-JAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRÓBABLE.
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PRIMTS; PR01303; CRGMSPRZOITE.
SMART, SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; D26255; O22QAB.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M15104; AAA29532.1; -.
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CSP_PLACL P08675;

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Query Match Best Local Si Matches 10,

SEQUENCE

SIGNAL DOMATN DOMAIN REPEAT

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CSP_PLACM
P08676;
              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN.
17 x 11 AA TANDEM REPEATS OF [DG]-G-A-A-A-A-G-G-G-N.
                                                                                                             CIRCUMSPOROZOITE PROTEIN.
17 X 9 AA TANDEM REPEATS OF A-G-N-N-A-A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                 Gaps
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Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Ususenzweig R.S., Enea V.;
"The circumsporozoite gene of the Plasmodium cynomolgi complex.";
Cell 48:311-319(1987).
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium cynomolgi (strain Gombak).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5830;
                                                                                                                                                                                       Length 398;
                                                                                                                                                                                     65.1%; Score 71; DB 1; Length 398 ilarity 47.6%; Pred. No. 0.0022; Conservative 8; Mismatches 3; Indels
                                                                                                                                                  6DFA2E8A62ED05BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PF00090; tsp_1; 1.
PRINTS, PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL 1 19
                                                                                                  PROBABLE.
          PIR: C26255, O220AS.
Interpro: IRR003667, Crcmsprzolte.
Interpro: IRR003667, Crcmsprzolte.
Interpro: IRR000684 i TSP1.
Pfam; PF00090; tsp_1; 1.
SMART; SR00209; TSP1; 1.
Malaria; Sporozolte; Repeat; Signal.
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                     364 DLETEVCTMDKCAGIFNVVSN 384
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                                                                                                                                                  398 AA; 37718 MW;
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EMBL; M15103; AAA29533.1; -.
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Best Local Similarity
Matches 10; Conserv
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SEQUENCE FROM N.A.
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P08674;
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InterPro; IPR000884; ...
R Pfam; PF00090; tsp_1; 1.
AR PRINTS; PR01030; CROMSPRZOITE.
BR SMART; SM00209; Tspl; 1.
BR Malaria; Sporozoite; Repeat; Signal.
CIGNAL 1 19 CICUMSPOROZOITE PROTEIN.
20 419 CICUMSPOROZOITE PROTEIN.
314 AA TANDEM REPEATS OF N-A-MY; 8F46CDD8AIB4EFF4 CRC64; ...+h 419;
                                                                                                                                                                                                                                                                                                                                                             Plasmodium cynomolgi (strain Mulligan/NIH).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 1; Length 419; Pred. No. 0.0023;
65.1%; Score 71; DB 1; Length 401; 47.6%; Pred. No. 0.0022;
                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87102878; PubMed-3802196;
Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzweig R.S., Enea V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                                      419 AA
           47.6%; Pred. ....
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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367 DLETEVCTMDKCAGIFNVVSN 387
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01-FEB-1996 (Rel. 33, Last seq
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385 DLETEVCTMDKCAGIFNVVSN 405
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                                                                                  1 DIEKKICKMEKCSSVFNVVNS 21
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47.6%;
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                                          Conservative
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Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                    STANDARD;
                 Best Local Similarity
Matches 10; Conserv
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de Stricker K. Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K. Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ26941; CAB64167.1;
InterPro; IPR000884; TSP1.
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            025836
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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100.0%; Pred. No. 8.9e-10;
ive 0; Mismatches 0;
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burnese field isolates and from laboratory strains.";

submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJZ6961, CAB64180.1;

InterPro; IPR000864; TSP1.

InterPro; IPR000864; TSP1.

InterPro; PR001303; CRCMSPRZOITE.

SMATT, SMO0209; LSP1; 1.

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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and

Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/Genbank/DDBJ databases.

EMBL; AJZ69957; CAB64237.1;

InterPro; IPR00084; TSP1.

InterPro; IPR000864; TSP1.

Pfam: PP00090; tSp_1: 1.

PRINTS; PR01303; CRCMSPRZOITE.
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Ebkaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TAXID=833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MNY-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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100.0%; Pred. No. 8.9e-10;
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GE STRICKER K., Vunst J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodlum
falciparum glutamater rich protein (GIMEP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
IMMETER: AJG6948; TRB1.1:
InterPro: IPR003063, TSP1.1:
InterPro: IPR003067; Cromsprzoite.
Prim: PF00090; tsp.1:
PRINTS: PR01303; CRCMSPRZOITE.
STRAIN:
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STRAIN-LI:
GRAIN-LI:
GESTICKET K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum quitamater rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL. Algobysi. CAB64176.1;
InterPro: IPRO00084: TSP1.

InterPro: PRO00090; Crcmsprzoite.

Ffam: PRO00090; ESP_1: 1.

SMART: SM00209; TSP1: 1.
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Bukswyota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Ekkaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
NCBL_TAXID=8933;
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80 AA; 9046 MW; BA7689D18F031C3E CRC64;
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01-MNY-2000 (TrEMBLrel. 13, Last sequence update)
01-MNY-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AA.
   80 AA.
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       PRT;
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nes 21; Conservative
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       PRELIMINARY;
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Matches 21;
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DT 01-MA
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CRCUMSPOROZOITE PROTEIN (FRAGMENT).
CS.
Elasmodium falciparum.
Elasmodium falciparum.
Pubar-yota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 80;
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Best Local Similarity 100.0%; Pred. No. 8.9e-10;
Matches 21; Conservative 0; Mismatches 0; Indels
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InterPro; IPR000084; TSP1.
InterPro; IPR003067; Cremsprzoite.
Pfam: PF00090; tsp_1, 1.
PRINTS: PR01303; CRCMSPRZOITE.
SMART: SM0209; TSP1; 1.
NON_TER
80 80
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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100.0%; Pred. No. 8.9e-10;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 21; Conservative
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2910P3
1D 0910P3
AC 0910P3
DT 01-MAY'
DT 01-MA
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090004
AC 090004
AC 090004
DT 01-MAX
DT 01-MAX
DE CS
CS DLASMO
CO NOS DLASMO

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                 85 F F P R P R P F F S
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

General Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

A de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

The Sequence variation in the non-repeat region of the Plasmodium

falciparum glutamate rich protein (GLDRP) from Brazil, Senegalese, and

REAL SECOND REPOSED TO THE EMBL/GenBank/DDBJ databases.

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

REAL, AJZ6963; CAB64182.1;

REAL: AJZ6963; CAB64182.1;

RICETPOS IPRO03067; CTCMSPIZOITE.

PRAM: PF00090; tsp_1; 1.

REAL: AND TERM SECOND SECOND
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STRAIN-E04363.

SEQUENCE K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the Plasmodium falciparum glutamate rich protein (GLÜRP) from Brazil, Senegalese, and Burnese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Plasmodium falciparum.
Enkaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                            100.0%; Score 109; DB 5; Length 80; 11arity 100.0%; Pred. No. 8.9e-10; Conservative 0; Mismatches 0; Indels
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2 21; Conservative 0; Mismatches 0; Indels es 21; Conservative 0; Mismatches 0
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NON_TER 80 80
SEQUENCE 80 AA; 9002 MW; ICEEAE08E6C9E976 CRC64;
     80 AA; 9047 MW; BA769C90DB031C3E CRC64;
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O9U0P5;
O1-MAY-2000 (TEMBLrel. 13, Created)
O1-MAY-2000 (TEMBLrel. 13, Last sequence update)
O1-MAY-2001 (TEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 DIEKKICKMEKCSSVFNVVNS 80
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                                                                                                                                                                                                                                                                                                                                                  1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                       Query Match
Best Local Similarity
Matches 21; Conserv
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Best Local S.
Matches 21
     SEQUENCE
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Q9U0P6
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RA SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA GESTICKER K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

RA de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

RA Sequence variation in the non-repeat region of the Plasmodium

RT Sequence variation in the non-repeat region of the Plasmodium

RT Sequence variation in the non-repeat region of the Plasmodium

RT Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

RE SUBMITTED SEQUENCE CAR64181.1;

DR FMBL; AJZ69968, CAB64187.1;

DR InterPro; IPR003884; TSP1.

DR InterPro; IPR003884; TSP1.

DR Pfam; PF001303; CRCMSPRZOITE.

DR Pfam; PF001303; CRCMSPRZOITE.

DR SMART; SM00209; TSP1.

SMART; SM00209; TSP1.
                                                                                                                                                                                                         TATALN-B1896;
TATALN-B1896;
de Stricker Ki, Vuust J. Jepsen S., Oeuvray C., Theisen M.;
de Stricker Ki, Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
Burnese field isolates and from iaboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EnterPro; IPR000848; TSP.;
InterPro; IPR000848; TSP.;
InterPro; IPR00090; ESP.];
PRINTS; PR01193; CRCMSPTCOITE.
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=6833;
                                                                 Piasmodium falciparum.
Eukaryoca: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBi_TaxID=6833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 109; DB 5;
100.0%; Pred. No. 8.9e-10;
Live 0; Mismatches 0;
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100.0%; Pred. No. 8.9e-10;
tive 0; Mismatches 0;
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CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Matches 21; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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NON_TER
SEQUENCE
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Q9TW97
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The State of the Plasmodium of State of the Plasmodium of State of State
                          de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
Interpro; IPR000084; TSP1.
Interpro; IPR000067; Cromsprzoite.
Pfam: PP00090; tsp_l: 1.
PRINTS: PR01303; CRCMSPRZOITE.
SMART; SW00209; TSP1: 1.
NON_TER 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
100.0%; Score 109; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 8.9e-10;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 80;
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 109; DB 5; 18 Best Local Similarity 100.0%; Pred. No. 8.9e-10; Matches 21; Conservative 0; Mismatches 0;
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0900D1;
01-MAY-2000 (TERMELREL 13,
01-MAY-2000 (TERMELREL: 13,
01-JUN-2001 (TERMELREL: 137,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
STRAIN-D4405;
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Q900P1
ID Q900P1
AC Q1-MAY
DT 01-MAY
DT 01-JUN
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Q9U0P2
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                                         100.0%; Score 109; DB 5; 100.0%; Pred. No. 8.9e-10;
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                                                                                                                 Mismatches
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PROSITE; PS50092; TSP1; 1.
SMART; SM00209; TSP1; 1.
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                 Conservative
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Best Local Similarity
Matches 21; Conserv
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Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ269944; CAB64179.1;

InterPro; IPR000884; TSP1.

InterPro; IPR000884; TSP1.

InterPro; IPR000895; CRMSPRZOITE.

Pfam; PF00090; tsp_1; 1.

PRINTS; PR01303; CRCMSPRZOITE.
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NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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                                                                           80 AA
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                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
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SEQUENCE FROM N.A.
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SEQUENCE
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Q9TW76
RESULT
Q9TW83
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STRAIN-M11, AND D7;
STRAIN-M11, AND D7;
Ge Stricker K. , Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodium falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269960; CAB64172.1; -.
EMBL; AJ269947; CAB64172.1; -.
EMBL; PR000884; TSP1.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
Length 80;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 AA; 9123 MW; 4614EEC68F0B1434 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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January 29, 2002, 10:21:43; Search time 310.82 Seconds (without alignments) 2:145 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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59
1 WSPCSVTCG 9
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Maximum DB seq length: 2000000000
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Perfect score:
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A_Geneseq_1101:*

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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/SIDSB/gogdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gogdata/geneseq/geneseqp/AA1999.DAT:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Thrombospondin pep	Peptide of the inv	Thrombospondin syn	Thrombospondin syn	Thrombospondin syn	Plasmodium falcipa	Synthetic peptide	Circumsporozoite p	Circumsporozoite p	Circumsporozoite p	Circumsporozoite
	QI	AAR13626	AAW97439	AAW81490	AAW81491	AAW81478	AAY70284	AAP60413	AAR51428	AAR51429	AAR51430	AAR51431
	ВВ	12	20	20		20		7		15		15
	Ouery Match Length DB ID	6	6	6	6	σ	6	13	16	18	18	18
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100,0
	Score	59	59	59	59	59	59	59	59	59	59	59
	Result No.	-	7	m	4	s	9	7	œ	σ	10	11

New peptide fragments and analogues of thrombospondin - useful for inhibiting tumour metastasis, as clotting agents and to promote or inhibit cell adhesion and immune modulation.

XYLL

Circumsporozoite p P. falciparum circ Peptide RII derive Amino acid sequenc Circumsporozoite p P. falciparum circ	Peptide used for F P. falciparum CSP: Peptide used for F P. falciparum circ	Consensus critomos Thrombospondin rel P. falciparum circ Circumsporozoite a Circumsporozoite a Amino acid sequenc	Synthetic peptide NSI_BRINGTELED. NSIBIRDFAUTH plasm NSI_BIRDFAUTH. P NSI_BIRDFAUTH + (NSI_BIRDFAUTH	Recombinant vaccin Plasmodium cynomol Sequence encoded b CS protein of mala Sequence encoded b RTS protein. Syn RTS* protein. Syn Antigenic protein Circumsporozoite (Amino acid sequenc
5 AAR51432 9 AAW59270 2 AAB49237 0 AAY03674 5 AAW59271	000000	22 AAB40115 12 AAR13504 19 AAR59273 11 AAR07290 20 AAX03681	4 0 11 0 0 0 0 0	AAY70278 AAP70709 AAP83144 AAP60416 AAR80835 AAR87796 AAR87797 AAR87797 AAR87797 AAR87797 AAR87797
18 18 18 18 20 20 21 21 23 1			327 329 319 319 327 1335 135	
100.0 100.0 100.0 100.0	100.00	100.00	100.00	1000.0 1000.0 1000.0 1000.0 1000.0 1000.0
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ALIGNMENTS

AAR1	RESULT 1 AAR13626 .
ΩI	AAR13626 standard; peptide; 9 AA.
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AC	AAR13626;
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DI	31-OCT-1991 (first entry)
XX	
DE	Thrombospondin peptide pl.
XX	
ΚW	Antiviral agent; wound healing; platelet aggregation; thrombotic;
ΚW	thrombolytic.
X	
SO	Synthetic.
XX	
PN	EP443404-A.
X	
PD	28-AUG-1991.
XX	
PF	11-FEB-1991; 91EP-0101908.
XX	
PR	
PR	22-FEB-1990; 90US-0483527.
XX	
ΡA	(GRAC) GRACE W R & CO-CONN.
PA	(MEDI-) MED COLLEGE OF PENNSYLVANIA.
XX	
Ιd	Deutch AH, Tuszynski GP;
×	
DR	WPI; 1991-254044/35.

Gaps

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Sequences AAW81478 to AAW81491 represent syntehtic peptide analogs of thrombospondin (thrombin sensitive protein or 1859) that retain thrombospondin (thrombin sensitive protein or 1859) that retain mimicking a biological activity. The invention provides a method for (a) mimicking a biological activity of thrombospondin; (b) promoting thromboils activity of thrombospondin (b) promoting thrombospondin other than thromboils activity. The method comprises administering any of these peptides. Biological activities of thrombospondin include cell adhesion-promoting activity, cell mitogenic activity, cell chemotactic activities, haemostatic activities, and
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombospondin; thrombin sensitive protein; TSP; cell-adhesion; mitogenic activity; chemotactic; haemostatic; tumour; microbial; parasite; metastasis; platelet aggregation; fibrinolytic; malaria; immune modulation; wound healing; atherosclerosis; angiogenesis; complement modulator; diagnostic reagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for mimicking or inhibiting thrombospondin activity - using thrombospondin peptides
myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures.
                                                                                                                                                        ö
                                                                                                                                                       Indels
                                                                                                                   Match 100.0%; Score 59; DB 20; Local Similarity 100.0%; Pred. No. 4.3e+05; Nes 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note≈ "n-formyl-tryptophan"
                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombospondin synthetic analog compound p5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GRAC ) GRACE & CO-CONN W R. (UYAL-) UNIV ALLEGHENY HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Column 29; 19pp; English.
                                                                                                                                                                                                                                                                                                            AAW81490 standard; peptide; 9 AA.
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92US-0896527.
93US-0110146.
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                                                                     9 AA;
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Modified-site
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19-DEC-1994;
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation; neurite defaalculation; regeneration; nervous system cell; nerodegenration; Alzhaiemer's; Parkinson's disease; multiple sclerosis; myopathy; synapse formation; neuroblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97439-41 represent sequences that are not contained within a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasiculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple sclerosis and
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                 The peptide may have an NH2 gp on Gly(9) (peptide p6) and Trp(1) may be formylated (peptide p5). The peptide is a synthetic fragment of human thrombospondin and comprises the sequence motif of Robson et al (Nature (1988) 333:79-82). It has thrombospondin-11ke activity and can be used:
(1) to inhibit throwur cell metastasis and atherosclerosis:
(2) to promote or nhibit platelet aggregation, anglogenic activity, thrombotic or thrombolytic activity, immune modulaton and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell cultures
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                    (3) to promote wound healing; and (4) as an antiviral agent (interferes with cell adhesion). The peptide is prepa by std. synthesis techniques. See also AAR1367-R13641.
                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 12;
100.0%; Pred. No. 4.3e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW97439 standard; peptide; 9 AA.
                   Claim 3; Page 26; 30pp; English.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAU-) UNIV AUVERGNE.
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thrombospondin include cell adhesion-promoting activity, cell mitogenic activity, cell chenciactic activities, haemostatic activities, and activities that derive from these activities, e.g. tumour-cell, microbial or parasite metastasis activity, platelet aggregating activity, fibriolythic activity and immune modulation. The peptides are capable of inhibiting tumour metastasis. The peptides are useful in wound healing, atherosclerosis, malaria, thrombotic and thrombolytic conditions and anglogenesis, and as cell attachment promoters, complement modulators
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100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW81478 standard; peptide; 9 AA
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Best Local Similarity 100.
Matches 9; Conservative
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  activities that derive from these activities, e.g. tumour-cell, microbial or parasite meteastasis activity, platelet aggregating activity inbrinds are metages activity and immune modulation. The peptides are capable of inhibiting tumour metastasis. The peptides are useful in wound healing, atherosclerosis, malaria, thrombotic and thrombolytic conditions and anglogenesis, and as cell attachment promoters, complement modulators and diagnostic reagents.
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                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for mimicking or inhibiting thrombospondin activity - using thrombospondin peptides
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                                                                                                                                                                                                                                        Length 9;
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                                                                                                                                                                                                                                      100.0%; Score 59; DB 20;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW81491 standard; peptide; 9
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90US-0483527.
92US-0896527.
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                         Local Similarity
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1 wspcsvtcg 9
                                                                                                                                                                        9 AA;
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20-AUG-1993;
19-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1999
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Matches
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EP166410-A.
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ID AAR5:
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activities that derive from these activities, e.g. tumour-cell, microbial or parasite metastasis activity, platelet aggregating activity, fibrinolytic activity and immune modulation. The peptides are capable of inhibiting tumour metastasis. The peptides are useful in wound healing, atheroscierosis, malaria, thrombotic and thrombolytic conditions and anglogenesis, and as cell attachment promoters, complement modulators and diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetaenus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1, AMA-1; erythrocyte binding antigen-175; BBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                      Gaps
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                                                                                                                                                            Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum SSP-2 antigenic epitope, P547
                                                                                                                                                            DB 20; I
4.3e+05;
hes 0;
                                                                                                                                                            Query Match 100.0%; Score 59; DB Best Local Similarity 100.0%; Pred. No. 4.3 Matches 9; Conservative 0; Mismatches
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                               AAY70284 standard; peptide; 9 AA.
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                                                                                                                                                                                                                  1 WSPCSVTCG 9
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1 wspcsvtcg
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  of
for
                                                                                                                                                                                              Gaps
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antiparasitic activity and can used for treatment and prevention malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used detecting P. falciparum in biological samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 13; 0.013;
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                                                                                                                                               Ouery Match 100.0%; Score 59; DB 21; Best Local Similarity 100.0%; Pred. No. 4.39+05; Matches 9; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    AAP60413 standard; Protein; 13 AA.
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(USGO ) US GOVERNMENT.
(USSA ) US SEC OF THE ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sporozite; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmoium falciparum.
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Best Local Similarity
Matches 9; Conserv
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AAR51428;

31-MAR-1994

NAME OF COLOR OF STREET OF

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The sequences given in AAR51427-35 are peptide fragments derived from region II+ of the circumsporozoite (CS) protein derived from various Plasmodium species. These peptides fragments may be used as an inhibitor for the binding of CS polypeptides to receptors of hepatocytes from malaria-susceptible mammals. These peptides can be administered to malaria susceptible mammals to prevent infection, and they can be used to produce antibodies which can be used to produce antibodies which can be used to prevent infection. The peptides were tested for inhibition of CS binding to liver sections or to the human hepatocyte cell line HepG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region II+; circumsporozoite; CS; Plasmodium; inhibitor; binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide(s) corresp. to Region II+ of circumsporozoite - are used for inhibiting hepatocyte invasion by malarial sporozoites for preventing malaria infection
                                                                                                                                                                                                                 Peptide(s) corresp. to Region II+ of circumsporozoite - are used for inhibiting hepatocyte invasion by malarial sporozoites for preventing malaria infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 15; Length 18; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indels
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                                                                                                                                       Sinnis
                                                                                                                                       Nussenzweig V,
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                                                                                                                                                                                                                                                                                                    Claim 8; Page 32; 42pp; English.
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                                                         92US-0947033.
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                93WO-US08800.
                                                                                               (UYNY ) UNIV NEW YORK STATE
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                                                                                                                                       Frevert U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium knowlesi.
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Best Local Similarity
Matches 9; Conserv
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                17-SEP-1993;
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                                                                                                                                       Cerami C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                Region II+; circumsporozoite; CS; Plasmodium; inhibitor; binding; receptor; hepatocytes; malaria-susceptible; mammal; infection; antibody; liver; human hepatocyte cell line; HepG2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide(s) corresp. to Region II+ of circumsporozoite - are used for inhibiting hepatocyte invasion by malarial sporozoites for preventing malaria infection
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                                                                            Circumsporozoite protein region II+ peptide #2.
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                                                                                                                                                                                                                                                                                                                                                             92US-0947033.
                                                                                                                                                                                                                                                                                                                       93WO-US08800
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                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-118161/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium malariae.
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Best Local Similarity
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                                                                                                                                                                                                Plasmodium vivax.
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Sequence

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31-MAR-1994

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The sequences given in AAR51427-35 are peptide fragments derived from region II to of the circumsporozoite (CS) profetin derived from various plasmodium species. These peptides fragments may be used as an inhibitor for the binding of CS polypeptides to receptors of hepatocytes from malaria-susceptible mammals. These peptides can be administered to malaria susceptible mammals to prevent infection, and they can be used to produce antibodies which can be used to prevent infection. The peptides were tested for inhibition of CS binding to liver sections or to the human hepatocyte cell line HepG2.
                                                                                                                                                                                                                                                                                                                                                                                                                Region II+; circumsporozoite; CS; Plasmodium; inhibitor; binding; receptor; hepatocytes; malaria-susceptible; mammal; infection; antibody; liver; human hepatocyte cell line; HepG2.
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                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                          Circumsporozoite protein region II+ peptide #6.
                                               0; Mismatches
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                                                                                                                                                                                                                                             AAR51432 standard; peptide; 18 AA.
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     100.0%;
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Best Local Similarity 100.
Matches 9; Conservative
  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                          1 WSPCSVTCG 9
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                                        The sequences given in AAR51427-35 are peptide fragments derived from Pregion II + of the actrounsporzozie (CS) protein derived from various Plasmodium species. These peptides fragments may be used as an inhibitor for the binding of CS polypeptides to receptors of hepatocytes from malaria-susceptible mammals. These peptides can be administered to malaria susceptible mammals to prevent infection, and they can be used to produce antibodies which can be used to prevent infection. The peptides were tested for inhibition of CS binding to liver sections or to the human hepatocyte cell line Hepd2.
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                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 15; Length 18; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circumsporozoite protein region II+ peptide #5.
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          Claim 8; Page 32; 42pp; English
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
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CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                                                                            The present invention relates to a first generation recombinant adenoviral vector, part of which integrates into a host cell genome. Twinverted terminal repeats (ITRs) allow integration of a transgene into the host genome. The invention can be used to make 'gutless' vectors for gene therapy, e.g. of sickle cell anemia or thalassemia (targeting hematopoietic cells) or atherosclerosis or restenosis (targeting endothelial cells), or more generally a wide range of genetic diseases, cancers and infectious diseases.
                                                                                                                                                                                                               Recombinant adenoviral vector containing transgene, used to produce gutless vectors for gene therapy, targetable to selected cells and lacking antigenicity \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the malaria (M) string CTL epitope TRAP AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating CD8-positive \mathtt{T} cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and \mathtt{HIV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McMichael AJ;
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                                                                                                                                       Farrar D, Papayannopoulou T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 59; DB 22; 100.0%; Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Smith GL;
                                                                                                                                                                                                                                                                                            Example 2; Page 97; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY03674 standard; peptide; 20 AA.
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  01-JUN-2000; 2000WO-US15442.
                                      99US-0137213.
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Plebanski M, Schneider J,
                                                                                                                                     Shayakhmetov D,
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                                                                                                (UNIW ) UNIV WASHINGTON
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Matches 9; Conser
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                                        01-JUN-1999;
                                                        22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW59270-W59274 are fragments of malarial circumsporozoite (CS) region II isolated from Plasmodium falciparum. These fragments can be used as ligands in a method for the targeted delivery of nucleic acid to cells in culture or cells in vivo, especially where the cells are hepatocytes. Therapy of diseases such as cancer, malaria, hepatitis, cystic fibrosis, hypercholesterolaemia, phenylketonuria and haemophilia is mentioned. CS polypeptides are liver cell specific with rapid hepatic invasion. They are more efficient than the prior art asialocrosomucoid (ASOR) ligands, of which there may be an accumulation in certain diseases due to
                                                                        Malaria; gene therapy; hepatocyte; liver; circumsporozoite; ligand; targeted delivery; therapy; disease; cancer; hepatitis; cystic fibrosis; hypercholesterolaemia; phenylketonuria; haemophilia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complexes for targetted delivery of nucleic acids to hepatocytes containing Plasmodium circumsporozoite polypeptide as targetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adenoviral vector; inverted terminal repeat; ITR; gene therapy; sickle cell anemia; thalassemia; atherosclerosis; restenosis;
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                                      P. falciparum circumsporozoite region II peptide fragment.
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Pred. No. 0.017;
Mismatches 0; Indels
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100.0%; Pr
tive 0;
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27-AUG-1998
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The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The Kits of the invention comprises (i) as priming composition, a source of one or more CD8+ T-cell [Cytotoxic T lymphocytes-(CTL)] composition a source of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the composition a source of CTL epitopes, with a least one CTL epitope the composition impaired recombinant powirus vector [WV) plus a carrier. If the source of CTL epitopes in (i) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or unnours, specifically against malaria parasites such as P. falciparum, or HIV, and specifically against malaria parasites such as P. falciparum, or HIV, and also used for protective response against melanoma and cancer of breast or colon, and generally wherever a strong CD8+ response is protective. The boosting composition may be used alone to boost a naturally primed cresponse against malaria. The specified pvv provide an excellent booster effect, better than that from wild-type poxvirus, resulting in complete rather than partial protection against approxozoite challenge. Also Pvv are sets to use than wild-type virus. Sequences AAV03661-680 represent CTL.
infection, also epitope strings from Plasmodium and HIV
                                                            Claim 38; Page 19; 85pp; English.
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Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative '0; Mismatches 0; Indels

20 AA;

Sequence

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1 WSPCSVTCG 9

3 wspcsvtcg 11

Search completed: January 29, 2002, 10:21:43 Job time: 419 sec

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Sequence 11, Appl Patent No. 5171843 Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 10, Appl Sequence 8, Appl Sequence 8, Appl Sequence 8, Appl Sequence 8, Appl Sequence 9, Appl Sequence 18, Appl Sequ
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Patent No. 5200397
GENERAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: Tuszynski, George Paul
TITLE OF INVENTION: Peptide Fragments and Analogs of
TITLE OF INVENTION: Thrombospondin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. R. Grace & CO.-Conn.
                                                US-07-862-0218-16
PCT-US93-03164-16
US-08-02-18-12
US-08-313-28-12
PCT-US93-03164-12
US-08-313-28-12
PCT-US93-03164-12
US-08-313-28-10
US-08-313-28-10
US-08-488-273-8
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US-07-646-531D-9
US-07-646-531D-18
                   5171843-9
US-08-799-173A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTER READABLE FORM:

EDOMUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/646,531D

ATTONEY/AGENT INFORMATION:

NAME: APPLED, Vanessa L.

REGISTRATION NUMBER: 3323

REFERENCE/DOCKET NUMBER: 01-7896

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                5426100-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: W. R. Grace & Co.-Conn. STREET: 7379 Route 32 CITY: Columbia STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-07-646-531D-1
 1 WSPCSVTCG
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   RESULT
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Sequence 15, Appl
Sequence 16, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 34, Appli
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Sequence 5, Appli
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1.521 Million cell updates/sec
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                                                                                                                         Search time 133.18 Seconds
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Sequence 3
Sequence 3
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-646-531D-15
US-08-488-273-1
US-08-488-273-14
US-08-488-273-14
US-08-488-273-14
US-08-858-273-14
US-08-955-602A-1
US-08-955-602A-2
US-08-955-602A-2
US-08-956-659B-9
US-08-956-659B-18
US-08-956-659B-18
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3-08-313-288B-18
5-08-760-797A-1
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                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
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                                                                                                                       January 29, 2002, 10:24:03
                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                   US-09-763-397A-8
59
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Match Length
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                                                                                                                                                                                            Title:
Perfect score:
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                                                                                      OM protein
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                                                                                                                                                                                                                                                                                                                   Searched:
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105-06-488-273-1

1 Sequence 1 Application US/08488273

1 Sequence 1 Application US/08488273

1 Sequence 1 Application US/08488273

2 Sequence 1 Application US/08488273

2 SEPTICANT: Tuszynski, George P. ApplicANT: Tuszynski, George P. TITLE OF INVENTION: THROMOSPONDIN NUMBER OF SEQUENCES: 15

2 CONTRESSEE: PARTITCH SCHWARZE JACOBS & NADEL, P.C. STREET: Philadelphia STREET: 1501 Market Street, 36th Floor CITY: Philadelphia STREET: DCOUNTRY: USA STREET: PC-DOS/MS-DOS SOFTWARE: Pennsylvania COUNTRY: USA STREET: PC-DOS/MS-DOS SOFTWARE: PLORATION DATA: PC-DOS/MS-DOS SOFTWARE: PLING DATE: 19-DEC-1994

2 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/896,527

3 PRIOR APPLICATION NUMBER: US 07/896,527

3 PRIOR APPLICATION NUMBER: US 07/896,527

3 PRIOR APPLICATION NUMBER: US 07/896,527

4 PRIOR APPLICATION NUMBER: US 07/896,527

5 FILING DATE: 20-AGG-1993

5 PRIOR APPLICATION NUMBER: US 07/896,527

5 FILING DATE: 20-AGG-1993

5 PRIOR APPLICATION NUMBER: US 07/896,527

5 FILING DATE: 19-DEC-1994

5 FILING DATE: 19-DEC-1994

5 FILING DATE: 20-AGG-1993

5 PRIOR APPLICATION NUMBER: US 07/896,527

5 FILING DATE: 19-DEC-1994

5 FILING DATE: 19-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0;
                                                       CURRENT AFFLLTAION DAYS
PULICATION NUMBER: US/07/646,531D
FILING DATE: 19910131
ATTORNEY/GENY INFORMATION:
NAME: AAPPLEDY, Vanessa L.
REGISTATION NUMBER: 01-7896
FELECHORE (301) 531-4515
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: PEPLICE
CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: PEPLICE
CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: AMINO ACID
   SOFTWARE: Word Perfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WSPCSVTCG 9
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COTHER INFORMATION: formyl-tryptophan and the glycine at position 9 is carboxyami
US-07-646-531D-15
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Sequence 16, Application US/07646531D

Patent No. 5200397

GENERAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: TUSZYDSKI, George Paul
TITLE OF INVEWTION: Thrombospondin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Grace & Co.-Con.
STREET: 7379 Route 32
CITY: Columbia
STATE: Maryland
COMPTRY: USA

ZIP: ZJONTRY: USA
ZIP: ELOPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: ELOPPY disk
COMPUTER: IBM PC COMPALIALE
COMPUTER: STEM: PC-DOS/MS-DOS
US-07-646-531D-15

Sequence 15, Application US/07646531D
Patent No. 5201037
GENERAL INFORMATION:
APPLICANT: Deutch, Alan Howard
APPLICANT: Tuszynski, George Paul
TITLE OF INVENTION: Thrombospondin
TITLE OF INVENTION: Thrombospondin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. R. Grace & CO.-Conn.
STREET: 7379 Foute 32
CITY: Columbia
STREET: USA
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 59; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.0
CURRENT APPLICATION NOWER:
FILING DATE: 19910131
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Appleby, Vanessa L.
REGISTRATION NUMBER: 3327386
REFERENCE/DOCKET NUMBER: 01-7896
TELECOMMUNICATION INORMATION:
TELEPHONE: (301) 531-4515
INPORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear MOLECULE TYPE: peptide FERTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WSPCSVTCG 9
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us-09-763-397a-8.rai

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10.5-08-408-273-14

1 Sequence 14, Application US/08488273

2 Sequence 17. Application US/08488273

3 Patent No. 549652

5 GENERAL INFORMATION:

APPLICANT: Deatch, Alan H.

CONTRY: USA

CONTRY: DEATCH NOWBER: USA

CLASSIETCATION NOWBER: USA

FILING DATE: 19-DEC-1994

PRIOR APPLICATION NOWBER: USA

PRIOR APPLICATION NOWBER: USA

PRIOR APPLICATION NOWBER: USA

PRIOR APPLICATION NOWBER: USA

FILING DATE: 19-DEC-1994

PRIOR APPLICATION NOWBER: USA

ATOMER'S LEARY NOWBER: USA

PRIOR APPLICATION NOWBER: USA

TELECOMMUNICATION NOWBER: USA

TELECOMMUNICATION
                                                                                                                                            the tryptophan at position 1 is n-formyl-tryptophan."
                                                                                                                                                                                                                                              the glycine at position 9 is carboxyamide."
                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                  MAME/KEY: Peptide
COCATION: 9
COCATION: 9
OTHER INFORMATION:
COTHER INFORMATION:
US-08-488-273-13
                                                                                                                      LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                    NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WSPCSVTCG 9
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                 STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELERA: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRNEENENENESTES:
STRNDENESTES:
                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-488-273-1
                                                                                                                                                                                                                                                                                                                                                                         1 WSPCSVTCG 9
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US-08-488-273-13
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Ouery Match 100.0%; Score 59; DB 6; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6+65; Matches 9; Conservative 0; Mismatches 0; Indels Matches
RESULT 8
5426100

PATENT NO. 5426100

PATENT NO. 5426100

TITLE OF INVENTION: PIPTIDE FRACMENTS AND ANALOGS OF

TITLE OF INVENTION: PIPTIDE FRACMENTS AND ANALOGS OF

TITLE OF INVENTION DATA:

CURRENT APPLICATION NOWBER: US/08/110,146

FILING DATE: 20-ADC-1993

PRICK APPLICATION NOWBER: 896,527

FILING DATE: 09-ADV-1992

APPLICATION NUMBER: 483,527

FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 59;
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REPERREMCE/COCKET NUMBER: UTSC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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; LENGTH: 9
5426100-1
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US-08-395-602A-1
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(Sequence 1, Application US/08858971

) Sequence 1, Application US/08858971

) Patent No. 5886142

(GENERAL INFORMATION:

) TITLE OF INFORMATION:

NUMBER OF SEQUENCES:

ADDRESSEE: Jane Massey Licata, Esq.

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

CONVENTED NOT THE CONTROL OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 59; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 0; Indels Maches 0; Indels
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ZIP: 08002

COUNTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IEM 486 WINDOWS FOR WORKGROUPS
SOFTWATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWATS: WORDERERET 5.1
CURRENT APPLICATION DATA:
FILING DATE: herewith
CLASSIFICATION WINDER: US/08/858,971
FILING DATE: herewith
FILING DATE: TO FOR SEQ ID NO: 1:
FILING DATE: HEREWITH
FILING D
                                                                                                                                                                                                                                                                                                                      the glycine at position 9 is carboxyamide glycine."
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Best Local Similarity 100.
Matches 9; Conservative
        LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                , NAME/KEY: Peptide LOCATION: 9 OTHER INFORMATION: t , OTHER INFORMATION: 1 US-08-488-273-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-858-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WSPCSVTCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WSPCSVTCG 9
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DB 1; Length 18;

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Gaps
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100.0%; Score 59; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kuo, M. Tien
APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,602A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UTSC:410/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/021,625D
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: United States of America 21P: 77210
                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-021-625D-2; Sequence 2, Application US/08021625D; Patent No. 5976851; GENERAL INFORMATION:
                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATORNEY-AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFRENCE/POCKET NUMBER: UTSC:
TELECHOME: (512) 418-3000
TELERA: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-395-602A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (/15,
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                    Houston
                                            Texas
                                                          COUNTRY: Un
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                                                                                                                                                                                                               Sequence 1. Application US/08021625D
Fatent No. 5976851
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 2; Length 18; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. Application US/08395602A
Sequence 2. Application US/08395602A
Batent No. 5766899
GENERAL INFORMATION:
APPLICANT: Nuo, M. Tien
APPLICANT: Ding, Zhi-Ming
TITLE OF INVENTION: Targeted Nucleic Acid Delivery into
TITLE OF INVENTION: Liver Cells
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
Pred. No. 0.01; 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/021,625D
FILING DATE: 16-FEB-1993
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100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10.12.
CLASSIEGATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
RECISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
RELECOMMUNICATION INFORMATION:
TELEFAX: (713) 789-2679
TELEFAX: (713) 789-2679
TELEFX: 79-0924
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                  Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
US-08-021-625D-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 WSPCSVTCG 10
                                                                                                  2 WSPCSVTCG 10
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                                                                           1 WSPCSVTCG 9
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                                                                                                                                                                              RESULT 10
US-08-021-625D-1
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US-08-986-659B-33
; Sequence 33, Application US/08986659B
; Petent No. 6171591
; GENERAL INFORMATION:
; APPLICANT: Hall, Stephen G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TURBER OF ENVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6171591th Wacker Drive, 36th Floor
; CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DAPA:
FILING DATE: 08-D08C-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/386,659B
FILING TATA:
PRIGN APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION ...

FILING DAME:
ATTORNEY/AGENT INFORMATION:
NAME: TAILVALDIS CEPUTILIS
REGISTRATION NUMBER: 20,818
REFERENCE/DOCKET NUMBER: 20,818
REFERENCE/TOOKKET NUMBER: 2549.0
TELECHOMICLATION INFORMATION:
TELECHOMICLATION INFORMATION:
TELECHOME: 312-580-1189
INFORMATION FOR SEC ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGALIC ...
LENGALIC ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: peptide US-08-986-6598-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 WSPCSVTCG 10
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                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chi
STATE: IL
COUNTRY:
ZIP: 6060
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                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 59; DB 2; Length 23; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
CITY: Chicago
STATE: 11
COUNTY: USA
COMPUTEY: USA
COMPUTEY: THE FLORM:
MEDIUM TYPE: Florpy disk
COMPUTEY: THE FLORM:
MEDIUM TYPE: PREABLE FORM:
MEDIUM TYPE: PREABLE FORM:
MEDIUM TYPE: PROPEY disk
COMPUTEY: THE FLORE COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
CHREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,659B
FILING DATE: 08-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/986,659B
FILING DATE: MEDICATION DATA:
APPLICATION NUMBER: US/08/986,659B
FILING DATE: MEDICATION DATA:
APPLICATION NUMBER: US/08/986,659B
FILING DATE: MEDICATION DATA:
APPLICATION NUMBER: US/08/986,659B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Olson & Hierl, 1rd.
STREET: 20 No. 6171591th Wacker Drive, 36th Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08986659B
Patent No. 6171591
GENERAL INFORMATION:
APPLICANT: Hall, Stephen G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Talivaldis Cepuritis
REGISTRATION NUMBER: 20,818
REFERENCE/DOCKET NUMBER: 569.
TELECOMMUNICATION INFORMATION:
TELEFRAN: 312-580-1180
TELEFRAN: 312-580-1180
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 aming acids
             , INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
'GOROLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-986-6598-9
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US-08-986-659B-9
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0
Query Match 100.0%; Score 59; DB 4; Length 23; Best Local Similarity 100.0%; Prod. No. 0.013; Matches 9; Conservative 0; Mismatches 0; Indels Matches 9.
                                                                                                         STATE: IL.
COUNTRY: USA
ITP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
```

RESULT 14

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SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/986,659B
FILING DAFE: 08-DEC-1997
CLASSIFICATION: 424
PROR APPLICATION NUMBER: 20,818
REJENSATION NUMBER: 20,818
REFERENCE/DOCKET NUMBER: 549.0
FELENOMUNICATION INFORMATION:
RECOMMUNICATION INFORMATION:
FELENOMUS TELEPAX: 312-580-1180
FELENOMUS CHARACTERISTICS:
FELENOMUS CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FELENOMUS CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FELENOMUS CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FERENCH OF SEQ ID NO: 34:
STRANDEDNESS: N/A
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-986-659B-34

QUERTY MATCh
BOST LOCAL SIMILATITY 100.0%; Pred: NO: 0.017;
MATCHES 9; CORSETVALIVE 0; MISMATCHES 0; Indels 0; Gaps 0;
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Search completed: January 29, 2002, 10:24:03 Job time: 509 sec

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14.5
Compugen Ltd.
   GenCore version
Copyright (c) 1993 - 2000
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 protein search, using sw model OM protein

(without alignments)
4.729 Million cell updates/sec January 29, 2002, 10:26:36; Search time 144.96 Seconds Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-763-397A-8 59 1 WSPCSVTCG 9 Perfect score: Sequence: Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	circumsporozoite p			circumsporozoite p			circumsporozoite p		circumsporozoite p	circumsporozoite p	circumsporozoite p	circumsporozoite p	thrombospondin-rel	sporozoite surface	hypothetical prote	circumsporozoite p	circumsporozoite p					circumsporozoite p	circumsporozoite p		hypothetical prote	F-spondin - rat	E.		
SUMMARIES	ID	OZZOAB	OZZQAL	A39756	OZZOAS	OZZÕAC	S05428	OZZQAF	OZZQAM	A54533	A54504	A54529	A60610	S04531	A46283	T21371	A29319	OZZOKU	OZZQAK	A32068	OZZQAV	A48571	D41156	C41156	A41156	T34212	A38152	JC5928	T18856	T00017
	DB	-	-	7	Н	Н	7	Н		7	~	~	7	~	7	N	~	٦	-	7	٦	7	~	~	~	~	~	~	7	7
	Length	378	378	388	398	401	405	412	419	424	~	442	485	559	574	2165	343	351	363	367	378	386.	387	387	395	802	807	1074	1444	951
d	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.9	94.9	94.9	94.9			94.9	94.9	ಶ	e.	93.2	٠	٠	89.8
	Score	59	59	59	59	59	59	59	29	59	29	29	29	59	59	59	26	26	26	26	56	26	26	26	26	55	55	52	52	53
	Result No.	-	7	٣	4	S	9	7	Ф	თ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

hypothetical prote	circumsporozoite p	circumsporozoite p	F-spondin precurso	hypothetical prote	hypothetical prote	hypothetical prote	thrombospondin 1 p	thrombospondin 1 p	thrombospondin 2 p	thrombospondin 2 p	thrombospondin pre	procollagen N-endo	brain-specific and	properdin precurso	properdin - mouse	
T34395	A44969	OZZOMY	A47723	T16892	T14764	T00326	TSHUP1	A40558	TSHUP2	A42587	A39804	T18517	T00028	S29126	S05478	
7	7	-	7	~	7	~	Н	7	ч	7	-	7	7	Н	7	
2167	264	367	803	860	868	984	1170	1170	1172	1172	1178	1205	1522	469	437	,
88.1	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	84.7	83.1	
52	21	21	51	51	51	51	51	51	51	51	51	51	51	20	49	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Circumsporozoite protein precursor - Plasmodium cynomolgi (strain Berok)
N.Alternate names: major sporozoite surface antigen
C.Species: Plasmodium cynomolgi
C.Species: 10.5ep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C.Accession: D26255
R.Salinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Ene
R.Salinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Ene
R.Stile: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878
A;Reference number: A90889; MUID:87102878
A;Recossion: D26255
A;Molecule type: DNA
A;Residues: 1-378 cGAL>
C;Comment: There are three distinct regions in the mature circumsporozoite protein, thoolic membrane-anchoring sequence.
C;Comment: There are 10 tandem copies of a 9-residue repeat
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: sporozoite; surface antigen; tandem repeat
E;1-19/Domain: signal sequence #status predicted <SIG>
F;20-3784/Region: 9-residue repeats
F;303-356/Domain: thrombospondin type 1 repeat homology <THRI>

Gaps Query Match 100.0%; Score 59; DB 1; Length 378; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 9; Conservative 0; Mismatches 0; Indels

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313 WSPCSVTCG 321 1 WSPCSVTCG 9 ò g

Circumsporozoite protein precursor - Plasmodium cynomolgi (strain London)
N;Alternate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Dectes: Plasmodium cynomolgi
C;Accession: A26555
R;Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Ene
Cell 48, 311-319, 1987
A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878

A; Molecule type: DNA A; Residues: 1-378 <GAL>
C; Comment: There are three distinct regions in the mature circumsporozoite protein, t obic membrane-anchoring sequence.
C; Comment: There are 19 tandem copies of a 6-residue repeat and 6 copies of an 11-res

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RESULT 5

ORZOAC
CITCUMSportozoite protein precursor - Plasmodium cynomolgi (strain Gombak)

(Species: Plasmodium cynomolgi
C:Species: Plasmodium cynomolgi
C:Accession: E2625
C:Accession: E2625
A:Title: The Circumsporcozoite gene of the Plasmodium cynomolgi complex.
A:Title: The Circumsporcozoite gene of the Plasmodium cynomolgi complex.
A:Reference number: A30889; MUID:87102678
A:Reference 
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CiSpecies; Plasmodium falciparum
C;Species: Species: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
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100.0%; Score 59; DB 1; Length 401;
Best Local Sinitarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels
            Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           333 WSPCSVTCG 341
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                                                                                                                                                   1 WSPCSVTCG 9
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NiAternate names: major sporozoite surface antigen
Ci Species: Plasmodium cynomolgi
Ci Species: Plasmodium cynomolgi
Ci Species: Plasmodium cynomolgi
Ci Species: Plasmodium cynomolgi
Ci Species: Jo-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
Ci Accession: C26225
Ridalinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea, A.Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A:Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A:Reterence number: A90889; MUDD:87102878
A:Anchecula: type: Dax
A:Residues: 1-398 cGAL>
C:Comment: There are three distinct regions in the mature circumsporozoite protein, the object membrane anchoring sequence.
C:Comment: There are 16 tandem copies of a 9-residue repeat and 3 copies of a 17-residue C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C:Reywords: sporozoite; surface antigen; tandem repeats
F:197comain: signal sequence #status predicted <SIGS
F:20-398/Product: circumsporozoite protein #status predicted <AMT>
F:20-398/Product: circumsporozoite protein #status predicted <AMT>
C:Comment: The copies of a presidue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ticumsporozoite protein - Plasmodium reichenowi
Specias: Plasmodium reichenowi
Joate: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
Accession: A39756
- Biol. Chem. 266. 6666-6689, 1991
- Biol. Chem. 266. 6666-6689, 1991
- Reference number: A39756; MUID:91201303
- Accession: A39756; MUID:91201303
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C.Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology C.Reywords: sporozoite; surface antigen; tandem repeat F.1-19/Domain: signal sequence #status predicted <SIG> F.20-378/Product: circumsporozoite protein #status predicted <AMAT> F.30-3178/Product: circumsporozoite protein #status predicted <AMAT> F.22-217/Region: 6-residue repeats F.32-277/Region: 11-residue repeats F.303-356/Domain: thrombospondin type 1 repeat homology <THRI>
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A.RATROSIGUES: 1-188 GLALA.
A.GTROSIGUES: 1-188 GLALA.
A.GTROSIGUES: 1-188 GLALA.
C.SADEGIAMIN: CALCAMINESPORTOSIGN: TAIRCAMARDSOGNIG TYPE 1 repeat homology F: 312-366, Domain: thrombospordin type 1 repeat homology CHRI>
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100.0%; Score 59; DB 2; Length 388; Best Local Similarity 100.0%; Pred. No. 0.037; Matches 9; Conservative 0; Mismatches 0; Indels Matches
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circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)
C;Species: Plasmodium malariae
C;Date: 06-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
C;Accession: A54504
R;Lal, A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; McCutcha Mol. Blochem. Parasitol. 30, 291-294, 1988
A;Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Reference number: A54504; MUID:89040027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome) (Species: Plasmodium falciparum (Cipaciparum Cipacies: Plasmodium falciparum Cipacies: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 Cipacession: A54529 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 Cipacession: A54529 #s.T.

#Not Notice Construction: A1. Schwarz, N.T.

#Not Notice Construction in the circumsporozoite protein gene of Plasmodium falcipar A; Feference number: A54229; MUID:87115616 #s.Accession: A54529 #s.Accession: A54
                                                                                                                                                                                                                                                                                                                  Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain T4, Tha Cispecies: Plasmodium falciparum
Cispecies: Plasmodium falciparum
Cispecies: 28-Ocr-1994 #sequence_revision 28-Ocr-1994 #text_change 09-Jun-2000
CiAccession: A54533
Mol. Blochem. Parasitol. 24, 289-294, 1987
A;Title: Circumsporozoite gene of a plasmodium falciparum strain from Thailand. A;Reference number: A54533; MUID:B7315205
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 obEL>
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A; Residues: 1-429 <LAL>
A; Cross-references: 68:J03992; NID:g160220; PIDN:AAA29557.1; PID:g160221
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C; Keywords: tandem repeat
F; 354-407/Domain: thrombospondin type 1 repeat homology <THRI>
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C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F; 348-402/Domain: thrombospondin type 1 repeat homology <THR1>
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100.0%; Score 59; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels
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has 0; Indels
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100.0%; Pred. No. 0.04;
tive 0; Mismatches 0; Indels
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354 WSPCSVTCG 362
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364 WSPCSVTCG 372
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                1 WSPCSVTCG
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OZZOAM

Circumsporozoite protein precursor - Plasmodium cynomolgi (strain Mulligan/NIH)

N.Alternate names: major sporozoite surface antigen

C.Species: Plasmodium cynomolgi

C.Species: Bozoita in 20.2625

R.Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea, Cell 48, 311-319, 1987

A.Fitle: The circumsporozoite gene of the Plasmodium cynomolgi complex.

A.Accession: Bozois

C.Superfamily: Circumsporozoite protein; Actures

F.119/Pomaln: signal sequence #status predicted <AMT>
F.30-419/Pomaln: thrombospondin type I repeat homology <ATHRI>

F.344-397/Domain: thrombospondin type I repeat homology <ATHRI>

A.Accession of the Accession of the Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Species: Plasmodium falciparum falciparum) (isolate IMTM22)
Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22)
CiSpecies: Plasmodium falciparum
CiSpecies: Saissey, 1804
Recession: A03384
R.Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W.T.
Science 225, 535-559, 1984
A.Title: Structure of the gene encoding the immunodominant surface antigen on the sporoz
A.Reference number: A03388; MUD:84250215
A.Molecule type: DNA
A.Residues: 1-412 cDAM>
A.Tossion: Antigen on the sporoz
A.Tossion: Antigen on the sporoz
A.Tossion: A.Tossion on the sporoz
C.Comment: Residues 1-16 are the probable signal sequence.
C.Comment: Residues 1-16 are the probable signal sequence.
C.Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the C.Superfamily: circumsporozoite protein; thrombospondin type I repeat homology CTHR1>
F.336-390/Domain: thrombospondin type I repeat homology CTHR1>
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A;Residues: 319-336,354-373 cLOC> C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology F;329\cdot383/{\rm Domain}: thrombospondin type 1 repeat homology 
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                            Length 405;
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                                                                                                                                                                                                                                       ; Score 59; DB 2;
; Pred. No. 0.039;
0; Mismatches 0
                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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Best Local Similarity 100.8
Matches 9; Conservative
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4

F;240-287/Domain: thrombospondin type 1 repeat homology <THR1>

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Sporocoite surface protein 2 - malaria parasite (Plasmodium falciparum) (strain NF54) N.Alternate names: thrombospondin-related anonymous protein (TRAP) (Species: Plasmodium falciparum (Species: Plasmodium falciparum) (Species: Plasmodium falciparum) (Species: Plasmodium falciparum) R.; Rogers, M.O.; Mallk, A.; Mellouk, S.; Nakamura, K.; Rogers, M.D.; Szarfman, A.; Gor A.Title: Characterization of Plasmodium falciparum sporozoite surface protein 2. A.; Reference number: A46283; MUID:93028427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1,
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A; Reference number: 219949
A; Recession: T24896
A; Accession: T24896
A; Status: pre-liminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2165 < WI2>
A; Residues: 1-2165 < WI2>
A; Cross-references: EMBL: 269361; PIDN: CAA93288.1; GSPDB: GN00022; CESP: F25H8.3
A; Experimental source: clone T13H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Aclecule type: DNA
A;Residues: 1-2165 GMIL>
A;Residues: EMBL:269360; PIDN:CAA93287.1; GSPDB:GN00022; CESP:F25HB.3
A;Cross.references: EMBL:269360; PIDN:CAA93287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA A;Residues: 1-574 <ROG> A;Residues: 1-574 <ROG> A;Cross-references: GB:WA4013; NID:g160690; PID:g160691 C;Superfamily: thrombospondin type 1 repeat homology F;240-287/Domain: thrombospondin type 1 repeat homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F25H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T21371; T24896
R;Gājādsty, S.
Ssubmitted to the EMBL Data Library, February 1996
A;Reference number: Z19413
A;Accession: T21371
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                                                                                                100.0%; Score 59; DB 2.
ilarity 100.0%; Pred. No. 0.05;
Conservative 0; Mismatches
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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250 WSPCSVTCG 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Circumsporozoite protein precursor - Plasmodium brasilianum
Cispecies: Plasmodium brasilianum
Rid Glovanni, Lu.; Cochrane, A.H.; Enea, V.
Exp. parasitol. 70 373-381, 1990
A;Title: On the evolutionary history of the circumsporozoite protein in plasmodia.
A;Recession: A60610
A;Status: not compared with conceptual translation
A;Residues: 1485 cDIA
A;Residues: 1485 cDIA
A;Residues: 1485 cDIA
A;Residues: 1485 cDIA
A;Residues: 33-485-5498, 1988
A;Title: Circumsporozoite protein gene from Plasmodium brasilianum. Animal reservoirs fc
A;Residues: 33-485-5403
A;Residues: 33-485-5403
A;Residues: 33-485-5403
A;Residues: 393-485 cLAL
A;Cross-references: GB:303203; NID:g160212; PIDN:AAA29553.1; PID:g160213
C;Superfamily: circumsporozoite protein; tandem repeat
C;Reywords: sporozoite; surface antigen; tandem repeat
C;Reywords: sporozoite; surface antigen; tandem repeat
C;Reywords: sporozoite; surface antigen; tandem repeat
C;Cromain: signal sequence #status predicted cSIC>
F;11-485/Freduct: circumsporozoite protein; #status predicted cMAT>
F;114-369/Region: 4-residue repeats
F;114-369/Region: 4-residue repeats
F;114-463/Domain: thrombospondin type 1 repeat homology <TRRI>
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N.Alternate names: thrombospondin-related anonymous protein
C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Date: 07-Sep-1990 #text_change 09-Jun-2000
C.Accession: S04531
R.Robson, K.J.H.; Hall, J.R.S.; Jennings, M.W.; Harris, T.J.R.; Marsh, K.; Newbold, C.I.
Nature 335, 79-82, 1988
A.Fitle: A highly conserved amino-acid sequence in thrombospondin, properdin and in prot
A.Recence number: S04531; MUID:88318952
A.Rocession: S04531, MUID:88318952
A.Rocession: S04531
A.Rocession: S04531; MID:99977; PID:99978
A.Rocession: S04531; MID:99977; PID:99978
C.Superfamily: thrombospondin type 1 repeat homology
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                                                             A;Cross-references: GB:M15505; NID:q160214; PIDN:AAA29554.1; PID:q160215
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Reywords: tandem repeat
F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>
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                                                                                                                                                                                                                                                                                Length 442;
                                                                                                                                                                                                                                                                         Score 59; DB 2; Length 44; Pred. No. 0.041; 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;

Matches 9; Conservative 0;
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A; Molecule type: DNA
A; Residues: 1-442 <LOC>
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0; Mismatches 0; Indels 0; Gaps		
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0,		2002,
Matches 9; Conservative	1 WSPCSVTCG 9 304 WSPCSVTCG 1312	Search completed: January 29, 2002, 10:26:37 Job time: 648 sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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59
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution. SwissProt_39:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•	cri	P08672 plasmodium	4								_			a	P02894 plasmodium	P08675 plasmodium		Q03110 plasmodium		m	rattus n	l homo sa	062217 mus musculu	O9wuq1 rattus norv	P97857 mus musculu	Q9p2n4 homo sapien	P06914 plasmodium	P35447 xenopus lae	P98167 bos taurus	Q28178 bos taurus	5 homo	I mus m	095116 bos taurus	ношо
SUMMARIES	ID	S	CSP_PLARE	CSP_PLABR	CSP_PLAFO	CSP_PLACC	CSP_PLAFA	CSP_PLACM	CSP_PLAFT	CSP_PLAMA	CSP_PLAFW	TRAP_PLAFA	CSP_PLAVS	CSP_PLAKU	CSP_PLAKH	CSP_PLACL	CSP_PLAVB	CSP_PLASI	CSP_PLACG	TSP1_XENLA	FSPO_RAT	SM5A_HUMAN	SM5A_MOUSE	ATS1_RAT	ATS1_MOUSE	ATS9_HUMAN	CSP_PLAYO	FSPO_XENLA	SSPO_BOVIN	TSP1_BOVIN	TSP1_HUMAN	SP1	TSP2_BOVIN	TSP2_HUMAN
	Length DB	378							424 1													1074 1												1172 1
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	Score	59	59	59	59	59	59	59	99	29	59	0,1	56	26	36	56	26	26	26	9	52	S	CC.	50	50	70	7.	7	51	51	51	51	51	51
	Result No.	П	~	m	4	ın.	9	7	œ (10	1.		13	14	15	16	17	18	91.	20	21	77	23	47	57	97	/7	87	5.5	30	31	32	33

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511 511 521 531 544 648 648	PLIGNMENTS CLT CSP_PACE CSP_PACE STANDARD; DHT; 378 AA. 01-JAN-1988 (Rel. 06, Last sequence update) 01-JAN-1988 (Rel. 06, Last sequence update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS). Plasmaddium cynomolgi (strain Berck). CARCATOLE Alveolata; Apicomplexa; Haemospori MCBI_TAXID=5828; [1] SECUENCE FROM N.A. MEDLINE=87102878; Pubmed=3802196; Galinski M.R., Arnot D.E., Cochrane A.H., Bar "The circumsporozoite gene of the Plasmodium cell 48:311-319(1987). PROMENE RRE ARE 10 TANDEM COPIES OF A SI BY A 6-RESIDUE INCOMPLETE REPEAT) AND 3T RESIDUE REPEAT (FOLLOWED BY 3 SHORTER, IN- FRESIDUE REPEAT (FOLLOWED BY 3 SHORTER, IN- FRESIDUE REPEAT (FOLLOWED BY 3 SHORTER, IN- NENSINGER ANTIGEN ON THE SPORGZOITE (THE IN- MISCELLANEOUS: THE CIRCUMSPORGZOITE (THE IN- WERTERRATE HOST).	monthies requires a license agreement (or send an email to license@isb-sib.ch) EMBL, M5104; AAA29532.1; PIR, D26255; OZZQAB. InterPro; IPR000884; TSP1. PERMY: PR00090; tsp_1; 1. PRINTS; PR01303; CRCMSPRZOITE. SMART; SW00209; TSP1; 1. MALATIA; SP00209; TSP1; 1. MALATIA; SW00209; TSP1; 1. SMART; SW00209; TSP1; 1. MALATIA; SW00209; TSP1; 1. SMART; SW00209; TSP1; 1. MALATIA; SW00209; TSP1; 1. SMART; SW00209; TSP1; 1. MALATIA; SW00209; TSP1; 1. REPEAT 20 378 CIRCUMSPORD DOMAIN 97 192 A0 3 x 16 AA 7 REPEAT 252 260 REPEAT 261 268 SEQUENCE 378 AA; 36286 MW; 779BA08IC
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between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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CIRCUMSPOROZOITE PROTEIN.
62 X 4 AA TANDEM REPEATS OF N-A-N-P.
CO31EEFBE2235604 CRC64;
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                                                                                                                                                                                                                                                                                                                                                     Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91201303; PubMed-2016283;
Lal A.A., Goldman I.F.;
"Circumsporozoite protein gene from Plasmodium reichenowi, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 59; DB 1; Length 388; Best Local Similarity 100.0%; Pred. No. 0.0092; Matches 9; Conservative 0; Mismatches 0; Indels
100.0%; Score 59; DB 1; Length 378; 100.0%; Pred. No. 0.009;
                                          Indels
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0
                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
00-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 AA.
                                                                                                                                                                                                                               388 AA.
                                        0; Mismatches
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InterPro; IPR003067; Cromsprzoite.
InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01303; CRCMSPRZOITE. SMART; SM00209; TSP1; 1.
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                                        Conservative
                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATE HOST)
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Query Match
Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
                                                                                                                        313 WSPCSVTCG 321
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ID CSP_P
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DT 01-JA
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MISCELLANBOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate vaccine antigen.";
Nucleic Acids Res. 17:5854-5854(1989).
                                                                                                                                                                                                                                              MEDLINE-88186854; Pubmed-3128542;
Lal A.A., la Cruz V.F., Collins W.E., Campbell G.H., Procell P.M.,
McCutchan T.F.;
                                                                                                                                                                                                                                                                                                                                                            "Circumsporozoite protein gene from Plasmodium brasilianum. Animal
                                                                                                                                                                                                                                                                                                                                                                                          reservoirs for human malaria parasites?";
J. Biol. Chem. 263:5495-5498(1988).
-!- FUNCTION: THE CIRCUMSPORZOITE PROTEIN IS THE IMMUNODOMINANT
SUBFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
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                                                                                                                              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 59; DB 1; Lengtn 35. 100.0%; Pred. No. 0.0093; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANDEM REPEATS OF G-N-A-A.
B32944419BC600AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSP_PLAFO STANDARD; PRT; 397 AA. P19597; 025798; 01-FEB-1991 (Rel. 17, Created) 30-MAY-2000 (Rel. 39, Last sequence update) CAUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
01-JAN-1990 (Rel. 13, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate NF54)
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HSSP; P04002; 1WFA.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50092; TSP1; 1
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                               Plasmodium brasilianum.
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us-09-763-397a-8.rsp

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SEQUENCE FROM N.A.
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P02893;
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                                                                                                                                       -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
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43 X 4 AA TANDEM REPEKTS OF N-A-N-P.
A -> ANPNANPNA (IN REF. 4).
9E81146F59EBGERA GRO64;
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                                                Davis J.R., Cortese J.F., Herrington D.A., Murphy J.R., Clyde I
Thomas A.W., Bagar S., Cochran M.A., Thanassi J., Levine M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROXOITE PROTEIN PRECURSOR (CS).
Plasamodium cynomolgi (strain Ceylon).
EUKALYOCE: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=5829;
                                                                   Hackett C.S.;
"Plasmodium falciparum: in vitro characterization and human infectivity of a cloned line ";
Exp. Parasitol. 74:159-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 59; DB 1; Length 397; 100.0%; Pred. No. 0.0093; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
        Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
                                                                                                                                                                                                                                                                                                                                                         EMBL; X15363; CAA33421.1; -.
EMBL; M32892; AAA29521.1; -.
EMBL; M22982; AAA29527.1; -.
PIR; S05428; S05428.
PIR; A45527; A45527.
InterPro; IPR003067; Cromsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                     SEQUENCE FROM N.A. MEDLINE-89364998; PubMed-2671723;
                           SEQUENCE FROM N.A.
MEDLINE-92155298; Pubmed-1346766;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42646 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00090; tsp_1;
PRINTS; PR01303; CRCMS
                                                                                                                                                                                                                VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 WSPCSVTCG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WSPCSVTCG 9
Campbell J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSP_PLACC
P08673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIRCUMSPOROZOITE PROTEIN.
17 x 9 AA TANDEM REPEATS OF A-G-N-N-A-A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                       -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                       "The circumsporozoite gene of the Plasmodium cynomolgi complex."; Cell 48:311-319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 1; Length 398; 100.0%; Pred. No. 0.0094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; Core Pred. No. 0.0094; Indels
MEDLINE-87102878; PubMed-3802196;
Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzweig R.S., Enea V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6DFA2E8A62ED05BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M15103; AAA29533.1; -.
PIR; C26255; 0220AS.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-84250215; PubMed-6204383;
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SMART; SM00209; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000884; TS
Pfam; PF00090; tsp_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398
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Best Local Similarity
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SMAKK; SMULZUS, 1011, 1.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL 20 419 CIRCUMSPOROZOITE PROTEIN.
CHAIN 20 419 CIRCUMSPOROZOITE PROTEIN.
NAMATN 99 314 54 X 4 AA TANDEM REPEARS OF N-A-[DG]-G.
InterPro; IPR000884; TSP1.
Pfam; PF00009; tsp_1; 1.
PRINTS; PR01303; CRCMSPR20ITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity
Matches 9; Conserv
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DOMAIN
SEQUENCE
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

GAIGASH PUBMEd-3802196;

GAIGASH N.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,

Nussenzweig R.S., Enea V.;

Nussenzweig R.S., Enea V.;

Cell 48:311-319(1987).

-!- MISCELLANEOUS THE CIRCUMSPORCZOITE PROTEIN IS THE IMMUNDOMINANT

SURFACE ANTIGEN ON THE SPORGZOITE (THE INFECTIVE STAGE OF THE

MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRARE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
         THE REPEAT SEQUENCES
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01-JAN 1988 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 37, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Elasmodium cynomolgi (Strain Mulligan/MIH).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 59; DB 1; Length 412; Best Local Similarity 100.0%; Pred. No. 0.0096; Matches 9; Conservative 0; Mismatches 0; Indels
         ANCHORING THE PROTEIN TO THE CELL MEMBRANE. TY WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMICARITY: CONTAINS I TSP TYPE-I DOMAIN.
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BIR; A03388; OZZOAF.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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InterPro; IPR003067; Crcmsprzoite.
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P08676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **MEDILINE-97312505; Pubmed-3306373; ***MEDILINE-97312505; Pubmed-3306373; ***MEDILINE-97312505; Pubmed-3306373; ***MEDILINE-97312505; Pubmed-9731050; Paliand...; Paliand...;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRÓBABLE.
CRUMASPOROZOITE PROTEIN.
45 X 4 AA TANDEM REPRETS OF N-A-N-E.
710AB14238786CD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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01-JAN-1990 (Rel. 13, Last annotation update)
20-AUG-2011 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PREDUKSOR (CS).
ELMRATYOTA: Alveolata: Apicomplexa; Haemosporida: Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 1; Length 424; Conservative 0; Mismatches 0; Indels Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                              100.0%; Score 59; DB 1; Length 419; 100.0%; Pred. No. 0.0098; Dred. No. 0.10098; Pred. O; Mismatches 0; Indels
                                               8F46CDD8A1B4EFF4 CRC64;
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Interpro; IPR000844; TSP1.
Pfan; PF00099; LSP_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SW00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45610 MW;
99 314 5
419 AA; 38924 MW;
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                                                                                                                                              Ouery Match
Best Local Similarity 10v...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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CSP_PLAMA

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                                                                                                                                                                                                  falciparum.";
MOL. Biochem. Parasitol. 22:101-108(1987).

-1- EUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
VERTEBRATE HOST).

-1- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
WOULD BE THE SUBFACE ANTIGEN OF THE ORGANISM.

-1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88318952; PubMed-3045563; Robson K.J.H., Hall J.R.S., Jennings M.W., Harris T.J.R., Marsh K., Newbold C.I., Tate V.E., Weatherall D.J.; Marsh K., Newbold C.I., Tate Sequence in thrombospondin, properdin and in proteins from sporozoites and blood stages of a human malaria
                                                                                                                                                         Lockyer M.J., Schwarz R.T.; "Strain variation in the circumsporozoite protein gene of Plasmodlum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 CIRCUMSPOROZOITE PROTEIN.
320 47 X 4 AA TANDEM REPEATS OF N-A-N-P.
47402 MW; BD57A9A152B85E03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasite.";
Nature 135:79-82(1988).
-! - DURING ERYTHROCYTIC STAGE OF
глаsmodnum falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 59; DB 1; Length 442; 100.0%; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 15, Last sequence update)
THROMBOSPONDIN RELATED ANONYMOUS PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                   MEDLINE=87115616; PubMed=3543671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M15505; AAA29554.1; -. PIR; A54529; A54529.
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Best Local Similarity 100..
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                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE—89040027: Pubmed=3054537;

Lal A.A., la Cruz V.F., Campbell G.H., Procell P.M., Collins W.E., McGutchan T.F.;

McGutchan T.F.;

Mol. Blochem. Parasitol. 30:291-294(1988).

-I- FUNCTION: THE CIRCUMSPOROZOITE (THE IMMUNDOMINANT SURFACE ANTIGEN ON THE SPORGZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSOUITO THE THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSOUITO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSOUITO THE
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NCBI_TaxID=5858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 59; DB 1; Length 429; 100.0%; Pred. No. 0.01; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIRCUMSPOROZOITE PROTEIN.
4 AA TANDEM REPEATS.
3629D641D1C0BB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSP_PLAFW STANDARD; PRT; 442 AA. P08307; 01-402-1988 (Rel. 08, Created) Claud-1988 (Rel. 08, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                              429 AA
                                                                                                                                                                                                                                                                                             CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03992; AAA29557.1; -. PIR; A54504; A54504. HSSP; P04002; 1WFA. InterPro; IPR003067; Crcmsprzoite. InterPro; IPR003084; TSP1. Pfam; PF00090; tsp. 1: 1. PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal
                                                                                                                                                                              PRT;
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                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                     Plasmodium malariae.
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Matches 9; Conserv
                                        358 WSPCSVTCG 366
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                1 WSPCSVTCG 9
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P13815;
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SEQUENCE
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SIGNAL

CSP_PLAFW

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CROSS-LINKING TO FACTOR 3(A) (POTENTIAL).

CELL ATTRACHMENT SITE.

N-LINKED (GLCNAC, ...) (POTENTIAL).

N-LINKED (GLCNAC, ...) (POTENTIAL).
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SEQUENCE FROM N.A.

MCUtchan T.F., Lal A.A., de la Cruz V.F., Miller L.H., Maloy W.L.,
Charoenvit Y., Beaudoin R.L., Guerry P., Wistar R. Jr., Hoffman S.L.,
Hockmeyer W.T., Collins W.E., Wirth D.;
Sequence of the immundominant epitope for the surface protein on
sporozoltes of Plasmodium vivax.";
Science 230:1381-1383(1985).
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SIMILARITY: IT IS POSSIBLE THAT TRAP IS THE P.FALCIPARUM HOMOLOG OP THE 66 KDA BROTEIN FROM P.KNOWLESI.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
SIMILARITY: CONTAINS 1 VWFA DOMAIN.
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MEDILINE-87194878; PubMed=2437120;
MEDILINE-87194878; PubMed=2437120;
MEDILINE-97194878; PubMed=2437120;
"Evolution of the immunodominant domain of the circumsporozoite protein gene from Plasmodium vivax. Implications for vaccines.";
J. Biol. Chem. 265:6464-6467(1987).
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01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) (FRAMENT).
Plasmodium vivax (strain Salvador I).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
9; Conservative
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250 WSPCSVTCG 258
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76
307
132
310,
460
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P13826;
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SITE
CARBOHYD
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CARBOHYD
SEQUENCE
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CSF_PLAVS
CSF_PLAVS
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                                                                                                                                                                                                                                                                     Gaps
                                                                 THE REPEAT SEQUENCES
FUNCTION: THE CIRCUMSPOROZOITE PROPEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                     ٥;
                                      Plasmodium knowlesi (strain nuri).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5852;
                                                                                                                                                                                                                                           94.9%; Score 56; DB 1; Length 343; 88.9%; Pred. No. 0.025; 1ive 1; Mismatches 0; Indels
                                                                                                                                                                                            G-Q-P.
308EFD5BBC15DFC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Repeat; Signal.
19 PROBABLE.
351 CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                        13.40G-1987 (Rel. 05, Created)
13.40G-1987 (Rel. 05, Last sequence update)
20.40G-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
                                                                                                                                                                                                                                                                                                                                                                                 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003067; Cromsprzoite.
InterPro; IPR00804; TSP1.
IPfam; PF00090; tSp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
SIGNAL
20 351 CIRCUMSI
                                                                                                                                                                                                         34155 MW;
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PIR; A26253; OZZQKU.
                                                                                                                                                                                                                                                        Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                           343 AA;
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278 WTPCSVTCG 286
                                                                                                                                                                                                                                                                                            1 WSPCSVTCG 9
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P04922;
                                                                                                                                                                                                           SEQUENCE
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Search completed: January 29, 2002, 11:13:39 Job time: 815 sec
  Query Match
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RA Godson G. N., Ellis J., Svec P., Schlesinger D.H., Nussenzweig V.;

RA Godson G. N., Ellis J., Svec P., Schlesinger D.H., Nussenzweig V.;

RT Identification and chemical synthesis of a tandemly repeated througenic region of Plasmodium knowlesi circumsporozoite protein.";

RL Nature 305:29-33(1983).

CC SURFACE ANTIGEN ON THE SPOROZOITE PROTEIN IS THE IMMUNODMINANT CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE CC VERTEBRATE HOST).

CC VERTEBRATE HOST).

"TEACHLIANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR THE CC TERMINAL REGION IS PROBABLY USED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIRCUMSPOROZOITE PROTEIN.
12 x 12 AA TANDEM REPEATS OF N-A-G-Q-P-Q-A-Q-G-D-G-A.
                                                                                           Gaps
 15 X 9 AA TANDEM REPEATS OF A-A-G-A-G-G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-84026486; PubMed-6313209;
Ozaki L.S., Svec P., Nussenzweig R.S., Nussenzweig V., Godson G.N.;
"Structure of the plasmodium knowlesi gene coding for the circumsporozoite protein.";
Cell 34:815-822(1983).
                                                                                            ö
                                                                                                                                                                                                                                                                                                Plasmodium knowlesi (strain H).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                 Length 351;
                                                                                           0; Indels
                         A85E87A152E6485B CRC64;
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                                                                DB 1;
0.026;
                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
                                                                                                                                                                                                                  363 AA
                                                                                           Mismatches
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Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SMO0209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                Score 56;
Pred. No. (
              E-0-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A03389; OZZOAK.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                          34782 MW;
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                                                                94.9%;
88.9%;
                                                               Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                  STANDARD;
 235
                         351 AA;
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286 WTPCSVTCG 294
                                                                                                                    1 WSPCSVTCG 9
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101
                                                                                                                                                                                                               CSP_PLAKH
P02894;
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 DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzavelg R.S., Enea V.;
"The circumsporozoite gene of the Plasmodium cynomolgi complex.";
Cell 48:311-319(1987).
-!- MISCELLAMBOUG: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INPECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 X 11 AA TANDEM REPEATS OF G-N-Q-A-G-G-
                                                      Gaps
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SIMILARITY: CONTAINS I TSP TYPE-1 DOMAIN.
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18 X 6 AA TANDEM REPEATS OF D-G-A-R-A-
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P08675;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
20-AG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium cynomolji (strain London).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Score 56; DB 1; Length 363;
Pred. No. 0.027;
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR00084; TSP1.
Pfam; PF00090; LSP_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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94.9%;
88.9%;
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Matches 8; Conservative
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Matches 8; Conser
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298 WTPCSVTCG 306
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313 WSPCTVTCG 321
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STRAIN-LEDS:

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Plasmodium falciparum (isolate 165).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5840;
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Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 9; Conservative 0; Mismatches 0; Indels
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73 AA; 8233 MW; 53524145A58E52E8 CRC64;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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1 WSPCSVTCG 9
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us-09-763-397a-8.rspt

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SEQUENCE FROM N.A.
STRAIN=KI;
STRAIN=KI;
SEQUENCE TO N. S. SEQUENCE TO S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodium
sequence variation in the non-repeat region of the Plasmodium
falchparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burnese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/Genbank/DDBJ databases.

EMBL, AJS6946; CAB6417.1;
InterPro; IPR0030467; Cromsprzoite.
Pfam; PF00090; tspl: 1.
PRINTS; PR01303; CRCMSPRZOITE.
PROSITE; PS50092; TSPI: 1.
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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burnee field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJS6941, CABC4168.1;

Interpro: IPR003067; Cremsprzoite.

Pran, PF00090; tspl.1;

SMART, SM00209; TSP1; 1.
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Eukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Best Local Similarity 100.0
Matches 9; Conservative
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                                                                                                      28 WSPCSVTCG 36
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Q9U0Q1
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Q9U0Q3
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And e Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

And Estricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

And Sequence variation in the non-repeat region of the plasmodium at falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and an electron glutamate rich protein (GLURP) from Brazil, Senegalese, and an electron glutamate (SEP-1999) to the BMBL, AJ269945; CAB64243.1; -CAB64243.1; -CAB64243.1; -CAB64243.1; -CAB64243.1; -CAB64243.1; -CAB6424.1; -CAB6424.1;
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STRAIN-B1:
Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum quitamater rich protein (GluRP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALZ6941: CABG4167.1;
InterPro: IPR0030684; TSP.1.
InterPro: IPR0030684; TSP.1.
InterPro: PR003090; tsp.1.1.
FRINTS; PR01303; CRCKSPROITE.
SWART; SM00209; TSP1; 1.
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Pussmodium falciparum.
Bukaryota: Alveolata: Apicomplexa: Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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NON_TER 80 80
SEQUENCE 80 AA; 9102 MW; A3283B70CEE50FDE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                   O90002; ENBLIMINANY: PRT; 79 AA.
01-MAY-2000 (TEMBLE: 13, Created)
01-MAY-2000 (TEMBLE: 13, Last sequence update)
01-JUN-2001 (TEMBLE: 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
CS.
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Best Local Similarity 100.0
Matches 9: Conservative
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Best Local Similarity 100.1
Matches 9; Conservative
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STRAIN=M4;

Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, A1269957; CAB64237.1;

InterPro: IPR000884; TSP1.

InterPro: IPR0003067; Crcmsprzoite.

Pfam; PF00090; tsp_1; 1.

PRINTS; PR01303; CRCMSPRZOITE.

SMART; SMO0209; TSP1; 1.
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CS.
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Pred. No. 0.0037;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269951: CAB64176.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1: 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1: 1.
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80 AA; 9032 MW; ADED6F0E266AD98E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Pred. No. 0.0037;
Mismatches 0;
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Best Local Similarity 100..
Lag 9; Conservative
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Matches 9; Conservative
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Plasmodium falciparum.
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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLUPP) from Brazil, Senegalese, and
Burmese fleld isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ269948, CAB64173.1;
InterPro: IPR000884; TSP1.
InterPro: IPR003067; Crcmsprzoite.
Pfam; PR00090; LSP.1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 59; DB 5; Length 80; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
                                                                                       Similarity 100.0%; Score 59; DB 5; Length 80; Similarity 100.0%; Pred. No. 0.0037; 9; Conservative 0; Mismatches 0; Indels
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NON_TER 80 80
SEQUENCE 80 AA; 9046 MW; BA7689D18F031C3E CRC64;
                                        4204EEC68F0B1434 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                             80 AA.
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80 AA;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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28 WSPCSVTCG 36
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28 WSPCSVTCG 36
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   NON_TER
NON_TER
SEQUENCE
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Gaps

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RESULT 09U0P9

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SEQUENCE FROM N.A.
STRANT=D4396;
STRANT=D4396;
STRANT=D4396;
Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium falciparum glutemater rich protein (GLIMPP) from Brazil, Senegalese, and Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJZ96967; CAB64186.1;
InterPro; IPR000864; TSP1.
InterPro; IPR000864; TSP1.
InterPro; IPR000969; TSP1.
SPRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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                                             Plasmodium falciparum.
Eukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
VCDI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 59; DB 5; Length 80; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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80 AA; 8988 MW; 0E7689D18F031B53 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2010 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROFEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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28 WSPCSVTCG 36
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Q9U0P4;
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                            de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmase field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ26961. CAB64180.1; -.
InterPro: PR000884 TSP1.
InterPro: PR000884 TSP1.
PRINTS; PR001909: tsp.1; 1.
PRINTS; PR01913: GRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-04264.
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GIURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the BMBL/GenBank/DDBJ databases.
InterPro: IPR000884; TSP1.
InterPro: IPR000884; TSP1.
InterPro: IPR000091; Cromsprzoite.
Pfam: PF000999; LSP1: 1.
PRINTS: PR01303; CRCMSPRZOITE.
SWART: SM00209; TSP1: 1.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TAXID=9833;
                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 59; DB 5; Length 80; Best Local Similarity 100.0%; Pred. No. 0.0037; Matches 9; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created),
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MON-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AA.
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Matches 9; Conserv
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SEQUENCE FROM N.A.
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28 WSPCSVTCG 36
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Q9U0P5
ID Q9U0P5
AC Q9U0P5
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Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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Best Local Similarity 100.
Matches 9; Conservative
                          9; Conservative
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Query Match
Best Local Similarity
Matches 9; Conserv
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28 WSPCSVTCG 36
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                                                                                                                                                                                                                     de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutanate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269969; CAB64188.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Cromsprzoite.
Pfam; PP00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SNART; SM00209; TSP1; 1.
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STRAIN—D4416;

Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Ge Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese fleld isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/PDBJ databases.

EMBL: AJ269970; CAB64189.1;
InterPro; IPR000884; TSP1.
InterPro; IPR00096; TSP1.
InterPro; IPR00090; tsp_1; 1.
PRINTS: PR01303; CRCMSPRZOITE.

SMART; SM00209; TSP1: 1.
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NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 59; DB 5; Length 80; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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9015 MW; 1CF404B8FB142C73 CRC64;
                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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Best Local Similarity 100.
Matches 9; Conservative
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80 AA;
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STRAIN-D4405;
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28 WSPCSVTCG 36
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Q9U0P3;
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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ26978; CAB641971;
InterPro; IPR000884; TSP1.
                                                           Gaps
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NCBI_TaxID=5833;
100.0%; Score 59; DB 5; Length 80; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
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100.0%; Pred. No. 0.0037;
Live 0; Mismatches 0;
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CarA gene product. Bacterlophage 192 Malic enzyme #1 Murine FGF-8

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Peptide(s) recognising or inducing cytotoxic T lymphocytes useful in vaccines against malaria or HIV-2, derived from specific antigen and human leukocyte antigen contg. class I restricted epitope
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                                                                       AARO6464
AAY49850
AAY33356
AAW80482
AAX49324
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AAB07813
AAY28428
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AAB07821
AAB07822
AAY38892
AAY38893
AAY95241
AAM01053
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AAY08218
AAW144465
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AAB18270
AAY87855
AAU03676
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AAB80922
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92GB-0017704.
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 03-APR-1992;
20-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR43243;
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 P. falciparum live
Amino acid sequenc
Cytotoxic T lympho
Plasmodium falcipa
Amino acid sequenc
Recombinant vaccin
P.falciparum LSA g
Zea mays protein f
Zea mays protein f
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Plasmodium falcipa
                                                                                     (without alignments)
2.145 Million cell updates/sec
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                                                                        Search time 310.82 Seconds
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                          522463 seqs, 74073290 residues
                                                                        January 29, 2002, 10:21:43;
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Maximum Match 100%
Listing first 45 summaries
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AAR78844
AAY03663
AAY0285
AAY70285
AAY7027
AAY027
AAY033138
AAG33138
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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111... 112... 114... 116... 119... 120... 120...

Score

Result . 9 δλ QQ

us-09-763-397a-9.rag

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CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide (i.e. AAR78824 R78853) and a lipid conjugated helper T cell inducing peptide. The compsn. induces a CTL response to bacterial, viral or tumour Ags, and is therefore useful in the treatment and prevention of diseases associated with the Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g. hepatitis B
                                                                                                                                                                                        P. falciparum liver Ag 1786-1794 cytotoxic T lymphocyte epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of the malaria (M) string CTL epitope Ls6.
                                                                                                                                                                                                             Liver Ag 1786-1794; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte; viruses; parasites; tumours; antigens; treatment; disease prevention; cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 50; DB 16; ilarity 100.0%; Pred. No. 4.3e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ceut RW, Grey H, Sette AD, Vitiello MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 17; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03663 standard; peptide; 9 AA.
                                                                                                    AAR78844 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                            94US-0197484
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                             Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 9; Conserv
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                  WO9522317-A1.
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                                                                                                                                                              27-MAR-1996
                                                                                                                                                                                                                                                                                                                                     24-AUG-1995
                                                                                                                                AAR78844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local
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ID AAR7
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                          The sequence is that of peptide 1s6 which is recognised by, or can induce, cytotoxic.T lymphocytes. It may be useful in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential P.falciparum HLA epitopes are peptides derived from antiqens shown to be targets of CTL recognition and which are capable of binding with high affinity to a specified HLA class 1 molecule. Although they have not been shown to be recognised by CTL grown from malaria-exposed individuals their ability to bind to the relevant class 1 molecule indicates that they are likely to be presented on the surface of malaria-infected hepatocytes in vivo. The present sequence is a potential HLA-B7 epitope derived from liver-stage antignen-1. The use of this peptide (or its variants or longer peptides comprising it) as a CTL inducer for immunisation against malaria in HLA-B7 individuals is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                           Liver-stage antigen; LSA-1; human leucocyte antigen; HLA; class 1; HLA-B7; potential epitope; malaria; vaccine; CTL induction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plebanski
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum peptide(s) · useful in vaccine for immunising against malaria
                                                                                                                                                                                                                                                                                                                                                                                  .Plasmodium falciparum HLA-B7 potentíal epitope 1s6.
                                                                                                                                Score 50; DB 14;
Pred. No. 4.3e+05;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 21; 23pp; English.
                                                                                                                                                                                                                                                                                           AAR87311 standard; peptide; 9 AA.
 Claim 6; Page 30; 35pp; English
                                                                                                                                Ouery Match

Best Local Similarity 100.0%;

Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94GB-0006492.
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-B7; potential epito
cytotoxic T lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
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                                                                                       9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9526982-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                   16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1995.
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Best Local Si
Matches 9
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                                                                                                                                                                                                                                                                                                                        AAR87311;
                                                                                        Sequence
                                                              malaria.
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cytostatic; immunostimulant; cellular immune response inducer;
             protozoacide; leukaemia; cancer
                                                                                                                                            19-FEB-1999;
                                                                                                                                                                                              Shinbara N,
                                                                                         24-AUG-2000
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AAY70285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The Kits of the invention comprises (1) as printing composition, a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)] cepitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (1), with this source being a non-replicating or replication impaired recombinant poxvirus vector (FVV) plus a carrier. If the source of CTL epitopes in (i) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune (ii) is from a different virus. The kits are used to generate an immune specifically against malaria parasites such as P. falciparum, or HIV, and also many other bacterial, viral or parasitic pathogens or tumours, specifically against malaria parasites against melanoma and cancer of breast or colon, and generally wherever a strong CD8+ response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than half from wild-type poxvirus, resulting in complete cather than partial protection against sporozoite challenge. Also PVV are affect, the na wild-type poxvirus, resulting in complete
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falciparum; viral; bacterial; parasitic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                          Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; immune response; infectious disease; malaria; cytotoxic T cell;
                                                                                                                                                                                              Hill AVS, McMichael AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide epitopes of the malaria (M) string
            melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                             Hanke T, Smith GL;
                                                                                                                                                                                                                                                                                                                             Claim 38; Page 18; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB23658 standard; Peptide; 9 AA.
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                                                                                                                 98WO-GB01681.
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                                                                                                                                                                    (ISIS-) ISIS INNOVATION LTD
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Schneider J,
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'malaria; parasite; P.
                                   Plasmodium falciparum
                                                                                                                                                                                                                                   WPI; 1999-070325/06.
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Best Local Similarity
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                                                                                                                                                                                            Blanchard T,
Plebanski M,
                                                             WO9856919-A2
                                                                                                                09-JUN-1998;
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T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence regereseits a specifically claimed CTL epitope for use in a fused protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 53; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    (SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                          99JP-0041535.
                                                                                                                                                                                                                               18-FEB-2000; 2000WO-JP00941
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPIVQYDNF 9
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Homo sapiens.
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Blanchard T,
Plebanski M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δŏ
                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the antigenic epitope P595, derived from
liver stage antigen-1 (LSA-1) of Plasmodium falciparum. It is used
liver stage antigen-1 (LSA-1) of Plasmodium falciparum. It is used
in the construction of recombinant protein CONIMALVAC-1, which
antificable in unitistage malarial vaccine. The recombinant
protein comprises, melittin signal Peptide, (His)6 tag,
corollar protein (CSP), sporozoite surface protein-2 (SSP-2),
circumsporozoite protein (CSP), sporozoite surface protein-1 (MSP-1),
liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1),
liver stage antigen-1 (LSA-1), merozoite surface protein-1
(MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175
(MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175
(MSP-179), rhopty associated protein-1 (AMA-1) and gamete specific
antigen, Pfg27. These epitopes were obtained at different stages of the
antigen, Pfg27. These epitopes were obtained at different stages of the
antigen, Pfg27. These epitopes were obtained at different stages of the
cativity and can used for treatment and prevention of malarial
confections. Anti-CDC/NIMALVAC-1 antibodies can be used for detecting
confections. Anti-CDC/NIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic I lymphocyte; boosting; poxxirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                  Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of the malaria (M) string CTL epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 21; I 100.0%; Pred. No. 4.3e+05; Limited and the score of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                          (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY03681 standard; protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 16; 52pp; English.
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                                                                                                                                                                                                              Shi YP, Hasnain SE;
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                                                          99WO-US18869.
                                                                                                       98US-0097703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                           WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KPIVQYDNF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-1998
                                                                 19-AUG-1999;
                                                                                                         21-AUG-1998;
                     02-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                     Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
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The invention relates to methods and reagents for generating a protective CC CD8+ T-cell immune response against at least one target antigen. The kits CD8+ T-cell (syttoxic T lymphocytes-(CTL)) epitopes of the target antigen, plus a carrier and (li) as boosting composition, a source of one or antigen, plus a carrier and (li) as boosting composition a source of CTL epitope the same as used in (li), with this source being a non-replicating or replication-impaired recombinant this source being a non-replicating or replication-impaired recombinant comparisons viral vector (PVV) plus a carrier. If the source of CTL epitopes in povavirus vector (PVV) plus a carrier. If the source of CTL epitopes in comparisons the strict are used to generate an immune response (prophylactic or the rapeutic) against pathogens or fumours, specifically against malaria creaspines against melanoma and cancer of breast or colon, and generally response against melanoma and cancer of breast or colon, and generally wherever a strong CD8+ response is protective. The boosting composition wherever a strong CD8+ response is protective. The boosting composition complete rather than that from wild-type poxvirus, resulting in complete rather than partial contains and contains against melanome and contains and contains against melanome and exceptive. The boosting composition complete rather than partial and contains and conta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; recall epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen: Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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McMichael AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
23..350
         Hill AVS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
         Hanke I, H
Smith GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70278 standard; Protein; 350 AA.
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 20; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                   Gilbert SC,
Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                           WPI; 1999-070325/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wild-type virus.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                      The 3' part of the P.falciparum liver-stage specific antigen (LSA) gene codes for a polypeptide sequence which carries a T cell epitope characteristic of a protein produced in hepatocytes infected with P.falciparum. The polypeptide can be used in the preparation of vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                    Polypeptide(s) derived from liver stage of Plasmodium falciparum - for vaccination against, treatment of and diagnosis of malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 50; DB 13; Length 493; 100.0%; Pred. No. 0.047; ive 0; Mismatches 0; Indels 0
                                                                                                                                                    Guerinmarchand C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays protein fragment SEQ ID NO: 40107
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                                                                                                                                                                                                                                                                                          Claim 2; Fig 8-10; 81pp; French.
                                                                                                                                                    Druilhe P, Guerin-Marchand C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
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99US-0129845.
99US-0130077.
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                                                 92WO-FR00104.
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                                                                                 91FR-0001286.
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les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays subsp. mays.
                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                      WPI; 1992-299985/36.
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370 kpivgydnf 378
                                                                                                                                                                                                                                                                                                                                                                                                                               493 AA;
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                                                                                                                                                                                                        N-PSDB; AAQ28119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
                                                 05-FEB-1992;
                                                                                   05-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
23-APR-1999;
                 20-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000,
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08-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG33138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), inver stage antigenic (SSP, sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), thopits associated protein-1 (RAP-1) and gamete specific antigen, Ffg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                          Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
/label- Mature_CDC/NIMALVAC-1
/note- "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malaria; hepatocyte; sporozoite; T-cell epitope; B-cell epitope; paludism; liver stage-specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 50; DB 21; Length 350; llarity 100.0%; Pred. No. 0.032; Conservative 0; Mismatches 0; Indels
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/label= repetitive_region
214..493
/label= non-repetitive_region
                                                                                                                                                                                      (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.falciparum LSA gene C-terminal region.
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                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR26944 standard; Protein; 493 AA.
                                                                                                                                                                                                                                        Shi YP, Hasnain SE;
                                                                                                                    99WO-US18869.
                                                                                                                                                      98US-0097703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
                                                                                                                                                                                                                                                                       WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KPIVQYDNF 9
                                                   WO200011179-A1.
                                                                                                                    19-AUG-1999;
                                                                                                                                                      21-AUG-1998;
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                                                                                   02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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PR 22-JUL-1999; 99US-0145088.
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PR 22-JUL-1999; 99US-0145087.
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PR 03-AUG-1999; 99US-0147304.
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PR 13-AUG-1999; 99US-0147304.
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990S-0123180.
990S-0123548.
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Pred. No. 6.1;
2; Mismatches
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Length 459;

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AAHS5304 to AAHS3970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG81454 to AAG8120, from Staphylococcus epidermidis. (II), given in AAG81454 to AAG8120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used to in vaccination. The nucleic acids (II) may be used to produce the containing them which are used to produce hosts cells which express the containing them which are used to produce acids) may then be collapseptides. The polypeptides (II) (and/or incleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the AAHS5090 represent specifically claimed s. epidermidis genomic DNA AAHS5090 represent specifically claimed s. epidermidis genomic DNA AAHS5090 represent oligourcleotide sequences and primers which are used in the exemplification of the present invention. AAHS5091 to sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing of the present specification, chowever the sequences are given in the disclosure for SEQ ID NO:4455 to 4472, on sequences are present for SEQ ID NO:4455 to 4472, on sequences are present for SEQ ID NO:4455 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                      S. epidermidis open reading frame protein sequence SEQ ID NO:1246.
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                                                                                         DB 21; Length 267;
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                                                                                         Score 38; DB;
Pred. No. 6.9;
                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 357; 2188pp; English
                                                                                                                                                                                                                                             AAG82076 standard; Protein; 459 AA.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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                                                                                          76.0%;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (I), given in AAG81454 to AAG81120, from Staphylococcus epidermidis.

(II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used (I) and (II) can have nucleic acids (I) way be used to produce the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the polypeptides (II) (and/or nucleic acids) may then be contained to accinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the transment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH5509 represent specifically claimed S. epidermidis genomic DNA AAH5509 represent oligourcleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to sequence listing of the present specification, conceaved the present specification of the present invention.

Sequences given in the sequence listing of the present specification, however the sequence listing of the present specification, conceaved the sequence listing of the present specification, however the sequence listing of the present specification, conceaved the sequence listing of the present specification, conceaved the sequence listing of the present specification.
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                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. epidermidis open reading frame protein sequence SEQ ID NO:2554.
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Pred. No. 13; 1; Indels
1; Mismatches 1; Indels
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Score 38; DB 22;
Pred. No. 13;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                              AAG82730 standard; Protein; 459 AA
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75.0%;
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N-PSDB; AAH53580.
                     Query Match
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Matches 6; Conserv
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343 piitydnf 350
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                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 69655
                                                                                         AAG54615 standard; Protein; 103 AA
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990S-0123548.
990S-0125788.
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99US-0138094
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343 piitydnf 350
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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06-APR-1999;
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AAGS4615
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Search completed: January 29, 2002, 10:21:44 Job time: 420 sec	
	Score 34; UB 21; Length 103; Pred, No. 16; 3; Mismatches 1; Indels 0; Gaps 0;
99999999999999999999999999999999999999	Query Match Best Local Similarity 55.6%; Matches 5; Conservative / 1 KPIVQYDNF 9 / 1 1 1 1 1 1 1 1 1

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ORGANISM: Plasmodium falciparum
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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1.521 Million cell updates/sec
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                                                                                                                                                                    January 29, 2002, 10:24:03; Search time 133.18 Seconds
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Compugen Ltd
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PCT-USS5-02121-21
US-08-468-5548-14
US-08-468-5798-14
US-08-468-5798-14
US-08-337-690A-2
US-08-337-690A-2
US-08-337-690A-2
US-09-137-690A-2
US-09-135-102-2
US-09-217-787-2
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US-09-217-787-4
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US-09-217-787-4
US-09-135-166-8
US-08-93-001-2
US-08-93-522A-1
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GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
                                                                                                                 OM protein
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                                                                                                                                                                       Run on:
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APPLICANT: Adrian V.S. Hill, et al:
APPLICANT: Adrian V.S. Hill, et al:
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERVTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
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US-09-135-166-6
US-08-942-046-4
US-08-942-046-6
US-08-942-046-6
US-08-942-046-6
US-08-942-046-6
US-08-448-438-1
US-08-448-438-4
US-08-992-176-5
US-08-992-176-5
US-08-448-438-6
US-08-448-438-6
US-08-448-438-7
US-08-448-438-7
US-08-448-438-6
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 is comparable comparable operating system: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1+

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: OCCODER 3, 1994
PRIOR APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: APILI 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1993
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APILI 5, 1993
ATTORNEY AGENT INFORMATION:
NAME: Lee Cheng
RESISTRATION NUMBER: 263-PPIR1577US
TELEPHONEY: (202) 721-8200
TELEPHONE (202) 721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263-PPIR1577US
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GENERAL INFORMATION:
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APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CT.L EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08468576B
Patent No. 595345
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: DATAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBLIAN TYPE: Floppy disk, 3.5 inch, 1.44 mb ENDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-D6S/MS-D0S SOFTWARE: Wordberfect 5.1+
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/318,856A
FLING DATE: October 3, 1994
FRIOR APPLICATION NUMBER: GB 92 08 068.8
FRIDK DATE: APRIL 3, 1992
FRIDK DATE: APRIL 3, 1992
FRIDK DATE: APRIL 3, 1992
FRIDK DATE: AUGUSE 20, 1992
FRIDK DATE: AUGUSE 20, 1992
FRIDK DATE: AUGUSE 20, 1993
FRIDK APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APRIL 5, 1993
ATTORNEY AGENT INFORMATION:
NAME: Long Change From The Programmer of the Company 
                                                                                                                                                                                                                                                                                       ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 263-PPIR1577US
TELECOMNUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEPHONE: (202) 721-8250
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 amino acid residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abua.
STREET: 600 ..
CITY: Tarrytown
TARY YOFK
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                       STREET: 2033 K St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 20006
                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10591-5144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPIVQYDN 8
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US-08-468-576B-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCE: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-105/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16 FEB-1995
                                                                                                     Query Match 100.0%; Score 50; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 50; DB 5; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 26-80G-1992
PRIOR APPLICATION DATA:
FILING DATE: 27-80F-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-8PR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-80G-1991
ATTORNEY/ACENT INFORMATION:
NAME: PARMED-100: SLEVEN W.
REGISTRATION NUMBER: 31,990
REFERENCE/POCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
PCT-US95-02121-21
; Sequence 21, Application PC/TUS9502121
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-318-856A-46
; Sequence 46, Application US/08318856A
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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MOLECULE TYPE: peptide
PCT-US95-02121-21
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STRANDEDNESS: unb
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Pred. No. 24;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road CITY: Tarrytown STRATE: New York COUNTRY: USA LINE 10591-5144
COUNTRY: USA LINE 10591-5144
COMPUTER READBLE FORM: WEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect CORENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,577B FILING DATE: O6-JUN-1995
CLASSIFICATION: 514
RPICR APPLICATION NUMBER: US 08/239,276
FILING DATE: O6-JUN-1995
FILING DATE: O8-MAY-1994
RPICR APPLICATION NUMBER: US 07/812,646
FILING DATE: O8-JUN-1992
PRICR APPLICATION NUMBER: US 07/812,646
FILING DATE: 14-JUN-1991
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08468577B
Patent No. 6001804
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
                                                                                                                                                                                                                                                                                                                                                               NAME: KUTE G. Briscoe
REGISTRATION NUMBER: 33,141
REGISTRATION NUMBER: MDI 251.5-KGB
TELECOMMUNICATION INFORMATION:
TELEPRONE: (914) 332-1700
TELEPRONE: (914) 332-1700
SEQUENCE CHARACTERISTICS:
                                                         PRIOR DATE:

APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-UN-1992
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-UN-1991
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: 04-DEC-1989
FILING DATE: 04-DEC-1989
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/41,703
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: KUTE G. BFISCOG
                     UMBER: US 08/239,276
05-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 264 amino acids TYPE: amino acid
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Best Local Similarity 55.uv
Ere 5; Conservative
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TOPOLOGY:
US-08-468-579B-14
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         WEDDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: System 7.5 SOFTWARE: WordPerfect CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION UNBER: US/08/468,576B FILING DATE: O6-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: US 08/239,276 FILING DATE: O5-MAY-1994 PRIOR APPLICATION NUMBER: US 07/872,646 FILING DATE: O8-JUN-1992 PRIOR APPLICATION NUMBER: US 07/872,646 FILING DATE: O8-JUN-1991 PRIOR APPLICATION NUMBER: US 07/715,181 FILING DATE: 14-JUN-1991 PRIOR APPLICATION DATE: US 07/441,703 FILING DATE: 04-DEC-1989 PRIOR APPLICATION NUMBER: US 07/312,543 FILING DATE: 17-FEB-1989 ATTORNEY/AGENT INFORMATION: NAME: KILING DATE: INFORMATION: NAME: KILING DATE: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08468579B
Patent No. 5981700
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
CITY: PatryLown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OOPERATING SYSTEM: System 7.5
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.7-KGB
TELECOMMUNICATION INFORMATION:
TELEFAX: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/468,579B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 264 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0uery Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurt G. Briscoe
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-468-5768-14
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US-08-468-579B-14
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                                                                                                                                                                 RESULT 8
US-09-048-887-2
US-09-048-887-2
; Sequence 2, Application US/09048887
; Patent No. 6166180
; GENERAL INFORMATION:
; APPLICANT: Korenberg, Julie R.
; APPLICANT: Yanakawa, Kazuhiro
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TOWERSPONDENCE 3:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; CARPESCE:
; STREET: 4370 La Jolia Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1190;
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Pred. No. 1.9e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,887
       100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALMOND, GEORGE PEACOCK COPELAND MCGOMAN, SIMON JAMES SEBAIHLA, MOHANMED COX, ANTHONY RICHARD JOHN HOLDEN, MATTHEW THOMAS GEOFFREY PORFER, LANGEN ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,690
FILING DATE: 09-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENG-DOCKET NUMBER: P-CE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08737825; Patent No. 5871922; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 66.0%; Sco
Best Local Similarity 100.0%; Pi
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4370 La Jolla VIII
CITY: San Diego
STARE: California
COUNTRY: United States
ZIP: 91212
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
     Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-048-887-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                           774 PIVQYD 779
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774 PIVQYD 779
                                                                          2 PIVQYD 7
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-737-825-3
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Patent No. 577368

GARRAL INFORMATION:
A PAPLICANT: Yamakawa, Kazuhiro
TITLE OF INVENTION: A NOVEL CHROMOSOME 21 GENE MARKER,
TITLE OF INVENTION: OPPOSITIONS AND METHODS USING SAME
WUMBER OF SEQUENCES:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET, 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STRAFE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 3; Length 264;
Pred. No. 24;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/337,690A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CE 2573
TELECOMMUNICATION INFORMATION:
TELEFAX: (619)535-9001
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 amino acids
TENGTH: 1190 amino acids
TENGTH: 1190 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989:
ATTORNEY/AGENT INFORMATION:
NAME: KURT G. BILSCOG
RGGISTRATION NUMBER: MDI 251.8-KGB
RGGISTRATION NUMBER: MDI 251.8-KGB
TELECOMUNICATION INFORMATION:
SUDURNEY ON SECOID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.0%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.08;
                                                                                                                                                                                                                                                                                                                                               LENGTH: 264 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-577B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KPIVQYDNF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-337-690A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-337-690A-2
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Gaps
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APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Sandy, Allen
APPLICANT: Randy, Allen
APPLICANT: Randy, Allen
APPLICANT: Randy, Allen
APPLICANT: Randy Allen
APPLICANT: Mashington
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.0%; Score 31; DB 2; Length 235; 71.4%; Pred. No. 83;
                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/580,545B

FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

REGISTRECOMMUNICATION NUMBER: 04473/068001

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 anino acids
TYPE: amino acids
TELET APPLICATION INFORMATION:
TELEFAX: 202/783-2331
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICALLO...
FILING DATE:
FLILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 26.55
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09262653A Patent No. 6166294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 235 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.0
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-5458-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-09-262-653A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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USA
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100 QPIVEYD 106
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COUNTRY: US,
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-262-653A-10
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APPLICANT: BYCROFT, BARRIE WALSHAM
APPLICANT: WILLIAMS, PAUL
TITLE OF INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENEM
NUMBER OF SEQUENCES: 12
CORRESSONDENCE ADDRESS:
ADDRESSEE: BLICh, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
COUNTRY: USA
STREET: Virginia
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: MISPOSOTY WORD97
CORPUTER: MICROSOTY WORD97
CORPUTER: MICROSOTY WORD97
CORPUTEN: MICROSOTY WORD97
CORPUTENT AND MICROSOTY WORD97

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APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Kolchi, Fujisawa
APPLICANT: Koshihiko, Mishiguchi
APPLICANT: Susumu, Nishiguchi
APPLICANT: Randy, Allen
APPLICANT: Randy, Allen
TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C. STREET: 601 Thirteenth Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08580545B Patent No. 5932713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASALFLATANION: 4.2.
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1009-
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.v.
6; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 KPGAQYDN 381
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US-08-580-545B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-737-825-3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09412102

Patent No. 6228922

GENERAL INFORMATION:
APPLICANT: USESEN, HOLLY J
APPLICANT: MEYER, TERRY E
TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
TITLE OF INVENTION: NEMATODES IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. MATTAY Spruill (Alston & Bird, LLP)
STREET: Railegh
CITY: Railegh
                                                                                                                             STATE: NC
COUNTRY: US
ZPE2
ZPE2
ZPE2
ZPE2
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWRE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/09/217,787
TITLE OF INVENTION: NEMATODES IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESCEDING ADDRESS:
ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Railegh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
OCMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/412,102
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SPIDILI, W. MANTRAY
REGISTRATION NUMBER: 32,943
REFERRENCE/COCKET UNMER: 518-18P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 220.
TELEFRAX: 919 420 220.
TELEFRAX: 919 880 210 0.
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/217,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-217-787-2
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                          Gaps
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                                                                                          0;
                                          Score 31; DB 4; Length 235;
Pred. No. 83;
2; Mismatches 0; Indels
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57.1%; Pred. No. 1e+02;
tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Sequence 2, Application US/09412102
Fatent No. 6228992
GENERAL INFORMATION:
APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E
ITILE OF INVENTION: GENES AND METHODS FOR CONTROL OF
ITILE OF INVENTION: NEMATODES IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. MURTAY Spruill (Alston & Bird, LLP)
STREET: 8055 Glenwood Ave. Suite 310
STREET: NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-217-787-2
US-09-217-787-3
Parent No. 6284948
| GENERAL INFORMATION:
| APPLICANT: MESEN, HOLLY J
| APPLICANT: MESEN, TERRY E
| TILLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW FC COMPUTER: IBW FC
COMPUTER: IBW FC
COMPUTER: PAPECONDALIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NORM: US/09/412,102
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/217,787
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SPCAILL, W. MUTEAY
RECISTRATION WIMBER: 57.943
REFERENCE/DOCKET WUMBER: 5718-
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 282 amino acids
amino acid
                                               Query Match 62.0
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: protein
US-09-412-102-2
                                                                                                                                                                          100 QPIVEYD 106
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Search completed: January 29, 2002, 10:24:04 Job time: 510 sec

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Pred. No. 1e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Score 31; DB 4; Length 285; Pred. No. 1e+02; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE W. MULTAY Spruill (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave. Suite 310
CITY: Rallegh
STREET: 3605 Glenwood Ave. Suite 310
CITY: Rallegh
STREET: 3605 Glenwood Ave. Suite 310
CITY: Rallegh
STREET: 3605 Glenwood Ave. Suite 310
STREET: 3605 Glenwood Ave. Suite 310
STREET: 3605 Glenwood Ave. Suite 310
ADDRESSEE Floppy disk
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,787
FILING DATE:
CLASSIFICATION:
NAME: SPILLIL, W. MULTAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
RECECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TREEFERX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: JESSEN, HOLLY J
APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E
TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
TITLE OF INVENTION: NEMATODES IN PLANTS
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
                                            5718-18P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-217-787-4
; Sequence 4, Application US/09217787
; Patent No. 6284948
; GENERAL INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 571:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                        32,943
                                                                                                      TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         62.0%;
57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-09-412-102-4
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; MOLECULE TYPE: protein
US-09-217-787-4
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18 KPVLEYD 24
                                                                                                                                                                                                                                                                                                                                                                                                            1 KPIVQYD 7
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Mon reb

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 10:26:37; Search time 144.96 Seconds (without alignments) 4.729 Million cell updates/sec Run on:

US-09-763-397A-9 50 1 KPIVQYDNF 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	liver stage antige	UL100 protein - hu	vacuolar protein s	hypothetical prote		_	٦	_	NADH dehydrogenase	hypothetical prote	hypothetical prote	probable cpsA prot	hypothetical prote	hypothetical prote	iron-sulfur cluste	UDPglucose 4-epime	conserved hypothet	conserved hypothet	COI intron 14 prot	probable permease	hypothetical prote	receptor like prot	probable transport	mt2 protein - rat	multidrug resistan	hypothetical prote	NADH dehydrogenase	transmembrane prot	TyB protein - yeas
SUMMARIES	ΩΙ	A45592	QQBEJ7	S62458	D82941	809799	T27444	B84062	D70153	D75388	E71677	S74561	A70569	T19918	T10155	B72272	T10498	B82887	G81010	G38888	G82032	T24784	T48176	S25576	S38400	S13426	T34329	E84948	JC5523	B22671
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ø	Query Match	100.0	78.0	76.0	72.0	72.0	72.0	70.0	68.0	68.0	68.0	68.0	68.0	0.89	67.0	99	99	0.99	0.99	0.99	99	99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
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TyB protein - yeas TyB protein - yeas	TyB protein - yeas	TyB protein - yeas	TyB protein - yeas	PBSX prophage ORF	N-(5'-phospho-D-ri	conserved hypothet	UTPglucose-1-pho	S fimbrial adhesin	glycosyltransferas	hypothetical prote	integral membrane	hypothetical prote	hypothetical prote	sucrose-6-phosphat
S57045 S69963	869957	569838	S69982	G69732	н64070	D30191	E64466	C49233	A84114	A83678	T44032	T32111	T23720	JH0754
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1755	1755	1755	1755	235	249	281	283	299	303	331	344	463	467	473
66.0	66.0	0.99	0.99	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0
е е е	33	33	33	32	32	32	32	32	32	32	32	32	32	32
30	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

```
liver stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Bate: 22-NNo-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jun-2000
C;Accession: S24597, A45592; S29393; S34842; B45592; C45592; D45592
R;Zhu, J; Hollingdale, M.
Submitted to the EMBL Data Library, November 1990
A;Reference number: S24597
A;Reference number: S24597
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1909 < CAHD>
A; Cross-references: EMBL:X56203; NID:99915; PID:99916
B; Zhu, J.; Hollingdale, M.R.
And. Biochem. Parasitol. 48, 223-226, 1991
A; Title: Structure of Plasmodium falciparum liver stage antigen-1.
A; Reference number: A45592; MUID:92107224
A; Accession: A45592.
RESULT
```

A; Residues: 1-195;638-688;1165-1215;1590-1909 <2H2>
A; Rolecule type: DNA
A; Residues: 1-195;638-688;1165-1215;1590-1909 <2H2>
A; Molecule type: DNA
A; Residues: 1-195;638-688;1165-1215;1590-1909 <2H2>
A; Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:75012, NCBIN:75014, R; Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Patarapotikul, J.; Beaudo Nature 329, 164-167, 1987
A; Title: A liver-stage-specific antigen of Plasmodlum falciparum characterized by gen A; Reference number: 829393; MUID:87315391
A; Residues: 223393
A; Status: preliminary
A; Residues: 323-387 <GUEL>
A; Residues: 323-387 <GUEL>
A; Cross-references: EMBL:M28266
A; Cross-reference number: S34842
A; Residues: 333-381 'HRAI 'GUEL>
A; Residues: 323-381 'HRAI 'GUEL>
A; Residues: 232-381 'HRAI 'GUEL>
A; Residues: EMBL:M28266
A; Note: difference at carboxyl end due to frameshift error
C; Comment: This protein is found as flocculent material in the parasitophorous vacuol C; Superfamily: trichohyalin; calmodulin repeat homology
C; Keywords: EF hand
F; 154-1629/Region: 17-residue repeats (A-K-E-K-L-Q-E-Q-C-S-D-L-E-Q-E-R-R)

ö Gaps ö Query Match 100.0%; Score 50; DB 2; Length 1909; Best Local Similarity 100.0%; Pred. No. 0.09; Matches 9; Conservative 0; Mismatches 0; Indels (

1 KPIVQYDNF 9 õ

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Nypothetical protein UL36 - human cytomegalovirus (strain AD169)
Nypothetical protein UL36 - human cytomegalovirus 5
A;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09799
R;Accession: S09799
R;Achee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.
Curr, Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovs
A;Accession: S0979
A;Accession: S0979
A;Accession: S0979
A;Accession: S0979
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1476 <CHE>
                                     Pupporhetical protein UU031 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Accession: DB2941
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to Genmank, Pebruary 2000
A;Befarence number: A82870
A;Reference number: A82870
A;Accession: DB2941
A;Status: preliminary
A;Accession: DB2941
A;Cross-references: GB.AE002103; GB:AF222894; NID:G6898977; PIDN:AAF30436.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X17403; NID:959591; PIDN:CAA35395.1; PID:e298606; PID:918139 A;Note: this sequence was submitted to the EMBL Data Library, December 1989 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27444
S;MoWirted to the EMBL Data Library, September 1997
A;Reference number: Z20368
A;Accession: T27444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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66.7%; Pred. No. 7.5;
live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 476;
Pred. No. 15;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%;
55.6%;
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Best Local Similarity bb...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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142 RPMVQYDDY 150
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51 KKLVQYENF 59
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A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 68/1
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                                                                                                                                                                                                                                                                                                                                                    Chacesion: S09865
Riche, M.S.: Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-conding content of the sequence of human cytomegalovirus A; Reference number: S09749; MurD: 90269039
A;Reference number: S09749; MurD: 90269039
A;Reference number: S09749; MurD: 90269039
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1372 CCHE>
A;Residues: 1372 CCHE>
A;Ross-references: EMBL:X17403; NID: 959591; PIDN: CAA35336.1; PID: 91780879
A;Note: possible protein-coding frames are given
A;Note: possible protein-coding frames are given
C;Superfamily: cytomegalovirus UL100 protein
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C;Species: Schizosaccharomyces pombe
C;Date: 16-May 1996 #sequence_revision 13-Mar-1997 #text_change 10-Dec-1999
C;Accession: S62488; T38569
R;Badcock, K.; Churcher, C.M.
submitted to the RMBL Data Library, October 1995
A;Reference number: S62445
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A.Molecule type: DNA
A.Rolecule type: DNA
A.Rolecu
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                                                                                                                                                                                                   UL100 protein - human cytomegalovirus (strain AD169)
C.Specides: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 31-Dec.1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
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A.Intross: 52/2: 121/3: 548/3
C:Superfamily: vacuolar protein sorting protein VPS45
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62.5%; Pred. No. 7;
iive 3; Mismatches (
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Best Local Similarity 62.5
Matches 5; Conservative
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1786 KPIVQYDNF 1794
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283 PIVOYDTF 290
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by totherical protein RP232 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: E71677
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: E7167
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-415 cAND>
A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14695.1; PID:g386
C;Genetics:
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
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A;Gene: RP232
C;Superfamily: Rickettsia prowazekii hypothetical protein RP232
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Pred. No. 12;
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C;Keywords: membrane-associated complex; NAD; oxidoreductase
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Pred. No. 34;
1; Mismatches
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77.8%;
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85.7%;
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Matches 7; Conservative
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Best Local Similarity
  11::: | | |
27 KPLLEVDNF 35
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39 KTIVQYANE 47
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206 PIVQHDN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Bacillus halodurans
C; Saccssion: B84062
R; Takami, H; Nakasone, K.; Takaki, Y; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A; Reference number: A83650; MUID:20263314
A; Accession: B84062
A; Accession: B84062
A; Accession: B84062
A; Reterences: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07017.1; GSPDB:GNOC
C; Genetics:
C; Genetics: Specimental source: strain C-125
C; Genetics: Specimental Source: strain C-125
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C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-oct-1999
C; Accession: D70153
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Reference number: A70100; MUID:98065943
A; Accession: D70153
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A;Residues: 1-129 <KLES
A;Cross-references: GB:AE001148; GB:AE000783; NID:g2688336; PIDN:AAC66810.1; PID:g268834
A;Experimental source: strain B31
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                       A;Cross-references: EMBL:299286; PIDN:CAB16542.1; GSPDB:GN00022; CESP:Y7A9C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BH3298 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                             Gaps
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Pred. No. 9;
3; Mismatches 1; Indels
                                                                                                                                                                                                 Length 544;
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Pred. No. 18;
2; Mismatches
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                                       A; Experimental source: clone Y7A9C
C; Genetics:
A; Genec ECSP: Y7A9C.1
A; Map position: 4
A; Introns: 27/1; 95/1; 296/3; 323/1; 391/3
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55.6%;
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66.7%;
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75.0%;
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
A; Residues: 1-544 <WIL>
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58 KPLVRIDNF 66
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808 PELQYDNF 815
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1 KPIVQYDNF 9

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hypothetical protein D - phage T4
C;Species: phage T4
C;Species: phage T4
C;Date: 16-Jul-1999
Esquence_revision 16-Jul-1999 #text_change 17-Nov-2000
C;Accession: T10155; T10156
E;Gacession: T10155; T10156
E;Gacession: T10155; T10156
E;Gacession: T10155
A;Title: Genes 55, alpha-qt, 47 and 46 of bacteriophage T4: the genomic organization A;Reference number: A91016; MUID:85257446
A;Accession: T10155
A;Accession: T10155
A;Accession: T10156
A;Residues: 1-264 GRA>
A;Accession: T10156
A;Residues: 38-264 GRA>
A;Accession: T10156
A;Essidues: 38-264 GRA>
A;Cross-references: EMBL:X01804; NID:g15229; PID:g15235
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Accession: B7272

A;Accession: B7272

A;Status: preliminary

A;Residues: 1-288

              A;Experimental source: clone C44B9
C;Genetics:
A;Gene: CESP:C44B9.4
A;Map position: 3
A;Introns: 22/3; 66/3; 190/3; 226/2; 320/1; 426/1; 470/1; 687/1; 756/3; 806/1; 867/1;
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iron-sulfur cluster-binding protein - Thermotoga maritima
c;Species: Thermotoga maritima
c;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: B72272
K;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hick Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                      68.0%;
ilarity 75.0%;
Conservative
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Matches 6; Conser
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881 PAVYYDNF 888
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C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S74561
B; Ranako, T: Sato, S:; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O; Kokumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
B; Takerence analysis of the genome of the unicellular cyanobacterium Synechocystis S. A; Reference number: S74322; MUID:97061201
B; A; Reference number: S74322; MUID:97061201
B; Status: nucleic acid sequence not shown; translation not shown
B; Status: nucleic acid sequence not shown; translation not shown
B; Residues: 1-512 ckan>
B; Residues: 1-512 ckan>
B; Residues: 1-512 ckan>
B; Rotoss-references: EMBL:D90900; GB:AB001339; NID:91651768; PIDN:BAA16713.1; PID:d101744
B; Rotos: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
G; Genetics:
B; A; Start codon: GTG
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Acces: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-oct-1999
C;Acces: 17-Jul-1998 #sequence number: Arguers, 3.; Barris, D.; Gordon, S;
A;Authors: Sqares, M; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Apostphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:9425987
A;Status: preliminar; nucleic acid sequence not shown; translation not shown
A;Residues: 1-512 CCOL>
A;Holecule type: DNA
A;Residues: 1-512 CCOL>
A;Holecule type: CCOL>
A;CLOSS-references: GB:295390; GB:AL123456; NID:93261766; PIDN:CAB08707.1; PID:e315866;
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A;Molecule type: DNA
A;Residues: 1-1204 <WLL>
A;Cross-references: EMBL:273424; PIDN:CAA97781.1; GSPDB:GN00021; CESP:C44B9.4
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C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C;Accession: T19918
R;McMurray, A.
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2; Mismatches
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Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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83 PVVSYDDF 90
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331 PVVRYDN 337
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                                                                         caenorhabdi
schizosacch
chlamydia t
                   streptococc
                           xylella fas
                                              bacillus su
                                                       euglena gra
caenorhabdi
                                                                                             saccharomyc
                                    klebsiella
                                                                                                       salmonella
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-9026039; PubMed-2161319;

MEDLINE-9026039; PubMed-2161319;

Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,

HOTSING I. T., Hutchison C. A. III, Kouzarides T., Martignetti J.A.,

Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;

"Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";

Cytomegalovirus strain AD169.";

Curr. Top. Microbiol. Immunol. 154:125-169(1990).

-: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-: SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
                                                                                                                                                                                                                                                                                                                 Lehner R , Meyer H., Mach M., Identification and characterization of a human cytomegalovirus gene coding for a membrane protein that is conserved among human
       P28321
Q54430
Q9pda6
Q48456
P54376
P54376
Q27516
Q09653
Q92370
P38850
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POTENTIAL.
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ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                Human cytomegalovirus (strain AD169).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GMYCOPROTEIN M.
GM OR UL100.
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                                                                                                                                   ALIGNMENTS
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         YKJ4_YEAST
SCRR_STRMU
CSD_XYLFA
YC10_KLEPN
GCS1_BACSU
YCX2_EUGGR
                                                                        YS24_CAEEL
TRPG_SCHPO
YHV4_YEAST
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Pfam; PF01528; Herpes_glycop; 1.
PRINTS; PR00333; HSVINTEGRLMP.
                                                                                                                                                                                                                                                                                                         MEDLINE-89342616; PubMed=2547996;
                                                                                                                                                                                                                                                                                                                                               herpesviruses.";
J. Virol. 63:3792-3800(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M28350; AAA45984.1; -. EMBL; X17403; CAA35336.1; -. PIR; S09865; QQBEJ7.
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caenorhabdi
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P13329 b
P13329 b
09mul6 m
09pq21 u
027520 c
P36370 p
P36370 p
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Q9zdu2
                  Compugen Ltd
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        4.5
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        GenCore version
Copyright (c) 1993 - 2000
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UL36_HCMVA
Y232_RICPR
CRK7_HUMAN
Y03E_BPT4
YCX3_MESVI
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YRV8_CAEEL
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YD34_METJA
VGLM_HSV6U
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SCRB_LACLA
YEJH_ECOLI
VEI_HPV03
NCPR_CANMA
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                             protein search, using
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.B., Kurland C.G.; The genome sequence of Rickettsia prowazekii and the origin of mitochomia."; Muture 396:133-140(1998).
                                Chee M.S., Bankker A.T., Beck S., Bohni R., Brown C.M., Cerny R., Chee M.S., Bankker A.T., Beck S., Bohni R., Martignetti J.A., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; Analysis of the protein-coding content of the sequence of human cytomegalovirus strain Immunol. 154:125-169(1990).

Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 476;
Pred. No. 6.3;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         EMBL; X17403; CAA35395.1; -.
PIR; S09799; S09799.
InterPro; IPR003360; US22.
Pfam; PF02393; US22; 1.
Hypothetical protein.
SEQUENCE 476 AA; 54981 MW; EDFFD4632CE0112C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN RP232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR0023372; Bac_P00_repeat.
Pfam; PF01011; Bacterial_P00; 6.
Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MADRID E;
MEDLINE-99039499; PubMed-9823893;
[1]
SEQUENCE FROM N.A.
MEDLINE=90269039; Pubmed=2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ235271; CAA14695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|:||||::
142 RPMVQYDDY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 5; Conserv
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Q9ZDU2;
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Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE STXBP/UNC-18/SEC1 FAMILY: STRONG, TO
YEAST VPS45.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
      56 N-LINKED (GLCNAC, .) (POTENTIAL).
113 N-LINKED (GLCNAC, .) (POTENTIAL).
42861 MW; F2F99BEC69BF8E32 CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C.
SPAC2G11.03C.
                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 558;
Pred. No. 2.8;
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                                                                                                       Score 39; DB 1; Length 372;
Pred. No. 1.1;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 254354; CAA91168.1; -.
InterPro; IPR001619; Sec1.
Pfam; PF00995; Sec1; J.
Hypothetical protein; Protein transport.
SEQUENCE 558 AA; 63551 MW; 2C138B7CDF5CFEA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UL36. HCMVA STANDARD; PRT; 476 AA. p16767; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) HYPOTHETICAL PROTEIN UL36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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62.5%;
                                                                                                                      78.0%;
87.5%;
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Best Local Similarity 8/...
Applied 7; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
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NCBI_TaxID=4896;
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nes 5; Conserv
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                       56
113
372 AA;
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283 PIVQYDTF 290
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Q09805;
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                              CARBOHYD
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-1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC2/CDKX SUBFAMILY.
                                                                Gaps
                                                                                                                                                                        CRK7_HUMAN STANDARD; PRT; 1490 AA.

20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
Rel. DIVISION CYCLE 2-RELATED PROTEIN KINASE 7 (EC 2.7.1.-) (CDC2-CRK7 OR KIAA0904.
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  "CRK7: a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                     Length 415;
                                                              0; Indels
46750 MW; EFAA3604D5B302B3 CRC64;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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                                    Score 34; DB
Pred. No. 14;
                                                            1; Mismatches
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam: PF00069; pkinase; I.
SMART: SM00220; S_TKC; I.
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99156230; PubMed=10048485;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 266-1262 FROM N.A.
                                    68.0%;
85.7%;
                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Pines J.N., Kelly E.;
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
415 AA;
                                    Query Match
Best Local Similarity
                                                                                                    1111:11
206 PIVQHDN 212
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                     2 PIVQYDN 8
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310 PGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQRSVSPYS
RRRS -> SSSRSRHSBISDVRLPLNSSLGAELSRKKKERA
AAAAAAAMDGKE (IN REF. 2).
639 G -> D (IN REF. 2).
745 R -> K (IN REF. 2).
1195 M -> T (IN REF. 2).
1195 M -> T (IN REF. 2).
1262 ACPPHILPP -> GRSWGGNAL (IN REF. 2).
AA; 164154 MW; 851E18DF3BD2B1A1 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 30.4 KDA PROTEIN IN AGT-GP55 INTERGENIC REGION (ORF D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage T4.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
T4-like phages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gram H., Rueger W.;
"Genes 55, alpha gt, 47 and 46 of bacteriophage T4: the genomic organization as deduced by sequence analysis.";
EMBO J. 4:257-264 (1985).
-i- SIMILARITY: TO PHAGE T4 MOBD AND Y04I.
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                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 1490;
Pred. No. 60;
3; Mismatches 0; Indels
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EMBL; X01804; CAA25939.1; ALT_INIT.
INTERPRO; IPR002711; HNH.
INTERPRO; IPR003615; HNH_nuc.
InterPro; IPR003647; Intron_nuc_1.
Pfam; PF01844; HNH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-85257446; Pubmed-4018026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO0507; HNHC; 1.
SMART; SMO0497; IENR1, 2.
EMPOCTHETICAL Protein.
SEQUENCE 264 AA; 30363 MW;
                                                                                                                                                                                                                                                                      68.0%;
62.5%;
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                      Query Match 68.0
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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68 KPLVEYDD 75
                                                                                  639
745
1195
1254
1490
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us-09-763-397a-9.rsp

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Best Local Similarity
Matches 5; Conserv
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"Isolation and expression of two cDNA clones encoding UDP-galactose epimerase expressed in guar endosperm.";
epimerase genes expressed in guar endosperm.";
submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-GIUCOSE = UDP-GALACTOSE.
-!- CATALYTIC ACTIVITY: UDP-GIUCOSE = UDP-GALACTOSE.
-!- PATHWAY: GALACTOSE METABOLISM AND BIOSYNTHESIS OF UDP-GALACTOSE AS PRECURSOR OF GALACTOLIPIOS AND CELL MALL POLYSACCHARIDES.
-!- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALACTOSE 4-EPIMERASE).

Cyamopsis terragonoloba (Guar) (Cluster bean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;

eurosids 1; Fabales; Fabaceae; Papilionoideae; Indigofereae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last amoctation update)
UDP-GLUCOSE 4-EPIMERASE GEP148 (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lemieux C., Otis C., Turmel M.; "Ancestral chloroplast genome in Mesostigma viride reveals an early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                           20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 30-4 KDA PROTEIN IN RPOZ-YCF20 INTERGENIC REGION.
Mesostigma viride.
                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 261;
Pred. No. 14;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F89E327F8810A074 CRC64;
       261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AA.
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NIES-296;
MEDLINE-20150907; PubMed-10688199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          branch of green plant evolution.";
Nature 403:649-652(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Chloroplast.
SEQUENCE 261 AA; 30378 MW; F89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF166114; AAF43882.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :11111 ::
252 RPIVQYSSY 260
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                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=41882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPIVQYDNF
                                                                                                                                                                                                                                            Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAEZ_CYATE
065781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyamopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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-i- CATALYTIC ACTIVITY: ATP + NICOTINATE RIBONUCLEOTIDE = DIPHOSPHATE + DEAMIDO-NAC!+).
-i- PATHWAY: DE NOVO BIOSYNTHESIS OF NAD.
-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE NADD FAMILY.
-i- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE YORO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
PROBABLE NICOTINATE-NUCLEOTIDE ADENYLYLTRANSFERASE (EC 2.7.7.18)
(DEAMIDO-NAD(+) PYROPHOSPHORYLASE) (DEAMIDO-NAD(+) DIPHOSPHORYLASE)
AUGOTINATE MONOUCLEOTIDE ADENYLYLTRANSFERASE) (NAMN
ADENYLYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
MCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01966; HD; 1.
SMART: SW00471; HDc: 1.
Transferase; NAD; Complete proteome.
DOMAIN
DOMAIN
SEQUENCE 392 AA; 46644 MW; 4897A34B2876725C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.0%; Score 33; DB 1; Length 350; llarity 62.5%; Pred. No. 19; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
Nature 407:757-762(2000).
                                                                                                           HSSP, P09147; IXEL.
Mendel; 29844, Cyate; 1265; 29884.
InterPro; IPRO01509; Epimerase.
Pfam; PF01370; Epimerase; 1.
Isomerase; NAD, Galactose metabolism; Multigene family.
NP_BIND 5 36
SEQUENCE 350 AA: 38772 ... NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SEROVAR 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE002143; AAF30881.1; -. InterPro; IPR002819; HD. InterPro; IPR003607; HDc. Pfam; PF01966; HD: 1.
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us-09-763-397a-9.rsp

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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus
                                                                                                                                                           an MHC-linked transporter.";
Nature 354:528-531(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.0
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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352
603
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78
120
169
205
297
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703 AA;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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532 EPLVQYDH 539
                   NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULES.
                                                                                                                                                                                                                                                                                                                                                haplotypes.
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TRANSMEM
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SEQUENCE
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VARIANT
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TAP1_RAT
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                                                         ö
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MANDOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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InterPro; IPR01128; Cyt_P450.
InterPro; IPR001128; Cyt_P450.
PRIATS: PR00067; P450.
PRINTS: PR00364; EP4501.
PROSTTE: PS00086: CYTOCHRONE_P450; 1.
Hypotherical protein; Oxidoreductase; Monooxygenase; Heme. BINDING 465 465 HEME (BY SIMILARITY).
SEQUENCE 519 AA; 60044 MW; 3AF37EDC43539D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 519;
                   Length 392;
                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gardner A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PUTATIVE CYTOCHROME P450 CYP13A1 (EC 1.14-.-).
              DB 1;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ABTGEN PEPTIDE TRANSPORTER 2 (APT2).
                                                                                                                                                                                                                                            519 AA
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                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 30;
1; Mismatches
                 Score 33;
Pred. No.
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              66.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match. 66.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
            Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                   CYP13A1 OR T10B9.8.
                                                                                                                       1 :: |||||
215 KHLISYDNF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||||||
92 VTQYDNF 98
                                                                                               1 KPIVQYDNF
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                                                                                                                                                                                                                                          YRV8_CAEEL
Q27520;
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P36372;
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TAP2_RAT
AD TAP2_RAT
DT AD372,DT 01-JUN
DT 01-JUN
DT 30-MAY.
DE ANTIGE
GN ABCB3 1
GN RETUS
OC EUKALYS
                                                                                                                                                                                                                       YRV8_CAEEL
                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                            SO DER REAL PROPERTIES OF STREET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 40:45-53(1994).
-!- FUNCTION: INVOLVED IN THE TRANSPORT OF ANTIGENS FROM THE CYTOPLASM
TO A MEMBRANE-BOUND COMPARTMENT FOR ASSOCIATION WITH MHC CLASS I
                                                            Powis S.J., Townsend A.R.M., Deverson E.V., Bastin J., Butcher G.W., Howard J.C.; Restoration of antigen presentation to the mutant cell line RMA-S by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBGUNIT: HETERODIMER OF TAP1 AND TAP2.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                    STRAIN-PVG-RT1L(LEW);
MEDLINE-94266341; PubMed-8206525;
Joly E., Deverson E.V., Coadwell W.L., Guenther E., Howard J.C.,
Butcher G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                   "The distribution of Tap2 alleles among laboratory rat RT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide transport; Transport; Transmembrane; ATP-binding; Polymorphism.

TRANSMEM 11 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
ATP (POTENTIAL).
V -> F (IN TAP2L).
K -> R (IN TAP2L).
W; E545993A8F784250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            725 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 42;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABC_trnsportr_tmem.
InterPro; IPR001687; ATP_CTP_A.
Pfam; PF00664; ABC_membrane; 1.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
SEQUENCE FROM N.A. MEDLINE-92100193; PubMed-1758495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X63854; CAA45339.1; -. EMBL; X75305; CAA53053.1; -. PIR; S19603; S19603.
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01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
30-MAY-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               34
45
48
103
106
112
151
154
157
201
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50 VTQYDNF 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IVQYDNF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAK1_CYPCA
Q09178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JAK1_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                            this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way undified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                  MULECLES.
- SUBUNIT: HETERODIMER OF TAP1 AND TAP2.
- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- SUBCELLUIAR LOCATION: THE APP-BINDING TRANSPORT PROTEIN FAMILY
- SIMILARITY: BELONGS TO THE APP-BINDING TRANSPORT
- (ABC TRANSPORTERS). MDR SUBFAMILY.
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
3FA7215D0AC22EE0 CRC64;
                                                                                                         MEDLINE-91080926; Pubmed-1979660;
Deverson E.V., Gow I.R., Coadwell W.J., Monaco J.J., Butcher G.W.
Howard J.C.;
                                                                                                                                       "MHC class II region encoding proteins related to the multidrug resistance family of transmembrane transporters."; Nature 348:738-741(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.0%; Score 33; DB Best Local Similarity 62.5%; Pred. No. 43; Matches 5; Conservative 3; Mismatches
      01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).
                                                                                                                                                                                                                                                                                                                                                                               EMBL; X57523; CAA40742.1; ALT_INIT.
EMBL; X10231; CAA71280.1;
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
InterPro; IPR00140; ABC_transportr.
InterPro; IPR00140; ABC_transportr_tmem.
InterPro; IPR001697; APC_Grambrane; 1.
Pfam; PF000064; ABC_Lran; 1.
SMARY; SM00382; AAA; II.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
137
184
225
318
                                                          Rattus norvegicus (Rat).
                                               ABCB2 OR TAP1 OR MTP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: || || :
544 EPLVQYDH 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KPIVQYDN 8
                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUOG_BUCAI
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TRANSMEM
TRANSMEM
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TRANSMEM
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NUOG_BUCAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ы
                                                                                                                                                                                                                                                         Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigenobu S., Matanabbe H., Hattori M., Sakaki Y., Ishikawa H.; Shigenobu S., Matanabbe H., Hattori M. Sakaki Y., Ishikawa H.; Genome sequence of the endocellular bacterial symbiont of aphids Buchnera Sp. APS.";
Buchnera Sp. APS.";
Buchnera Sp. APS.";
I. CAPALYIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
I. CAPALYIC ACTIVITY: NADH FE-4S. CLUSTER AND ONE 2FE-2S CLUSTER.
I. CAPACTOR: MAY BIND TWO 4FE-4S. CLUSTER AND ONE 2FE-2S CLUSTER.
I. SUBUNIT: COMPLEX OF 13 DIFFERENT SUBUNITS. SUBUNITS NUOCD, E, AND G CONSTITUTE THE PERIPHERAL SECTOR OF THE COMPLEX (BY SIMILARITY).
I. SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 180N-SULEUR (2FE-25) (POTENTIAL). | 180N-SULEUR (2FE-25) (POTENTIAL). | 45 | IRON-SULEUR (2FE-25) (POTENTIAL). | 180N-SULEUR (2FE-25) (POTENTIAL). | 103 | IRON-SULEUR (2FE-25) (POTENTIAL). | 110 | IRON-SULEUR (2FE-25) (POTENTIAL). | 111 | IRON-SULEUR (2FE-25) (POTENTIAL). | 154 | IRON-SULEUR (4FE-45) (POTENTIAL). | 154 | IRON-SULEUR (4FE-45) (POTENTIAL). | 157 | IRON-SULEUR (4FE-45) (POTENTIAL). | 157 | IRON-SULEUR (4FE-45) (POTENTIAL). | 103761 MW; Alchallocoby754 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NADH DEHYDROGENASE I CHAIN G (EC 1.6.5.3) (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWBL; AP001118; BAB12877.1; ...
Interpro; IPR001283; Complex1_75K.
Interpro; IPR001041; Ferredoxin.
Fran; PF00111; fer2; ...
FROSTE; PS00641; COMPLEX1_75K_1; 1.
PROSITE; PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_2; 1.
Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S; Complete protecome.
                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=TOKYO 1998;
MEDLINE=20445173; Pubmed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Gaps

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                                                                                                                                                                                                                                                                                               EHOLLHUMAN STANDARD; PRT; 1259 AA.
P48531 094742; 020mD4;
01-FRE-1996 (Rel. 33, Created)
20-MCG-2001 (Rel. 40, Last sequence update)
EPILEPSY HOLOPROSENCEPHALY CANDIDATE-1 PROTEIN (EHOC-1) (TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-97339461; PubMed-9196060;
Magamine K., Kudoh J., Kawasaki K., Minoshima S., Asakawa S., Ito F.,
Shimizu N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamakawa K., Mitchell S., Hübert R., Chen X.-N., Colbern S.,
Huo Y.-K., Gadomski C., Kim U.-J., Korenberg J.R.;
"Isolation and characterization of a candidate gene for progressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic organization and complete nucleotide sequence of the TMEM1 gene on human chromosome 21q22.3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 198:313-321(1997).
-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED.
-1- DISEASE: CANDIDATE FOR AUTOIMMUNE POLYGLANDULAR DISEASE TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; HominIdae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS GLU-257; MET-633 AND MET-726. MEDILINE-98036064; PubMed-9370297;
Lafreniere R.G., Ribar Z., Rochefort D.L., Han F.-Y., Fon E.A., Dube M.-P., Kang X., Baird S., Korneluk R.G., Rommens J.M., Rouleau G.A.,
                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE TMEM1 FAMILY.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 1187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic structure of the human GT334 (EHOC-1) gene mapping
                              Score 33; DB 1; Length 1156;
Pred. No. 73;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene on humán chromosome 21q22.3.";
Biochem, Biophys. Res. Commun. 235:185-190(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U19252; AACSO134.1; ALT_FRAME.
EMBL; ABO01523; BAA21099.1; -.
EMBL; U61500; AAC51826.1; -.
EMBL; U61501; AAB58468.1; -.
EMBL; U61501; AAB58468.1; JOINED.
EMBL; U61502; AAB58468.1; JOINED.
EMBL; U61503; AAB58468.1; JOINED.
EMBL; U61503; AAB58468.1; JOINED.
EMBL; U61504; AAB58468.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
MEDLINE=95359979; PubMed=7633421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myoclonus epilepsy on 21q22.3.";
Hum. Mol. Genet. 4:709-716(1995).
                              66.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GT334 PROTEIN).
                                                                              Conservative
                                                     Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                        489 RPVPOYKNF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                              1 KPIVQYDNF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TMEM1 OR EHOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APECED)
                                 Query Match
                                                                                                                                                                        QQ
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROTEIN KINASE 1.
PROTEIN KINASE 1.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FYSHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H HSSP; PI1362; IEGI.

R InterPro: PR000299; Band_4.1.

R InterPro: PR000299; Band_4.1.

R InterPro: PR000299; Band_4.1.

R InterPro: PR000299; Band_4.1.

R InterPro: PR000295; B41.

R NART; SM00295; B41.

R SMART; SM00295; B41.

R SMART; SM00295; B41.

R SMART; SM00295; B41.

R PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS50011; PROTEIN_KINASE_NEG.

M Transferaes Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                         DNA CELJ BIOL.

-1- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE IFN-ALPHA/BETA/GAWMA SIGNAL PATHWAY. KINASE PARTNER FOR THE INTERLEUKIN (1L)-2 RECEPTOR (BY SIMILARITY).

-1- CATALITIC ACTIVITY: APP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

-1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSCIATED (BY SIMILARITY).

-1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALITIC DOMAIN (BY SIMILARITY), WHILE THE PROBABLY CONTAINS THE CATALITIC DOMAIN (BY SIMILARITY).
TYROSINE-PROTEIN KINASE JAKI (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1).
                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97047914; PubMed-8892755;
Chang M.S., Chang G.D., Leu J.H., Huang F.L., Chou C.K., Huang C.J.,
                                                  Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinidae; Cyprinidae;
CKBI_TaxID=7962;
                                                                                                                                                                                                                                                                                               "Expression, characterization, and genomic structure of carp JAKI
kinase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
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257 257 V -> E.

633 633 I -> M FREQUESTA.

726 726 V -> M FREQUEST POLYMORPHISM).

726 726 V -> M FREQUEST POLYMORPHISM).

727 114 114 V -> M FREQUEST 3; AAB58468).

728 121 121 V -> A (IN REF. 3; AAB58468).

739 813 Y -> D (IN REF. 1).

740 910 K -> Q (IN REF. 3).

750 11559 AA; 142188 MW; E8AB6847050CFEOC CRC64;
EMBL, U61505, AABS8468.1; JOINED.
EMBL, U61506, AABS8468.1; JOINED.
EMBL, U61508, AABS8468.1; JOINED.
EMBL, U61508, AABS8468.1; JOINED.
EMBL, U61509, AABS8468.1; JOINED.
EMBL, U61510; AABS8468.1; JOINED.
EMBL, U61511, AABS8468.1; JOINED.
EMBL, U61512, AABS8468.1; JOINED.
EMBL, U61513, AABS8468.1; JOINED.
EMBL, U61514, AABS8468.1; JOINED.
EMBL, U61514; AABS8468.1; JOINED.
EMBL, U61515; AABS8468.1; JOINED.
EMBL, U61516; AABS8468.1; JOINED.
EMBL, U61519; AABS8468.1; JOINED.
MIRN GOZJOJ.

POLYMOTPHISM.
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Gaps

111111 774 PIVQYD 779 2 PIVQYD 7 ò qq

Search completed: January 29, 2002, 11:13:40 Job time: 816 sec

us-09-763-397a-9.rspt

Perfect score: Sequence: Scoring table:

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09prb4 ureaplasma
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09rc01 pseudomonas
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09rc1 bacilius ha
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09vu3 drosophila
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098rb6 caenorhabdi
099rh4 sphaerechin
09m1 deishmania
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STRAIN-FCCI/(N.)
STRAIN-FCCI/(N.)
Shan Z.X., Yu X.B., Li X.R., Ma C.L.;
Shan Z.X., Yu X.B.,
"Molecular cloning and structure of the 3' terminal of liver stage antigen-1 gene of Plasmodium falciparum isolate FCCI/HN.";
submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF246996; AAG12124.1; -.
EMBL; AF246996; AAG12124.1; -.
EXQUENCE 264 AA; 31006 MW; 1714D653EBD9D1D7 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN-1 (FRAGMENT).
Flasmodium falciparum.
Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 50; DB 5; Length 264; 100.0%; Pred. No. 0.025; Live 0; Mismatches 0; Indels
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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MEDIJNE-56(05765; PubMed=7477115;
Amada C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Fange C., Shi Y.P., Udhayakumar V., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
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STRAIN-KENTAN,
MEDLINE-96065765; PubMed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.,
"Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates."
Mol. Biochem. Parasitol. 71:291-294(1995).
EMB. 140887; AAC41597.1; -
SEQUENCE 280 AA; 32882 MW; 46763641C81AFC33 CRC64;
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             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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EMBL, L40886; AABS9232.1; -. INON_TER
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Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field hol. Biochem. Parasitol. 71:291-294(1995).
PRUE: L40884; AAB5920.1; -.
SEQUENCE 280 AA; 32926 MW; 467080F32FAEAD33 CRC64;
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MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
Wang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates:
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID~5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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MBL. L40885; AAB59231.1; -.
NON TER
SEQUENCE 280 AA: 32940 MW; E9708E3CFFAEA9CF CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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Plasmodium falciparum.
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                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                         STRAIN-KENYAN;
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                      STRAIN-KENYAN;
MEDIATRS-96662765; PubMed=7477115;
MEDIATRS-96662765; PubMed=7477115;
MEDIATRS-96662765; PubMed=7477115;
Rang C., Shi Y. P., Udhayawkunar V., Alpers M.P., Povoa M.M.,
Rawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
Mol. Blochem. Parasitol. 71:291-294(1995).
BMBL: L40890; AAC41600.1;
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MEDLINE-96065765; PubMed=7477115;
MEDLINE-96065765; PubMed=7477115;
MEDLINE-91065765; PubMed=7477115;
MEDLINE-96065765; PubMed=7477115;
MEDLINE-911 Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
"Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 71:291-294(1995).
EMBL: L40891; AAC41601.1;
BMD. TER
SEQUENCE 280 AA; 32989 WW; E96F812CFFREEED8 CRC64;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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100.0%; Score 50; DB 5; Length 280; Best Local Similarity 1100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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SEQUENCE FROM N.A.
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Q25850;
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                                                SEQUENCE FROM N.A.
MEDILINE-96065765; Pubbmed=7477115;
MEDILINE-96065765; Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-
specific avtigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
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MEDIZINE-96065765; Pubbmed-7477115;
MEDIZINE-96065765; Pubbmed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Flawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
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AC 025849;
DT 01.NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 01, Created)
DT 01-NOV-1998 (TrEMBLrel. 01, Last sequence update)
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DT 01-NOV-1998 (TrEMBLrel
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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100.0%; Score 50; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels
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SEQUENCE 280 AA; 32944 MW; 467085E23BABBC27 CRC64;
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EMBL; L40888; AAC41598.1; -.
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EMBL; L40889; AAC41599.1; -.
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SEQUENCE
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STRAIN-KENYAN;
MEDIATE-8065765; PubMed-7477115;
MEDIATE-8065765; PubMed-7477115;
Ang C., 26065765; PubMed-7477115;
Hawley W.A., Collins W.E., Lal A.A.; Little regions of the liver stage-specific artiagen-1 (LSA-1) of Plasmodium falciparum from field isolates.";

isolates.";

isolates.";
                    Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M., Hawley W.A., Collins W.E., Lal A.A.; "Sequence variations in the non-repetitive regions of the liver stagespecific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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SEQUENCE FROM N.A.
MEDLINE=96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
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Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                      Mol. Blochem. Parasitol. 71:291-294(1995).
BEME, 140835, AAB59234.1; -.
NON_TER 180 AA, 32938 MW; 46751C45F4DCBD33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA; 32966 MW; 61851C5AD6E1A211 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
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EMBL; L40836; AAC41604.1; -.
NON_TER
SEQUENCE 280 AA; 32966 WW; 61851C5AD6E
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     MEDLINE=96065765; PubMed=7477115;
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Q25854;
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STRAIN=KENYAN;
MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
Hawley W.A., Collins W.E., Lal A.A.;
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.';
Mol. Biochem. Parasitol. 71:291-294(1995).
EMBL: L40893; AAC416093.1; -.
SEQUENCE 280 AA; 32927 MW; 48706EPDCF40ADD3 CRC64;
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MEDIJNE=96065765; Pubmed=7477115;
MEDIJNE=96065765; Pubmed=7477115;
MEDIJNE=96065765; Pubmed=7477115;
MA., Collins W.E., Lal A.A.;
Mayer W.A., Collins W.E., Lal A.A.;
Sepenence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.;
MOL. Blochem. Parasitol. 71:291-294(1995).
MOL. TER
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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Q25853;
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025853
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025853
AC 025853
DT 01-NOV
DT 01-NOV
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OS PLASMO
OS PLASMO
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RN [1]
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025852
AC 025852
AC 025852
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DT 01.NOV
DT 01.NOV
DE 1.1VER
GN 1.58A-1.
OX NCBL_T
RN 1.58A-1.
OX NCBL_T
RN 1.5A-1.
RN 1.19
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STRAIN-BRAILLIAN;
MEDILINE-56065765;
PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.;
Mol. Blochem. Parasitol. 71:291-294(1995).
EMBI. 140909; AAB59229.1;
SEQUENCE 280 AA; 32850 MW; FDEE929F34DF68E9 CRC64;
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.;
Mol. Blochem. Parasitol. 71:291-294(1995).
EMBL: L40837; AAC41605.1; -.
SEQUENCE 280 AA; 32866 MW; 73164A709789DD31 CRC64;
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COSB89;
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CONOV-1996 (TrEMBLrel. 01, Last sequence update)
COLNOV-1998 (TrEMBLrel. 08, Last annotation update)
CIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
FLASH-1.
FLASH-1.
EURARYOCIA: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
EURARYOCIA: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 50; DB 5; Eength 280; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 9; Conservative 0; Mismatches 0; Indels
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157 KPIVQYDNF 165
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722889
AC 022889
AC 025889
DT 01.NOV
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CON NCBL_TASMO
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protein - protein search, using sw model

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Scoring table:

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US-09-763-397A-10

Title: Perfect score:

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S. epidermidis ope
Arabidopsis thalia
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Human CBT encoded
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Arabidopsis thalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elvin J, Gotch FM, Hill AV, McMichael AJ, Whittle HC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTL; vaccine; malaria; specific antigen-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
 AAG28610
AAG28609
AAG28609
AAG28609
AAG23106
AAG23106
AAG26206
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92GB-0017704.
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   04-MAY-1994 (first entry)
 WPI; 1993-336833/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1993;
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20-AUG-1992;
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   AAR43244;
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P. falciparum live
Peptide from P.fal
Amino acid sequenc
Cytotoxic T lympho
Plasmodium falcipa
Amino acid sequenc
Recombinant vaccin
P.falciparum LSA g
Novel bone marrow
Arabidopsis thalia
                                                                                                 January 29, 2002, 10:21:44; Search time 310.82 Seconds (without allyoments) 1.907 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Carbos | Carbon | C
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                         522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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AAR43244
AAR78842
AAW5465
AAW5465
AAX0361
AAX70286
AAX70278
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25.44.32 27.44.32 27.44.32 27.44.33 27.44.33

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DB

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxxirus vector; PVV; pathogen; tumour; malaria; parasite; P, falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The peptides AAW54559-W54809 are examples of peptides to which at least 1 (preferably 2) mannose can be attached to increase their uptake as antigens by antigen-presenting cells. Uptake of agonist mannosylated peptides by a considerable of a cell response, whereas uptake of antagonist peptides will increase the T cell response, whereas uptake of antagonist autoantigens can be used in treatment of type I diabetes, rheumatoid arthritis, graft rejection etc., also to induce T cell nor responsiveness. Vaccines containing mannosylated antigen are used to prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths and parasites.
                                                                                                                                                                                           Mannose; antigen; antigen-presenting cell; mannosylated peptide; {\tt T} cell; vaccine; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing uptake and presentation of antigen(s) - by adding mannose residue(s) to antigen for increasing T cell response, useful in, e.g. vaccines against viral infection(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                             Peptide from P.falciparum LS 1850-1857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 29; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY03661 standard; peptide; 8 AA.
                               AAW54665
ID AAW54665 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                   97WO-NL00536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koning F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-230631/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KPNDKSLY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drijfhout JW,
                                                                                                                                                                                                                                                                                             WO9813378-A1.
                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1996;
                                                                                                                           25-SEP-1998
                                                                                                                                                                                                                                                                                                                                 02-APR-1998.
                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY03661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                         AAW54665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAY03661
ID AAY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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                               The sequence is that of peptide ls8 which is recognised by, or can induce, cytotoxic T lymphocytes. It may be useful in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an antiquen (Ag) in a mammal comprises, a CTL Ag response inducing peptide (i.e. AAR7884-R78853) and a lipid conjugated helper T cell inducing peptide. The compsn. induces a CTL response to bacterial, viral or tumour Ags, and is therefore useful in the treatment and prevention of diseases associated with the Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g. hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. falciparum liver Ag 1850-1857 cytotoxic T lymphocyte epitope.
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                                                                                                                                                                 Length 8;
                                                                                                                                                                                                     Indels
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100.0%; Score 44; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                               100.0%; Score 44; DB 14;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitiello MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 17; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                     AAR78842 standard; peptide; 8 AA.
Claim 6; Page 30; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sette AD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-302545/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                                              8 AA;
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                                                                                                                                                                                                                                          1 KPNDKSLY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1996
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                                                                                                            Sequence
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WO200049041-A1.
              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                             protective CD8+ T-cell immune response against at least one target antigen. The kits of the invention comprises (1) as priming composition, a source of one or more CD8+ T-cell [cyttotoxic T lymphocytes-(CTL)] cepitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (1), with this source being a non-replicating or replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in (1) is a viral vector, then the vector in (11) is from a different virus. The kits are used to generate an immune ceponacy (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria parasites such as P. falciparum, or HIV, and also many other bacterial, viral or parasitic pathogens. The kits are also used for protective response against melanoma and cancer of breast or colon, and generally wherever a strong CD8+ response is protective. CT he boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster cffect, better than that from wild-type poxvirus, resulting in complete crather than partial protection against sporozoite challenge. Also PVV are setting epitopes of the malaria (M) string.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                         Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL; Immune response; infectious disease; malaria; cytotoxic T cell; CytoStatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.
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                                                                                                                                                                                                                                                                                                                   The invention relates to methods and reagents for generating a
                                                                                                                                                               Hill AVS, McMichael AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 44; DB 20;
100.0%; Pred. No. 4.3e+05;
tive 0; Mismatches 0;
                                                                                                                                                               Hanke T, I
Smith GL;
                                                                                                                                                                                                                                                                                          Claim 38; Page 18; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB23657 standard; Peptide; 8 AA.
                                                                                     98WO-GB01681
                                                                                                               97GB-0011957.
                                                                                                                                       (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                           Schneider J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
           Plasmodium falciparum.
                                                                                                                                                               Gilbert
                                                                                                                                                                                                   WPI; 1999-070325/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                 N-PSDB; AAX29201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA;
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                                   WO9856919-A2
                                                                                                                                                               Blanchard T,
Plebanski M,
                                                                                     09-JUN-1998;
                                                             17-DEC-1998
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The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by yttotoxic T cells and a protein containing the Arpase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed CTL epitope for use in a fused protein of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                    (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 53; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                             Yu1 K;
                                                                         18-FEB-2000; 2000WO-JP00941.
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Best Local Similarity 100.0
---- 8; Conservative
                                                                                                                                                                                                                                                                                                             Shinbara N, Udono H,
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                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-543748/49.
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                                                                                                                                                      19-FEB-1999;
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24-AUG-2000
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The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The kits of the invention comprises (1) as priming composition, a source of one or more CD8+ T-cell (cyctoxic T lymphocytes-(CTL)) epitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (1), with capture post proceeding a non-replicating or replication-impaired recombinant povarius vector (PVV) plus a carrier of the source of CTL epitopes in (i) is a vizal vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria parasites such as P. falciparum, or HIV, and also many other bacterial, carponse against melanoma and cancer of breast or colon, and generally response against melanoma and cancer of breast or colon, and generally merever a strong CD8+ response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than that confid-type poxvirus, resulting in complete rather than partial protection against sporozoite challenge. Also PVV are safer to use than
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; merozoite surface protein-1; MSP-1; merozoite surface protein-1; MSP-1; EBA-1175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pf927; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody; honey bea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Generating CD8-positive T cell response to target antigen using recombinant poxvirus – for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV
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23...50
1...5bl= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
  Smith GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                              Example 1; Page 20; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
  Schneider J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2000 (first entry)
                                                 WPI; 1999-070325/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11111111
29 kpndksly 36
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Plebanski M,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the antigenic epitope P596, derived from liver stage antigen-1 (LSA-1) of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (H185) 6 tag.

T-cell epitope from tetanus toxoid and 21 antigenic epitopes from clircumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), Hive stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27, These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial frections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                         Novel recombinant protein as vaccine for treating malarial infection comprises autigenic peptides obtained from different stages of plasmodium falotparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 44; DB 21; Length 8; Best Local Similarity 100.0%; Pred. No. 4.3e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of the malaria (M) string CTL epitope.
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                                                                                                                         USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY03681 standard; protein; 229 AA
                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 17; 52pp; English.
                                                                                                                                                                          Lal AA, Shi YP, Hasnain SE;
                                                 98US-0097703.
99WO-US18869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-GB01681,
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                                                                                               (NAIM-) NAT INST IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1999 (first entry)
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                                                                                                                                                                                                                        WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KPNDKSLY 8
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19-AUG-1999;
                                           21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39-JUN-1997;
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Nucleic acids encoding bone marrow polypeptides, useful in diagnostic
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epitope
with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xue AJ;
                                                                                                                                                                                                       Polypeptide(s) derived from liver stage of Plasmodium falciparum - for vaccination against, treatment of and diagnosis of malaria
                                                                                                                                                                                                                                                                              The 3' part of the P.falciparum liver-stage specific antigen (Ligene codes for a polypeptide sequence which carries a T cell epicharacteristic of a protein produced in hepatocytes infected with P.falciparum. The polypeptide can be used in the preparation of vaccines against malaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 13; Length 493;
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                   Druilhe P, Guerin-Marchand C, Guerinmarchand C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bone marrow polypeptide #126.
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                                                                                                                                                                                                                                                        Claim 2; Fig 8-10; 81pp; French.
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20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
30-NOV-2000; 2000US-0250683.
              92WO-FR00104.
                                                91FR-0001286
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Best Local Similarity 100.
است 8; Conservative
                                                                                  PASTEUR
                                                                                                                                                 WPI; 1992-299985/36.
N-PSDB; AAQ28119.
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Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488875/53.
N-PSDB; AAS23032.
                                                                                                                                                                                                                                                                                                                                                                                                   493 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 kpndksly 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KPNDKSLY 8
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                05-FEB-1992;
                                                05-FEB-1991;
                                                                                  (INSP ) INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (RAP-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Fig27. These epitopes were obtained at different stages of the life cycle of altsmodium falciparum CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                          Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria; hepatocyte; sporozoite; T-cell epitope; B-cell epitope;
paludism; liver stage-specific antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 350;
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/label= repetitive_region
214..493
/label= non-repetitive_region
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100.0%; Pred. No. 0.7
:ive 0; Mismatches
                                                                                                                                                   (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                              plasmodium falciparum life cycle
                                                                                                                                                                                                       Shi YP, Hasnain SE
                                                                                 99WO-US18869.
                                                                                                                   98US-0097703
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                      WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 AA;
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                                                                                                                                                                                                                                                        N-PSDB; AAZ51336
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              WO200011179-A1.
                                                                                 19-AUG-1999;
                                                                                                                   21-AUG-1998;
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                                              02-MAR-2000
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Key Region Region

AAR26944 RESULT

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9905-0134370
9905-013476
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9905-0135124
9905-0135629
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9905-0136021
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9905-0137528
9905-0137528
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990S-0138847
990S-0139453
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990S-0140933
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990S-0132485.
990S-0132486.
990S-0132863.
990S-0132863.
990S-0134218.
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99US-0142920.
99US-0142977.
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99US-0143624.
99US-0144005.
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990S-0144086.
990S-0144325.
990S-0144331.
990S-0144333.
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10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
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29-JUN-1999;
30-JUN-1999;
01-JUL-1999;
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18 - MAY - 1999;
19 - MAY - 1999;
20 - MAY - 1999;
21 - MAY - 1999;
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03-JUN-1999;
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07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999;
AND ANUL4602-ANUL4794 represent novel bone marrow polypeptides of the invention. The proteins and corresponding coding sequences may be used in the prevention, diagnosis and treatment of diseases associated with cinappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by rectifying mutations core depetions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the patient's own production of the polypeptides. Additionally, the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients and in assays to dientify modulators of their expression and activity.

The anti-bone marrow protein antibodies and antagonists may also be used as and an assays to identify modulators of their expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the protein is amples.

Co down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the protein is amples.

Co down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the protein is amples.

Co down regulate haematopoiesis activity, and consequently in the treatment of myelold or lymph cell disorders; in tissue regeneration, and be used to regulate haematopoiesis activity, and consequently in the treatment of myelold or lymph cell disorders; in tissue regeneration, and activity as an untititional supplement, and in treatment of immune disorders such as severe combined immunodeficiency (SCID).
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85.7%; Pred. No. 42;
1.ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 33894.
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                               Claim 10; Page 133; 392pp; English.
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990S-0123180.
990S-0125788.
990S-0126264.
990S-0126785.
990S-0128234.
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Best Local Similarity 85.7
Matches 6; Conservative
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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|140 pndkmly 146
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Pred. No. 52;
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28-Jul. 1999;
38-Jul. 1999;
39-Jul. 1999;
30-Aug. 1999;
31-Aug. 1999;
32-Aug. 1999;
33-Aug. 1999;
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ö ö This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating thelicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptit ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis. GHPO protein, Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease. New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Gaps Gaps .; 0 ö Query Match 77.3%; Score 34; DB 19; Length 380; Best Local Similarity 75.0%; Pred. No. 77; 77; Matches 6; Conservative 1; Mismatches 1; Indels Length 275; 1; Indels Tomb Oomen RP, (HUMA-) HUMAN GENOME SCI INC. (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. DB : Mismatches Claim 8; Page 1749-1751; 2054pp; English. Al-Garawi A, Kleanthous H, Miller C, Score 34; Pred. No. AAW98800 standard; Protein; 380 AA. 99US-0161405. 99US-0161406. 99US-0161359. 99US-0161361. 99US-0161920. 99US-0161922. 99US-0161993. 97US-0902615. 97US-0833457. 97US-0881227. 98WO-US06371. Match 77.3%; Local Similarity 85.7%; les 6; Conservative H. pylori GHPO 1287 protein. 31-MAR-1999 (first entry) WPI; 1998-542293/46. N-PSDB; AAX14519. Helicobacter pylori. 380 AA; 177 pndkmly 183 2 PNDKSLY 8 25.0CT-1999; 25.0CT-1999; 26.0CT-1999; 26.0CT-1999; 26.0CT-1999; 28.0CT-1999; 28.0CT-1999; W09843478-A1. 01-APR-1998; 29-JUL-1997; 01-APR-1997; 24-JUN-1997; 08-OCT-1998. AAW98800; Seguence Query Mai Best Loca Matches RESULT 1 g

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[4] In Ingth CDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide expension of the complementary strand of a polynucleotide which complementary in the specification, where the complementary strand of a polynucleotide sequence conformation of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 5'-end sequence and an oligonucleotide comprision of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or alagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and ANAS are present human annon acid sequences; AAB9346 to AAB936891 represent human annon acid sequences; AAB9346 to AAB936891 represent human annon acid sequences; and AAB13629 to AAB13620 complement of the complement of the exemplification considered on the assemblied of the complement 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 (ull-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs .
                                                                                                                                                                                                                                                                                                                                             Human: primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:11968.
                                                                                                                                                        AAB93106 standard; Protein; 903 AA.
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09-JUN-2000; 2000JP-02418997.
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App Appl Appl Appl Appl

Sequence Sequence Sequence Sequence

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APPLICANT: Adrian V.S. Hill, et al.
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
US-08-485-886-45
US-08-485-886-60
US-08-485-886-66
US-08-485-886-203
US-08-487-362-45
US-08-477-362-66
US-08-477-362-67
US-08-477-362-67
US-08-477-134-65
US-08-477-134-60
US-08-477-134-60
US-08-477-134-60
US-08-477-134-60
US-08-477-134-60
US-08-477-134-67
US-08-477-134-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPEFFECT 5.1+
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263-PPIR1577US
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CB93/007111
FILING DATE: April 5, 1993
ATTORNEY/AGRAT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO PCT/GB93/00711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-820
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08318856A Patent No. 5972351
GENERAL INFORMATION:
                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
    0000000000000000000
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RY: U.S.A.
20006
    RESULT 1
US-08-318-856A-2
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                                                                                                             ; Search time 133.18 Seconds (without alignments) 1.352 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, 1
Sequence 56, 1
Sequence 201,
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Sequence 1, 1
Sequence 1, 1
Sequence 2, 1
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Sequence 45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Seq
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Sequence 6
Sequence 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/FOTUS_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-08-318-856A-45
US-08-318-856A-45
US-08-318-856A-45
US-08-318-856A-45
US-09-092-409-56
US-09-092-409-56
US-09-139-802-201
US-07-749-541A-4
US-08-27-327-1
PCT-US95-03323A-2
US-08-25-477B-9
US-08-25-477B-9
US-08-533-669A-6
US-08-533-669A-6
US-08-533-669A-6
US-08-533-669A-6
US-08-533-699A-6
US-08-475-263-67
US-08-475-263-67
US-08-475-263-67
US-08-475-263-67
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                             January 29, 2002, 10:24:04
                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 sw model
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Gapop 10.0 , Gapext 0.5
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                                                                               · protein search, using
                                                                                                                                                                   US-09-763-397A-10
                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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Match 1
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Perfect score:
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No.
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Patent No. 5972351
GENERAL INFORMATION:
APLICAMT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIDARUM MHC CLASS ITTLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2031 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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100.0%; Score 44; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4

US-07-912-015-2

Sequence 2, Application US/07912015

Sequence 2, Application US/07912015

Patent No. 5283191

GENERAL INFORMATION:
APPLICANT: Wolfan, Robin Wilson
APPLICANT: Claessens, Johannes Antonius Joseph
APPLICANT: Claessens, Johannes Antonius Joseph
APPLICANT: Sondermeijer, Paulus Joseph
APPLICANT: Sondermeijer, Paulus Joseph
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READELE FORM:
MEDIIM TYPE: Floppy disk, 3.5 inch, 1.44 mb COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIGN SYSTEM: PC-DS_MS-DOS SOFTWARE: WORDPERCH 5.14
CURRENT APPLICATION NUMBER: US/08/318,856A
PRIOR APPLICATION DATE: OCLOBER 3, 1994
RILING DATE: APPLICATION DATA: APPLICATION NUMBER: GB 92 17 704.7
RILING DATE: APPLICATION DATA: APPLICATION NUMBER: GB 92 17 704.7
RILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: APPLICATION NUMBER: MO PCT/GB93/00711
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Organion Teknika Corporation
ADDRESSEE: Biotechnology Research Institute
STREET: 1330-A Piccard Drive
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY, CALCADANA IN AN ANABER A 40,949
REGISTRATION NUMBER: 263-PPIR1577US
REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ 1D NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTR: 9 amino acid residues
TELECOMMUNICATION acid residues
TELECOMMUNICATION acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-318-856A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KPNDKSLY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING TITLE OF INVENTION: CTL IMMUNITY NUMBER OF SEDURNCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS.DOS SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version will release #1.0, Version William APPLICATION DATE: PCT/USS5/02121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 44; DB 5; Length 8; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                       Ouery Match 100.0%; Score 44; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1.0e+06; Matches 9; Conservative 0; Mismatches 0; Indels Matches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-ARR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 13,990
REDERRANGE/POCKET NUMBER: 14137-26-4P
TELECOMMUNICATION NUMBER: 131,990
REDERRANGE/POCKET NUMBER: 14137-26-4P
TELECOMMUNICATION INFORMATION:
TELEBHOME: (206) 467-9600
TELEBHOME: (206) 467-9600
TELEBHOME: (415) 543-5043
INFORMATION FOR SED ID NO: 19:
SEQUENCE CHARACTERISTICS:
FENCETAL
                                                                                                                                                                                                                                                                                                                                    RESULT 2
PCT-0495-02121-19
FCT-0495-02121-19
Sequence 19, Application PC/TUS9502121
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-318-856A-45
; Sequence 45, Application US/08318856A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown ; MOLECULE TYPE: peptide PCT-US95-02121-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 8 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KPNDKSLY 8
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US-09-092-409-56
US-09-092-409-56
; Sequence 56, Application US/09092409
; Patent No. 6159478
; GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
sTREET: 1700 Lincoln Street, Suite 3500
                                                                                                                             DB 1; Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 364;
54;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.7%; Score 32; DB 62.5%; Pred. No. 54; tive 1; Mismatches
                                                                                                                                                                      1; Mismatches
                                                                                                                             Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION ONTELN. 05/00/02/100
ELASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-023
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERIFICS: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-139-802-201
; Sequence 201, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
                                                                                                                         Ouery Match 72.7%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 364 amino acids
amino acid
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Best Local Similarity 62.5
Matches 5; Conservative
  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-680-726A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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US-08-680-726A-56
Sequence 56, Application US/08680726A
Sequence 56, Application US/08680726A
Patent No. 5804197
GENERAL INFORMATION:
APPLICANT: Hannes, Elizabeth J.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATPORTENT NUMBER: US/08/680,726A
FILING DATE: 12-JUL-1996
ATPORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
TELEPHONE: (303) 863-9770
TELEPHONE: (303) 863-9770
TELEPHONE: (303) 863-923
INFORMATION FOR SEO ID NO: 56:
SEQUENCE CHARACTERISTICS:
TENDONE 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912,015
                                                                                                                                                                                            APPLICATION:
FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,211
FILING DATE: 16 NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: DONNE BOOMDE BOLOWICZ
REGISTRATION NUMBER: 32,196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (30.1258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 663 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-912-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
Maryland
(: U.S.A.
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| 99 KPDDKLLY 106
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                                                                                                                                                                                                         70.5%; Score 31; DB 1; Length 45; ilarity 71.4%; Pred. No. 8.3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An Anti-HIV Protein, TAP 29, From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/275,327
FILING DATE:
APPLICATION NUMBER: US/07/966,600
FILING DATE:
APPLICATION NUMBER: US/07/685,126
FILING DATE:
ATTORNEY/AGANT: CHANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Litrat, Shuuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: LEE-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-5197
TELEFAX: (202)737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-275-327-1
; Sequence 1, Application US/08275327
; Patent No. 553214
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lee Huang, Sylvia
APPLICANT: Huang, Philip L.
APPLICANT: Rung, Hsiang-fu
APPLICANT: Huang, Paul L.
APPLICANT: Huang, Peter
APPLICANT: Huang, Henry I.
APPLICANT: Chen, Hao-chia
TITLE OF INVENTION: An Anti-HIN
UNDERS OF SEQUENCES:
ADDRESSE: ADDRESS:
ADDRESSE: Browdy and Naimath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-275-327-1
TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                      ; NAME/KEY: TAP 29
US-07-749-541A-4
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  11:1 11
26 PNEKKLY 32
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                                                         FEATURE:
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   APPLICANT: Pasqualli, EIKK1
APPLICANT: Pasquallin, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
TITLE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1938-08-25
FARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1939-09-10
EARLIER APPLICATION NUMBER: 08/710,067
EARLIER PILING DATE: 1936-09-10
NUMBER OF SEQ ID NOS: 226-69-10
SEQ ID NO 201
LENGTH: 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-707-149-541A-4
Sequence 4, Application US/07749541A
Sequence 4, Application Sylvia
APPLICANT: Lee-Huang, Sylvia
APPLICANT: Huang, Pull L
APPLICANT: Huang, Philip L.
APPLICANT: Hang, Philip L.
APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.7%; Score 32; DB 4; Length 967; 71.4%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: USA

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CORTWARE: PATENTIN RC-BOS/MS-DOS
TILING DATE:
TILING DATE:
APPLICATION NUMBER: US/07/749,541A
FILING DATE:
APPLICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Living NUMBER: LEE-HUANG-3
FEFERENCE/DOCKET NUMBER: LEE-HUANG-3
FELECOMMUNICATION INFORMATION:
TELEPHANE: (202)62-5197
TELEFANE: (202)737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-139-802-201
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Query Match 68.2%; Score 30; DB 5; Length 345; Best Local Similarity 62.5%; Pred. No. 1.3e+02; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08225477B;
Sequence 9, Application US/08225477B;
Patent No. 5635370
GENERAL INFORMATION:
APPLICANT: Susan HOckfield
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: Luronan-Binding Protein
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Reens
STREET: 986 Bedford Street
CITX: Stanford
STATE: CT
COUNTRY: United States
ZIP: 06905
COMPUTPD PROTEIN
                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM 55/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03323A
FILING DATE: SUBmitted herewith
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATTONEY, AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 30,134
TELECHANNICATION INFORMATION:
TELECHANNICATION OF 94,174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,477B
FILING DATE: APTII 8, 1994
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KTINSKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 1751-P0004
TELEPHONE: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 345 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |||::
86 KPQDKSVW 93
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TOPOLOGY: LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-225-477B-9
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RESULT 10
PCT-US92-03089-1
Sequence 1, Application PC/TUS9203089
Sequence 1, Application PC/TUS9203089
Sequence 1, Application PC/TUS9203089
APPLICANT: Lee-Huang, Sylvia
APPLICANT: Huang, Hailip L.
APPLICANT: Huang, Pail L.
APPLICANT: Huang, Henry I.
APPLICANT: Huang, Henry I.
APPLICANT: Huang, Henry I.
APPLICANT: Chen, Hao-chia
TITLE OF INVENTION: An Anti-HIV Protein, TAP 29, From
TITLE OF INVENTION: Trichosanthes, DNA Coding Therefor and Therapeutic
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
STRFFT: STRFFT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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GENERAL INFORMATION:
APPLICANT: KUNSCH, ET AL.
TITLE OF INVENTION: Human B-Cell Translocation Genes-2 and 3
NUMBER OF SEQUENCES: 16
CORRESSONDERICE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 5; Length 45; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
ZIP: 20004
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03089
FILING DATE: 1992/0415
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: LEE-HUANG-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,528-5197
TELERAX: (202,737-3528
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.5%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4*
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSELAND
: NEW JERSEY
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Sever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11:1 11
26 PNEKKLY 32
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PCT-US95-03323A-2
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COLIXA COPPORATION
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: LEISHMANIA AND DIAGNOSIS OF LEISHMANIASIS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 COlumbia Center, 701 Fifth Avenue
                                                             Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 656;
                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTMARE: Patentin Release #1.0, Version #1.30 CURREWT APPLICATION NDATA: APPLICATION NUMBER: US/08/533,669A FILMS DATE: 22-SEP-1995 CLASSIFICATION: 424 ATTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 31,392 REFERENCE/DGOKET NUMBER: 210121.420 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2;
Pred. No. 2.7e+02;
1; Mismatches 2
                                                          Score 30; DB 5;
Pred. No. 1.4e+02;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wilding, Edvina Imogen
APPLICANT: Traini, Christopher M.
TITLE OF INVENTION: nrdE
FILE REFERENCE: GM0162
CURRENT APPLICATION NUMBER: US/09/132,028
CURRENT FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: ... USA
COUNTRY: 99104-7092
ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
...AURTER: IBM PC COMPATIBLE
...AURTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-533-669A-6
; Sequence 6, Application US/08533669A
; Patent No. 5834592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-00-132-028-2
; Sequence 2, Application US/09132028
; Patent No. 6222014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.2%;
62.5%;
                                                             68.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 656 amino acids TYPE: amino acid
                                                             Query Match 68.2
Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-533-669A-6
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Corixa
                                                                                                                                                                                                                   128 RPNDSGIY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 KPEQKSIY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 C
SITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KPNDKSLY 8
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                                                                                                                                                                                                                                                       NAME/KEY: cat brain BEHAB;
OTHER INFORMATION: polypeptide encod;
OTHER INFORMATION: ed by (and set out under) SEQ ID NO 2
US-08-225-477B-9
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OTHER INFORMATION: polypeptide encod-
OTHER INFORMATION: ed by (and set out under) SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 1; Length 378
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: St. Onge Steward Johnston & Reens STREET: 986 Bedford Street
CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9. Application PC/TUS9504353
SENERAL INFORMATION:
APPLICANT: Susan Hockfield
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCETWARE: Word Processor

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
FILING DATE:
PRIOR APPLICATION DATA:
ATORIELS APPLICATION DATA:
APPLICATION NUMBER: 08/225,477
FILING DATE: APTIL 8, 1994
ATORIELS APPLICATION NUMBER: 13243
REGISTRATION NUMBER: 1751-P0004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 303-324-6155
TELECOMMUNICATION OF 303-324
TELECOMMUNICATION OF 303-324-6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
                                                                                                                                         DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: cat cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: cat cortex
                                                                                                                                                                                                                                                                                                                                                                                                                       68.2%;
50.0%;
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 06905
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0 Matches 4; Conservative
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TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ||| :|
128 RPNDSGIY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KPNDKSLY 8
                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
PCT-US95-04353-9
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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Staphylococcus Aureus
US-09-132-028-2
US-09-132-028-2

Query Match
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPNDKSLY 8
| | | | | | |
| Db 108 KTNDKSQY 115

Search completed: January 29, 2002, 10:24:04
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January 29, 2002, 10:26:38; Search time 144.96 Seconds (without alignments) 4.204 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                     219241
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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44
1 KPNDKSLY 8
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                      Scoring table:
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uo	de antige	hypothetical prote	leotide e	ific DNA-	syntheta	o protein	hypothetical prote	nine gamm	probable cystathio	thrin - p	ypothetical prote	hypothetical prote	nthase (E	tetM 5'-region lea	mentation	cal prote	cal prote	Lryptophan synthas	ide ABC t	phosphoes	al target	alanyl am	nypothetical prote	ti-HIV pr	hypothet	hypothet	nthase (E	nembrane	cal prote
Description	liver stage	hypotheti	rad16 nucleotide	site-specific DNA	qlutamine syntheta	related to protein	hypotheti	cystathionine gamm	probable	myohemerythrin -	hypotheti	hypotheti	chitin synthase	tetM S'-r	sugar fermentation	hypothetical	hypothetical	tryptopha	oligopeptide ABC t	probable phosphoes	peroxisomal target	membrane alanyl am	hypotheti	TAP-29 anti-HIV pr	conserved hypothet	conserved hypothet	chitin synthase (E	probable membrane	hypothetical
) ; ; ; ;																												
	# 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1																												
ID	A45592	T27232	T37973	534433	G82631	T51085	T46066	B64533	D71973	S16190	T25773	542532	S55520	B56779	S77151	T17583	T23321	C43664	F72300	857592	T51817	A30325	696595	A39598	C70242	670231	F45189	S45857	T33622
DB		~	~	~	~	~	~	7	7	7	7	~	~	~	N	~	7	~	~	Н	~	~	7	~	7	~	~	~	7
% Query Match Length DB	1909	649	830	417	504	1246	344	380	380	120	166	403	760	28	237	240	405	406	655	692	728	69	2143	45	184	190	198	213	230
% Query Match	100.0	81.8	81.8	79.5	79.5	79.5	77.3	77.3	77.3	75.0	75.0	75.0	75.0	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	70.5	70.5	70.5	70.5	70.5	70.5
Score	44	36	36	35	35	35	34	34	34	33	33	33	33	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	31
Result No.	1	7	٣	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	58

1 KPNDKSLY 8

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hypothetical prote multidrug-efflux t probable transport hypothetical prote oligopetide trans hypothetical prote oligopetide trans hypothetical integ hypothetical prote appa, alpha-trehal probable N-arginin hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote chitch synthase (E chitin synthase (E	MENTS ite (Plasmodium falciparum) -Dec-1994 #text_change 09-Jun-2000 42; B45592; C45592; D45592 ber 1990 5; PID:99916 1 1	1909 <2H2> bone (KCBIN:75010, NCBIN:75012, NCBIN:75014, b.; Londono, A.: Patarapotikul, J.; Beaudo f Plasmodium falciparum characterized by gen	Galey, B.; Londono, A.; Patarapotikul, J.; Beaudo April 1992 ic antigen of plasmodium falciparum characterized ic antigen of prasmodium falciparum characterized due to frameshift error flocculent material in the parasitophorous vacuolulin repeat homology	(A-K-E-K-L-Q-E-Q-S-D-L-E-Q-E-R-R) ore 44; DB 2; Length 1909; ed. No. 1; Mismatches 0; Indels 0; Gaps 0;
27 27 27 27 27 27 27 27 27 27 27 27	ALIGNMENT parasite on 02-Dec S34842; November :99915; P	;1590-1; I backbo Galey, igen of	Galey, Aprill.c ant.	score Pred. Mism
DB1191 E64667 F71848 F71848 F71848 F71848 F621966 AB1287 E64427 E64427 E64427 E64427 E72293 F73293 F73293 F64693 F64693	3; , , , , , , , , , , , , , , , , , , ,	7 L . 19 S	'	10
0100000000000000	malari parum ce_revi ; S2939 Library 6203; N	ic ic	18266 11he, P Librar 1e-sepc CGUE2> 28266 oxyl en found	due re
260 4443 4443 4443 4443 550 550 10 1355 1154 188 188	LISA-1 - malar um falciparum # A4592; S293 ale, M. S24597 AHUDETA LIDEAR S24597 AHUN R. CEMBL:X56203; ale, M.R. itol 48, 223- itol 48, 223- itol 148, 223-	A 98-688:1165-1215;1 Eracted from NCBI. 7: Druilhe, P.; G. 198-specific antig 829393; MUID:8731	ss: EMBL'MA3266 F. C. C.; Druilhe, P. C. EMBL Data Library Liver-stage-sepciars 234842 c.	: 17-residue 100 larity 100 Conservative
νίνινινινίνινινινίνι	um #s # #s alle S22 EN EN EN EN AA AA AA	A 38-	CC.; BL. BL. CC.; Ver. S3 FA. CF. CF. CF. CF. CF. CF. CF. CF. CF. CF	17- rit
700770070070070070070070070070070070070	tigen smodi -1993 24597 Lingd Lingd Lingd 1909 1109 Paras Cure nber:	195;6 195;6 195;6 20 ex 20	and, ne EM a 11, a 11, a 14, a 14, a 14, a 18, a	gion: 17-r Similarity 8; Conser
	RESULT 1 A4559 liver stage antigen LSA-1 - malarii C;Species: Plasmodium falciparum C;Date: 22-Nov-1993 #sequence_revii C;Accession: 52459; A4559; S239, R;Zhu, J; Hollingdale, M. Submitted to the EMBL Data Library A;Reference number: 52457 A;Accession: 52457 A;Accession: 52457 A;Resident Pype: DNA A;Residues: 1-1909 CzHU A;Cross references: EMBL;X56203; N R;Zhu, J; Hollindale, M,R. Mol. Biochem. Parasitol: 48, 223-2; A;Title: Structure of Plasmodium fa A;Accession: 445592; MUID:9 A;Accession: A45592; MUID:9 A;Accession: A45592; MUID:9	sule typines: 1-: sequent a sequent	s reference to the form of the	154-1629/Reg
01000000000000000000000000000000000000	RESULT AA5592 AA5592 C.Speci C.Accee R.Zhu, R.Zhu, R.Reit A.Refer A.Nolce A.No	A, Molec A, Resic A, Note Nature Nature A, Titlk A, Acces A, Acces A, Statu A, Molec A, Molec	A, Cross submitti A, Desci A, Acces A, Acces A, Statt A, Molec A, Notes C, Comme C, Super C, Super Super Super Super Super Super Super Super Super Super Super Super Super Super Super	F;154-162 Query M Best Lo Matches

us-09-763-397a-10.rpr

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A.Molecule type: DNA
A.Rosidues; 1.417 < CHA1>
A.Molecule type: DNA
A.Rosidues; 1.417 < CHA1>
A.Rosidues; 1.417 < CHA1>
A.Rosidues; 1.417 < CHA1>
A.Rosidues; 1.417 < CHA1>
A.Cross-references: EMBL: M76435; NID:g149226; PIDN:AAA25090.1; PID:g149228
R.Chatterjee, D.K.; Hammond, A.W.; Blakesley, R.W.; Adams, S.M.; Gerard, G.F.
N.Title: Genetic organization of the KpnI restriction-modification system.
A.Reference number: S34431; MUID:92093610
A.Reference number: S34431; MUID:92093610
A.Reference number: S34431; MUID:92093610
A.Reference number: S34432
A.Rosidues; 4.75;93-142;340-359 < CHA2>
A.Rosidues; 4.75;93-142;340-359 < CHA2>
A.Rosidues; EMBL: M76435
A.Rosidues; EMBL: M76435
A.Rosidues; EMBL: Data Library, July 1991
A.Rocidue type: DNA
A.Rocidue type: DNA
A.Rocidue type: DNA
A.Rociduestic MBL: X61796; NID:g43887; PIDN:CAA43898-1; PID:g43889
A.Rociduestic methyltransferase; restriction modification system; S-adenosylmethionine
                                                                            site: Specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) KpnI - Klebsiell C; Species: Klebsiella pneumoniae A; Variety: APCC 55014 C; Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 05-May-2000 C; Accession: 534433; S31452; S21959 B: Chatterjee, D.K.; Hammond, A.W.; Blakesley, R.W.; Adams, S.M.; Gerard, G.F. A; Reference number: S34433 A; Accession: S34433
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Pred. No. 16;
2; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative 2
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182 QPDDKSLY 189
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Rossidues: 1-830 - 400RN
A.Rossidues: 1-830 - 400RN
A.Rossidues: Strain 972A; cosmid c19G10
R.Modo, V.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
Submitted to the EMBL Data Library, July 1999
A.Rocssion: T4056
A.Rocssion: T4056
A.Rottus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-830 - 4000
A.Rossreferences: EMBL:AL096788; PIDN:CAB46673.1; GSPDB:GN00067; SPDB:SPBC582.10c
A.Rossreferences: Strain 972h-; cosmid c582
A.Rossreferences: Strain 972h-; cosmid c582
A.Rossidues: 1-830 - 4002
A.Rossreferences: Strain 972h-; cosmid c582
A.Rossreferences: Strain 972h-; cosmid c582
A.Rossidues: SAC19G10.02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   radio nucleotide excision repair protein homolog - fission yeast (Schizosaccharomyces) (Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Jate: 00 20-Ber 1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C; Accession: T37973; T40569 R; Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. A; Reference number: 221759 A; Accession: T37973
                                                                                                                                                         Pypothetical protein V57G11C.20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2723
R;McMurray, A.
R;Refurray, A.
R;Reference number: Z20330
R;Reference number: Z20330
R;Scession: T2723
R;Reference number: Z20330
R;Reference number: Z20330
R;Scession: T27232
R;Reference number: Z20330

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 36; DB 2;
62.5%; Pred. No. 16;
iive 3; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 2;
Pred. No. 21;
1; Mismatches (
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: c
C; Genetics:
A; Gene: CESP:Y57G11C.20
A; Map position: 4
1850 KPNDKSLY 1857
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478 KPNDRNIY 485
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Genetics: <WOO2>
Gene: SPBC582.10c
Wap position: 2
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C; Species: Helicobacter pylori

A; Variety; strain J99

C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Jul-1999

C; Accession: D/1973

Nature 397, 176-180, 1999

A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

A; Reference number: A/1800; MUID: 99120557

A; Accession: D/1973

A; Status: preliminary

A; Status: preliminary

A; Status: creferences: GB:AE001449; GB:AE001439; NID:94154604; PIDN:AAD05677.1; PID:9415

C; Genetics:

A; Stene: metB

C; Superfamily: O-succinylhomoserine (thiol)-lyase
                                                                                                                                                                Cystathionine gamma-synthase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Titler The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-380 <TOM>
A;Cross-references: GB:AE000532; GB:AE000511; NID:g2313184; PIDN:AAD07176.1; PID:g231
C;Superfamily: O-succinylhomoserine (thiol)-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myohemerythrin - polychaete (Nereis diversicolor)
C;Species: Nereis diversicolor (sandworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Oct-1999
C;Accession: S16190
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24;
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Best Local Similarity 75.0 Matches 6; Conservative
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Matches 6; Conservative
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132 KPNTKALY 139
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132 KPNTKALY 139
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162 PNDKMLY 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T18N14.80 - Arabidopsis thaliana hypothetical protein T18N14.80 - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Species: 146066
R.Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, F. Submitted to the Protein Sequence Database, December 1999
A.Recreace number: 223013
A.Accession: T46066
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-344 < CBL>
A.Cross-references: EMBL:AL132968
A.Experimental source: cultivar Columbia; BAC clone T18N14
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A;Introns: 48/3; 144/1
A;Note: T18N14.80
C;Superfamily: Arabidopsis thaliana hypothetical protein T18N14.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1246 <SCH>
A;Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.190
A;Experimental source: BAC clone B2A19; strain OR74A
C;Genetics:
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                                                                                                                                                                          Score 35; DB 2; Length 504;
Pred. No. 20;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                related to protein kinase PAKI [imported] – Neurospora crassa
N;Alternate names: protein B2A19.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
51;
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Pred. No.
                     A;Contents: annotation
C;Genetics:
A;Gene: XF1842
C;Superfamily: glutamate--ammonia ligase
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Similarity 85.7%;
6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
A; Reference number: A59328
                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
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584 KPDEKSLY 591
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A; Introns: 95/2
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Chitin Synthase (EC 2.4.1.16) CSH1 - smut fungus (Ustilago maydis)
C;Species: Ustilago maydis (corn smut)
C;Accession: S5520
R;Xoconostle-Cazares, B.; Leon-Ramirez, C.; Ruiz-Herrera, J.
Submitted to the EmBL Data Library, June 1995
A;Description: Multiple chitin synthetase genes in Ustilago maydis. Cloning and chara A;Description: Multiple chitin synthetase genes in Ustilago maydis. Cloning and chara A;Setus: preliminary
A;Molecule type: DNA
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:X87748; NID:q861150; PID:q861151
C;Keywords: glycosyltransferase; hexosyltransferase
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                                                      Length 403;
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                                                 DB 2;
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Pred. No. 80;
2; Mismatches
                                            Score 33; DB 2
Pred. No. 42;
0; Mismatches
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Pred. No. 4.3;
2; Mismatches
                                            Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative (
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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458 RPGDKSIY 465
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S77151
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Cippedies: Synechococcus sp.
Cipaceise: Cipaceise: Synechococcus sp.
Cipaceise: Cipaceise: Synechococcus sp.
Airtie: Cloning and characterisation of genes for tetrapyrrole biosynthesis from the cyanecesion: Synechococcus sylosoperide as Anacystis nidulans R2
Airtie: Cloning and characterisation of genes for tetrapyrrole biosynthesis from the cyanecesion: Sylosoperide as Anacystis nidulans R2
Airtie: DNA
Airtie: Cloning and characteristic appethetical protein 1; tetratricopeptide repeat homology critis
Cisuperfamily: Synechococcus hypothetical protein 1; tetratricopeptide repeat homology critis
Figh: 351-384/Domain: tetratricopeptide repeat homology critis
R; Takagi, T.; Cox, J.A.

FEBS Lett. 285, 25-27, 1991
A; Title: Primary structure of myohemerythrin from the annelid Nereis diversicolor.
A; Reference number: S16190; MuID: 91293305
A; Accession: S16190
A; Status: preliminary
A; Status: preliminary
A; Residues: 1.120 < FEB>
C; Superfamily: hemerythrin
C; Superfamily: hemerythrin
C; Reywords: 1ron: oxygen carrier
F; 25, 54, 58, 75, 79, 108, 113/Binding site: 2Fe-O cluster (His, His, His, His, His,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125) Protein F47C10.2 - Caenorhabditis elegans
CSpecies: Caenorhabditis elegans
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CSpecies: Caenorhabditis elegans
CSPECIESTOR CAENORMAN
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Pred. No. 12;
0; Mismatches 1; Indels
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Pred. No. 17;
2; Mismatches
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71.4%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Matches 5; Conserv
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A;Map position: 5
A;Introns: 24/3; 75/1
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94 PNDKLLY 100
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73 PNDKTVY 79
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A; Reference number: S74322; MUID:97061201
A; Reference number: S77151
A; Status: nucled acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-237 «KAN>
A; Residues: 1-237 «KAN>
A; Residues: 1-237 «KAN>
A; Residues: 1-237 «KAN>
A; Coss references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17709.1; PID:g165279
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics:
A; Gene: sfsA
C; Superfamily: sugar fermentation stimulation protein
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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| 130 KPEEKSIY 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=972;
Wood V., Rajandream M.A., Barrell B.G., Davis P., Churcher C.M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE SNF2/Rab54 HELICASE FAMILY.
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             Q90374
Q28062
P79171
P30600
P19706
Q9xps9
P16025
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P22271
Q60676
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Pred. No. 12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 93.9 KDA HELICASE CS82.10C IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47086968FDD951CB CRC64;
                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                       830 AA
                                                                                                                                                                                      ALIGNMENTS
SWI6_YEAST
PRLR_COLLI
PGCB_BOVIN
AMPN_FELCA
CHS1_EXODE
                                                                  MYSB_ACACA
RPOD_WHEAT
RPOD_MAIZE
                                                                                                         APU_THETU
STCA_EMENI
PRO1_PHYPO
PPP5_MOUSE
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InterPro; IPR00140; Helicase_C.
InterPro; IPR000330; SNF2_N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SNART; SN00487; DEXDC; 1.
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ilarity 85.7%;
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Q10332;
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P56069
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P15144
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P55707
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P77510
Q50586
Q01033
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       100059 seqs, 36664827 residues
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OGL_ERWCA
PRRC_ECOLI
PGCB_FELCA
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CHS2_PHAEX
CHS2_XYLBA
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DPIB_ECOLI
FD25_MYCTU
VG48_HSVSA
                                                                                         January 29, 2002, 11:13:40
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Maximum Match 100%
Listing first 45 summaries
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METB_HELPJ
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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        **X MEDLINE=99120557; PubMed=9923682;

**A RIM R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,

**A Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G.,

**A Smith D.R., Monan B., Guild B.C., deJonge B.L., Carmel G.,

**A Trust T.A.; Caruso A., Unita Nickelsen M., Mills D.M., Ives C.,

**Clbson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**A Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**Trust T.J.; Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

**C. CATALYTIC ACTIVITY: O-SUCCINYL-L-HOMOSERINE + L-CYSTEINE **

**C. COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

**C. COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

**C. SUBORIT: HOMOTETAAMER (BY SIMILARITY).

**C. SUBORIT: HOMOTETAAMER (BY SIMILARITY).

**C. SUBORIT: HOMOTETAAMER (BY SIMILARITY).

**C. SIMILARITY: ELONGS TO THE TRANS-SULFURATION ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
CP-SUG-2001 (Rel. 40, Last annotation update)
CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) (CGS) (0-SUCCINYLHOMOSERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-26695, / ATC 700392;
MEDLINE-97394467; PubMed=9252185;
MEDLINE-97394467; PubMed=9252185;
MEDLINE-97394467; PubMed=9252185;
Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.K., Peterson J.D., Kelley J.M., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRIDOXAL PHOSPHATE (BY SIMILARITY). 358BEAE6C5C802BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 380;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro: IPR000277; Cys_Met_Meta_PP.
PR01273; Cys_Met_Meta_PP.
PR051TE: PS00868: CYS_MET_META_BP; FALSE_NEC.
Methionine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001449; AAD05677.1; -. HSSP; P06721; 1CL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 77.3%;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
BINDING 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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P56069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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A Gerard G.F.;
A Gerard G.F.;
Charterjee D. K., Hammond A. W., Blakesley R.W., Adams S.M.,
A Gerard G.F.;

"Genetic organization of the Kpn1 restriction-modification system.";

"Uncleic Acids Res. 19:6505-6509(1991).

"Incleic Acids Res. 19:6505-6509(1991).

"CATALYTOR THE DNA FROW CLEAVAGE BY THE KNPI ENDONUCLEASE.

"CATALYTIC ACITYITY: S. ADENOSYL-L-METHIONINE + DNA ADENINE -

"S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPRINE.

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"The Swiss Draw of the Commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/corrected)
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METB OR JHP0098.

Helicobacter pylori J99 (Campylobacter pylori J99).

Helicobacter.

Helicobacter.

NCBL PaxID=85963;
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                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
MODIFICATION METHYLASE KRNI (EC 2.1.1.72) (ADENINE-SPECIFIC METHYLASE KRNI) (M.KPNI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 35; DB 1; Length 417; 75.0%; Pred. No. 8.9; 0; Indels tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M76435; AAA25090.1; -
EMBL; M76435; AAA25090.1; -
EMBL; K21996; CAA4898.1; -
PIR; S21433; S3443.

PIR; S34433; S34433.

REBASE; 3345; M.KpnI.

InterPro; IPR00225; D21N6_mtfrase.

InterPro; IPR00241; N6_Mtase.

R interPro; IPR00262; N6_Mtase.

R pfam; PF01555; N6_Mtase; I.

PRINTS; PR00506; D21N6MTRASE.

R PROSIFE; PS00929; N6_Mtase; I.

R PROSIFE; PS00929; N6_Mtase; I.

R PROSIFE; PS00929; N6_Mtase; I.

R PROSIFE; PS00929; N6_Mtase; Restriction system.

SEQUENCE 417 AA, 47577 NW; 42BFAA6F772347BD CRC64;
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PRT;
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Best Local Similarity 75.v
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  STANDARD;
                                                                                                                                                            Klebsiella pneumoniae
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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182 QPDDKSLY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KPNDKSLY 8
                                                                                                                                                                                                    Klebsiella.
NCBI_TaxID=573;
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ID METB_HELPJ
AC Q9ZMW7;
  MTK1_KLEPN
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Gaps

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108
113
120 AA;
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140 KPTDKELY 147
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ACT_SITE
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DISULFID
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                      CARBOHYD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
         complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases. Y: AN ORTHOPHOSPHORIC MONOESTER + H(2)O = AN
                                                                                                                                                                                                                                                                                                                                                  PYRIDOXAL PHOSPHATE (BY SIMILARITY). 58A85489B05257ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                   -i- PATHWAY: SECOND STEP IN METHIONINE BIOSYNTHESIS.
-i- SUBDNAT: HOMOTETRAMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE TRANS-SULFURATION ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1; Length 380;
Pred. No. 13;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE ACID PHOSPHATASE B0361.7 PRECURSOR (EC 3.1.3.2).
                                                                                                                                                                                                                                                                                    Interpro; IPR000277; Cys_Met_Meta_PP.
Pfam; PF01053; Cys_Met_Meta_PP; 1.
PROSITE; PS00868; CXS_MET_METAB_PP; 1.
Methionine blosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AA.
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01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                             380 AA; 41118 MW;
                                                                                                                                                                                                                                                    EMBL; AE000532; AAD07176.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1994) to the EP-1- CATALYTIC ACTIVITY: AN ORTALYTIC ACTIVITY: ALCOHOL + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                  77.38;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U00031; AAA50626.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Du Z.;
                                                                                                                                                                                                                                                               HSSP; P06721; 1CL1.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                       Complete proteome.
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| 132 KPNTKALY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KPNDKSLY 8
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                                                                                                                                                                                                                                                                          rigR; HP0106;
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Q10944;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PPAY_CAEEL
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Gaps
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-!- FUNCTION: MYOHEMERYTHRIN IS AN OXYGEN-BINDING PROTEIN FOUND IN
THE RETRACTOR MUSCLES OF CERTAIN WORMS. THE OXYGEN-BINDING SITE
                                                                                                                                                         PUTATIVE ACID PHOSPHATASE B0361.7.
NUCLEDPHILIC ACCEPTOR (BY SIMILARITY).
BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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Phyllodocida; Nereididae; Neanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takagi T., Cox J.A.; Primary structure of myohemerythrin from the annelid Nereis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 1 AND 2 (BY SIMILARITY).
A793589D582E8B97 CRC64;
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HSSP; P20646; IRPT.
WormPep; B0361.7; CE00836.
InterPro: IPR000560; H1S_acid_phosphtse.
Pfam; PF00328; acid_phosphat; 2.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
Hypothetical protein; Signal; Glycoprotein; Hydrolase.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     BA265D808EC8B11C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metal-binding; Iron.
                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                     -i- SUBUNIT: MONOMER.
-i- TISSUE SPECIFICITY: MUSCLE.
-i- SIMILARITY: BELONGS TO THE HEMERYTHRIN FAMILY.
PIR: $16190; $16190.
HSSP, P02247; 2MHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOHEMERYTHRIN (MHR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB
Pred. No. 14;
0; Mismatches
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IRON 2
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IRON 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91293305; PubMed-2065779;
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75 IR
79 IR
108 IR
113 IR
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ilarity 75.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     47110
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                                                                                                                                                                                                                                       363
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nes 6; Conser
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MEDLINE=99061201; PubMed=8905231;
KARDAKO T., Sato S., Korani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                        STRAIN-RK32 A2B3;

MEDLINE-27086517; PubMed-8932711;

Xoconostle-Cazares B., Leon-Ramirez C., Ruiz-Herrera J.;

Xoconostle-Cazares B. Leon-Ramirez C., Ruiz-Herrera J.;

Two chitin synthase genes from Ustilago maydis.";

Microbiology 142:377-387(1996).

-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.

-!- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-N-ACETYL-BETA-D-GLUCOSAMINEL)](N) = UDP + [1,4-(N-ACETYL-BETA-D-GLUCOSAMINEL)](N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: PLASMA MEMBRANE-BOUND.
-:- SIMILARITY: BELONGS TO THE CHITIN SYMTHASE FAMILY.
                            EMBL; X87748; CAA61027.1; .
InterPro; IPR002923; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD03989; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 33; DB 1; Length 760; 62.5%; Pred. No. 44; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803),
Bacteria, Cyanobacteria, Chrococcales, Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                760 AA; 85181 MW; 9377000F57410993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 30, Last annotation update)
SUGAR FERMENTATION STIMULATION PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| |||:|
458 RPGDKSIY 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family
SEOUENCE 760 A
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FRANSFERASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFSA_SYNY3
P73664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SESA_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                       Gaps
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Last annotation update)
2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                       ö
                                                                                                                                                                                                                                                                       ullour 1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 45.0 KDA PROTEIN IN COBA 5'REGION.
Synethococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chrococccales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 33; DB 1; Length 403; 85.7%; Pred. No. 22; 1ve 0; Mismatches 1; Indels
                                  DB 1; Length 120;
                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPR 1.
TPR 2.
TPR 4.
TPR 4.
TPR 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760 AA.
                                                                                                                                                                                                                                       403 AA.
                                Score 33; DB 1
Pred. No. 6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPR repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X70966; CAA50301.1; -.
InterPro; IPR001173; Glycos_transf_2.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00535; .Glycos_transf_2; 1. Pfam; PF00515; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 316 TPR
317 350 TPR
351 387 TPR
403 AA; 44998 MW; 4
                                                                       ;
                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq.
15-JUL-1998 (Rel. 36, Last annot
HYPOTHETICAL 45.0 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Repeat; REPEAT 208 243
                                  75.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 85.7
Matches 6; Conservative
                                  Query Match 75.0
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHSX_USTWA STANDARD 099127 (15-1010-1999 (Rel. 38, Cl. 15-010-1999 (Rel. 38, Le. 30-MAY-2000 (Rel. 39, Le. CHTIN SYMTHASE I (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART: SM00028; TPR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 | | |
348 PNDPSLY 354
                                                                                                                               2 PNDKSLY 8
                                                                                                         2 PNDKSLY 8
                                                                                                                                                                                                                                 YCOA_SYNP7
P42460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                  RESULT 7
YCOA_SYNP7
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SEQUENCE TO 1908 / CE15;

X MEDLINE-21173698; PubMed-11259647;

X MEDLINE-21173698; PubMed-11259647;

RA Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Diecka I., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,

RA DEBOY R.T., Dodson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DEBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

KA DEBOY R.T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RT "Complete genome sequence of Caulobacter crescentus.";

RT "Complete genome Squent IS RESPONSIBLE FOR THE SYNTHESIS OF L-

TRYPTOPHAN FROM INDOLE AND L.SERINE + 1 (INDOL-3-YL)GLYCEROL 3-PHOSPHATE

C. I CATALYTIC ACTIVITY: L-SERINE + 1 (INDOL-3-YL)GLYCEROL 3-PHOSPHATE

C. I CATALYTIC ACTIVITY: L-SERINE + 1 (INDOL-3-YL)GLYCEROL CC

SERIES SHAMAY: LAST (FIFTH) STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

C. I SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY

C. I SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY

C. I SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY

C. I SUBUNIT STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                   Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88115177; PubMed-2828322;
Soss C.M., Winkler M.E.;
"Structure of the Caulobacter crescentus trpFBA operon.";
J. Bacteriol. 170:757-768(1988).
                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                    237 AA; 26847 MW; BECC025E7EB3298A CRC64;
                                                                                                                                                                                                                                                     Score 32; DB 1;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-CCT-1989 (Rel. 12, Created)
01-CCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRPB OR CC3544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TRPB FAMILY.
                                                                                                                                                                                                                                                                      Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M19129; AAA23057.1; -.
EMBL; AE006013; AAK25506.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                   72.78;
62.58;
                                                                                                                                          EMBL; D90908; BAA17709.1; -.
                                                                                                                                                                                                                                                Query Match 72.7's
Best Local Similarity 62.5's
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                         130 KPEEKSIY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=69394;
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                                                                                                                                                                                                                                                                                                                                   1 KPNDKSLY 8
  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRPB_CAUCR
P12290;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
TRPB_CAUCR
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SSSSSSSS₹8
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                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogawa H., Johzuka K., Nakagawa T., Leem S.H., Hagihara A.H.; "Functions of the yeast melotic recombination genes, MRE11 and MRE2."; Adv. Biophys. 31:67-76(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: EXONUCLEASE REQUIRED FOR REPAIR DURING VEGETATIVE GROWTH AND FOR INTITATION OF MEIOTIC RECOMBINATION THROUGH THE FORMATION OF DOUBLE-STRAND BREAKS (DSB), WORK IN COMPLEX WITH RAD50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Interaction of Mrell and Rad50: two proteins required for DNA repair and meiosis-specific double-strand break formation in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
STRAIN-SCARC / AB972;
Skelton J. Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paull T.T., Gellert M.; The 3-prime beautivity of Mrell facilitates repair of DNA double-strand breaks."; Paul 1:969-979(1998).
                                                                                                                                        99 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
43491 MW; 83A8161FF477511E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                              DB 1; Length 406; 36;
                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                     PROSITE; PS00168; TRP_SYNTHASE_BETA; 1.
Tryptophan biosynthesis; Pyridoxal phosphate; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-0CT-2001 (Rel. 40, Last annotation update)
DOUBLE-STRAND BREAK REPAIR PROTEIN MRE11.
MRE11 OR YMR224C OR YM9959.06C.
                                                                                                                                                                                                                                                                                                                                                                                                             692 AA.
                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                Score 32;
                                                Trp_synth_beta
                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-643 FROM N.A. MEDLINE-95309669; PubMed=7789757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95351198; PubMed=7625279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98315380; PubMed=9651580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae.";
Genetics 139:1521-1532(1995).
                                                                                                                                                                                                                72.7%;
75.0%;
                               Interpro; IPR001926; PALP.
Interpro; IPR000993; Trp_s
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                              Ouery Match
Best Local Similarity 75.0.
نمر 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogawa H.;
 P00933; 2TSY.
                                                                                                                                                            406 AA;
                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                     1 KPNDKSLY 8
                  TIGR; CC3544; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johzuka K.,
                                                                                                                                                                                                                                                                                                                                                                                                              MR11_YEAST
P32829;
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION
                                                                                                                                             BINDING
HSSP;
                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                           -:- COFACTOR: BINDS ONE ZINC ION.
-:- SUBCELLILAR LOCATION: TYPE II MEMBRANE PROTEIN.
-:- SUBCELLILAR LOCATION: TYPE II MEMBRANE PROTEIN.
-:- DISEASE: DEFECTS IN AND SEEM TO BE A CAUSE OF VARIOUS TYPES OF LEUKBUH OR LYMPHONA.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MI (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE PEPN SUBFAMILY.
-:- DATABASE: NAME=ROW; NOTE=CD guide CD13 entry;
-:- MATABASE: NAME=ROW; NOTE=CD guide CD13 entry;
-:- MATABASE: NAME=ROW; NOTE=CD guide CD13 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CYTOSOLIC SER/THR-RICH JUNCTION.
METALLOPROTEASE.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001930; Aladiptase.
InterPro; IPR001930; Zn_MTpeptdse.
InterPro; IPR000130; Zn_MTpeptdse.
InterPro; IPR00130; Zn_MTpeptdse.
Pro; IPR00756; ALADIPTASE.
PROSTTE; PS00142; ZINC_PROTEMSE; I
Hydrolase; Metalloprotease; Aminopeptidase; Zinc; Glycoprotein;
Sulfation; Transmembrane; Duplication; Signal-anchor; Polymorphism.
INIT_MET 0 BY SAMILARITY.
. Mutat. Suppl. 1:S158-S160(1998).
FUNCTION: ALSO SERVES AS A RECEPTOR FOR HUMAN CORONAVIRUS 229E.
CATALYTIC ACTIVITY: AMINOACYL-PEPTIDE + H(2)O = AMINO ACID +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X13276; CAA31640.1; -... EMBL; X13276; CAA31640.1; -.. EMBL; M25224; AAA31399.1; -.. EMBL; M55522; AAA83399.1; -.. EMBL; M55528; AAA83399.1; -.. EMBL; M55529; AAA83399.1; -.. MEROPS; M01.001; -.. MEROPS; M01.001; -.. MIM; 151530; -.. Table and table 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULPATION (POTENTIAL)
SULPATION (POTENTIAL)
N-LINKED (GLCNAC...) (IN-LINKED (GLCNAC...) (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
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/FTId=VAR_006728.
E -> V (IN REF. 3).
P -> L (IN REF. 3).
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                                                                                        OLIGOPEPTIDE.
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VARIANT
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TSSUB-intestinal epithelium;
MEDIINE-91268079; PubMed-1675538,
Shapiro L.H., Ashmun R.A., Roberts W.M., Look A.T.;
Sperate promoters control transcription of the human aminopeptidase
N gene in myeloid and intestinal epithelial cells.";
J. Biol. Chem. 266:11999-12007(1991),
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BEDIINE-29198086; PubMed-2564851;
LOOK A.T., Ashunn R.A., Shapiro L.H., Peiper S.C.;
"Human myeloid plasma membrane glycoprotein CD13 (gpl50) is identical to aminopeptidase N.",
J. Clin. Invest. 83:1299-1307(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Intestine:
MEDILINE-89005706; PubMed-2901990;
MEDILINE-89005706; PubMed-2901990;
MEDILINE-89005706; PubMed-2901990;
MOSTILET J., Cowell G.M., Koenigshoefer E., Danielsen E.M.,
Moeller J., Laustsen L., Hansen O.C., Welinder K.G., Engberg J.,
Hunziker W., Spiess M., Sjoestroem H., Noren O.;
"Complete amino acid sequence of human intestinal aminopeptidase N deduced from cloned CDNA."
FEES Lett. 238:307-314(1988).
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WAEDLINE-99112453; PubMed-9452074;
Lendeckel U., Wex T., Arndt M., Frank K., Franke A., Ansorge S.;
"Identification of point mutations in the aminopeptidase N gene by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p15144; 016728;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AMINOPEPTIDAS N (RC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150)
(MYELOID PLASHA MEMBRANE GIYCOPROTEIN CD13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 692;
Pred. No. 63;
1; Mismatches 1; Indels
                   EMBL; D11463; BAA02017.1; -.
EMBL; 249939; CAA90195.1; -.
PIR; S27428; S27428.
S205. S0004837; MREL1.
InterPro: IPR003701; DNA_repair.
InterPro: IPR000934; Ser_thr_phosphtse.
Pfam, PF02549; DNA_repair; Meiosis.
SEQUENCE 692 AA; 77650 MW; D584333228952B73 CRC64;
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                                                                                                                                                                                                                                                                                                                                                          72.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                          Query Match 72.7
Best Local Similarity 75.0
Matches 6; Conservative
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62 KPSKKSLY 69
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AC APDRAN
LIDAR AC P15144
AC P15144
DT 01-APR

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Hypothetical protein; T
TRANSMEM 40 62
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P38212;
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NON_TER
SEQUENCE
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YBL5_YEAST
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Proc. Natl. Acad. Sci. U.S.A. 88:6570-6574(1991).
-!- FUNCTION: CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION.
IT INACTIVATES EUKARYOTIC GOS RIBOSOMAL SUBUNITS.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: TO OTHER BATTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 1 RIP. PIR; A39598; A39598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
CHITIN SYNTHASE 1 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Tuberous root;
MEDLINE-91319727; PubMed-1713684;
Lee-Huang S., Huang P.L., Kung H.-F., Li B.-Q., Huang P.L., I Huang H.I., Chen H.-C.;
"TAP 29: an anti-human immunodeficiency virus protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 45;
Pred. No. 5.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN TAP-29 (RRNA N-GLYCOSIDASE)
                  Indels
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                  1;
                                                                                                                                                                                                                                                                                                                              Prichosanthes kirilowii (Mongolian snake-gourd)
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InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
Protein synthesis inhibitor; Hydrolase; Toxin.
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d. No. 91;
Mismatches
Pred. No.
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71.48;
71.48;
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                      Conservative
                                                                                                                                                                                            STANDARD;
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  Best Local Similarity
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                                                                                             94 PNDRGLY 100
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                                                        PNDKSLY 8
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P30598;
                                                                                                                                                                                      RIP2_TRIKI
P23029;
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01-NOV-1991
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SEQUENCE
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CHS1_USTMA
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                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                       "Classification of fungal chitin synthases.";
Proc. Natl. Acad. Sci. U.S.A. 89:519-523(1992).
-!- FUNCTION: PLAYS A MAJOR NOLE IN CELL WALL BIOGENESIS.
-!- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-BETA-D-GLUCOSAMINE)](N) = UDP + [1,4-(N-ACETYL-BETA-D-GLUCOSAMINYL)](N)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Bowen A.R., Chen-Wu J.L., Momany M., Young R., Szaniszlo P.J., Robbins P.W.;
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01-0CT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 23.9 KDA PROTEIN IN COQ1-UGAS INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002923; Chitin_synth.
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 198;
Pred. No. 26;
0; Mismatches 2; Indels
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Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST SSH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A2A399FCAB3EF3C3 CRC64;

    -!- SUBCELLULAR LOCATION: PLASMA MEMBRANE-BOUND.
    -!- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.

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75.0%;
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Matches 6; Conservative
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198 AA;
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SQ SEQUENCE 213 AA; 23886 MW; 0784FB182C16F1B0 CRC64;
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; 0; Gaps Query Match
70.5%; Score 31; DB 1; Length 213;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 1; Indels

Search completed: January 29, 2002, 11:13:41 Job time: 817 sec

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099369 heurospora
099855 gibberella
098ct8 arabidopsis
0996m2 crithidia f
001560 caenorhabdi
09v134 drosophila
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Q9ibu9 turkey herp
Q9e6p2 turkey herp
Q92547 homo sapien
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Shan 2.X., Yu X.B., Li X.R., Ma C.L.;
"Molecular 2.X., Yu X.B., Li X.R., Ma C.L.;
"Molecular cloning and structure of the 3' terminal of liver stage antigen-1 gene of Plasmodium falciparum isolate FCC1/HN.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF246996; AAG12324.1;
NON_TER
SEQUENCE 264 AA; 31006 MW; 1714D653E8D9DID7 CRC64;
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            090z98 P
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                 264 AA
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Q9P855
Q9SCT8
Q9U6M2
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Q9E6P2
Q92547
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Q9FIX4
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047736
09AI85
09AI78
09NPM1
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Q9PCD9
Q9EZV7
Q9CM43
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Copyright (c) 1993 - 2000 Compugen Ltd.
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STRAIN=KENYAN;
MEDIZINE=56065765; Pubbmed=7477115;
MEDIZINE=56065765; Pubbmed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasitol. 71:291-294(1995).
EWBL: L40887; AAC41597.1; -.
SEQUENCE 280 AA; 32882 MW; 46763641C81AFC33 CRC64;
                                                                                                                       Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M., Hawley W.A., Collins W.E., Lal A.A.; "Sequence variations in the non-repetitive regions of the liver stagespecific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last amoctation update)
11-NOV-1998 (TrEMBLrel. 08, Last amoctation update)
11-NOR-1998 (TrEMBLrel. 08, Last amoctation update)
11-NOR-1998 (TrEMBLrel. 08, Last amoctation update)
11-NOR-1998 (TrEMBLrel. ANTIGEN I (FRAGMENT).
11-SA-1.
Plasmodium falciparum.
Plasmodium falciparum.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5833;
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels
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Q25846;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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EMBL; L40886; AAB59232.1; -.
                                                                                       STRAIN=KENYAN;
MEDLINE=96065765; PubMed=7477115;
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SEQUENCE FROM N.A.
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MEDLINE=96665765; Pubbwed-7477115;
MEDLINE=96665765; Pubbwed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (L.SA-1) of Plasmodium falciparum from field isolates.
                                                                                                         STRAIN-KENYAN,
MEDLINE-9605765; Pubmed-7477115;
MEDLINE-9605765; Pubmed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
    Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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100.0%; Score 44; DB 5; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels
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MBLE, L40884; AAB59230.1; -.
NOM TER
SEQUENCE 280 AA: 32926 MW; 467080F32FARAD33 CRC64;
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SEQUENCE 280 AA; 32940 MW; E9708E3CFFAEA9CF CRC64;
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01-Nov-1996 (TrEMBLrel. 01, Last sequence update)
01-Nov-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
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EMBL; L40885; AAB59231.1; -.
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Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M., Hawley W.A., Collins W.E., Lal A.A.; "Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
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NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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EMBL: L40891; AAC41601.1; -.
NON_TER
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EMBL; L40890; AAC41600.1; -.
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MEDLINE=96065765; PubMed=7477115;
                    STRAIN-KENYAN;
MEDLINE-96065765; Pubmed-7477115;
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MEDLINE-96655765; PubMed-7477115;
MEDLINE-96657765; PubMed-7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
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Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
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Eukaryocia: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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EMBL; L40888; AAC41598.1; -.
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EMBL; L40889; AAC41599.1; -.
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MEDLINE=96065765; Pubmed=7477115;
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NCBI_TaxID=5833;
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Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.,
'Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.''
Mol. Biochem. Parasitol. 71:291-294(1995).
EMB., L40835; AAC41604.1:

NON_TER 1

SEQUENCE 280 AA; 32966 MW; 61851C5AD6E1A211 CRC64;
MEDLINE-96065765; PubMed-7477115; Alpers M.P., Povoa M.M., Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M., Hawley W.A., Collins W.E., Lal A.A.; Sequence variations in the non-repetitive regions of the liver stage-sequence variations. In the non-repetitive regions of the liver stage-isolates ". Sequence variation of plasmodium falciparum from field isolates." Non. Biochem. Parasitol. 71:291-294(1995).

Mol. Biochem. Parasitol. 71:291-294(1995).

SEQUENCE 280 AA, 32938 MW; 46751C45F4DCBD33 CRC64;
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Eukaryota; Alveclata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveclata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_FaxID=5833;
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MEDLINE-96065765; PubMed=7477115;
Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
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01-NOV-1996 (TrEMBLRel. 01, Last sequence update)
01-NOV-1998 (TREMBLRel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
LIVER STAGE-SPECIFIC ANTIGEN I (FRAGMENT).
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221 KPNDKSLY 228
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MEDLINE=96065765; PubMed=7477115;
MEDLINE=96065765; PubMed=7477115;
Mang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.";
                                                                     Yang C., Shi Y.P., Udhayakumar V., Alpers M.P., Povoa M.M., Hawley W.A., Collins W.E., Lal A.A.; Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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BMEL: L40893; AAC41603.1; -.
NON_TER
SEQUENCE 280 AA: 32927 MW; 48706EFDCF40ADD3 CRC64;
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EMBL; L40834; AAB59233.1; -.
1 1 1 1 SEQUENCE 280 AA; 32927 MW; E6648F85FBBAA245 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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           STRAIN=KENYAN;
MEDLINE=96065765; Pubmed=7477115;
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Hawley W.A., Collins W.E., Lal A.A.;
"Sequence variations in the non-repetitive regions of the liver stage-specific antigen-1 (LSA-1) of Plasmodium falciparum from field isolates.";
Mol. Biochem. Parasicol. 71:291-294(1995).
EMBL: L40837; AC41605.1; ...
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SEQUENCE 280 AA; 32866 MW; 73164A709789DD31 CRC64;
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MEDLINE-96065765; PubMed-7477115;
MEDLINE-96065765; PubMed-7477115;
Mang C., Shi Y. P., Udhayakumar V., Alpers M.P., Povoa M.M.,
Hawley W.A., Collins W.E., Lal A.A.;
Sequence variations in the non-repetitive regions of the liver stage-
specific antigen-1 (LSA-1) of Plasmodium falciparum from field
isolates.;
Mol. Biochem. Parasitol. 71:291-294(1995).
EMBL; L40908; AAB59228.1; -.
SEQUENCE 280 AA; 32936 MW; FDF9A29104C5A7E9 CRC64;
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LIVER STAGE-SPECIFIC ANTIGEN 1 (FRAGMENT).
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Merozoite surface

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Peptide #692 enco
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Peptide #5280 enco
Peptide #5413 enco
Peptide #5413 enco
Peptide #5418 e

Human protein tyro Human secreted pro Murine receptor-ty

Mouse RPTPa amino

Human RPTPa amino

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AAA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
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                                                                          The present sequence is the antigenic epitope P597, derived from merozoite surface protein. (MSP-1) of the asexual blood stage of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/MITMALWAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melitin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein. 2 (SSP-2), ilver stage antigen-1 (LSA-1), merozoite surface protein. 1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27 These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/MITMALWAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/MITMALWAC-1 antibodies can be used for calculated and precenting P. falciparum in biological samples.
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         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle ^{-}
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iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSP1EGF1A EGF1-like domain variant.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAR41354 standard; peptide; 49 AA.
                                                         Claim 2; Page 16; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92GB-0003821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93WO-GB00367.
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                                                                                                                                                                                                                                                                                                                                               1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                              1 nsgcfrhldereeckcll 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-288413/36.
                                                                                                                                                                                                                                                                                                            Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium yoelii.
                                                                                                                                                                                                                                                                  18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1992;
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR41354;
                                                                                                                                                                                                                                                                   Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAR41354
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Allelic variants of epidermal growth factor 1. or 2-like domains - of merozoite surface protein 1, produced recombinantly for malaria
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                              The sequence is that of an allelic variant of a merozoite surface protein-1 epidetmal growth factor (EGF) 1 like domain. It may be used alone or as part of a fusion protein of EGF-1-like and EGF-2-like domains in vaccines against malaria. When expressed recombinantly it is produced in a form indistinguishable from that in the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of an allelic variant of a merozoite surface protein-1 epidermal growth factor (SGF) 1 like domain. It may be used alone or as part of a fusion protein of EGF-1-like and EGF-2-like domains in vaccines against malaria. When expressed recombinantly it is produced in a form indistinguishable from that in the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epidermal growth factor 1; merozoite surface protein 1; malaria;
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                                                                                                                                                                                                                                                                                                                                               Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "introduced to facilitate cleavage
  from recombinant protein"
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 105; DB 14;
Pred. No. 7.2e-08;
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 105; DB 14;
100.0%; Pred. No. 7.2e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blackman MJ, Chappel JA, Holder AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSP1EGF1B EGF1-like domain variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR41355 standard; peptide; 49 AA.
Claim 1; Fig la; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1b; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nsgcfrhldereeckcil 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-288413/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
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Matches

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16

Uthaipibull C;

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The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-1_4_2, and MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "amino acids derived from P. falciparum MSP1 p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel variants of the C-terminal fragment of Plasmodium merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surface protein-1, useful as vaccines for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                               Merozoite surface protein; protazoacide; vaccine; malaria
                                                                                                                                                                                                                                                                                                                                                               Syed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 22;
Pred. No. 1.5e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Morgan W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               Holder A, Birdsall B, Feeney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 15; 126pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
llarity 100.0%;
Conservative 0;
                                                Merozoite surface protein-119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                      99GB-0009072.
99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                           (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                       20-APR-2000; 2000WO-GB01558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 nsgcfrhldereeckcll 44
            27-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..95
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum,
                                                                                                                Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-015762/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                  WO200063245-A2.
                                                                                                                                                                                                                                                    20-APR-1999;
13-MAY-1999;
25-MAY-1999;
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                                                                                                                                                                                     26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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ID AAW3
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              δ
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            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of plasmodium MSP-142, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of plasmodium MSP-1, and mSP-1, and present sequence is the wild-type MSP-1 protein. This sequence was used to generate the variants of the present invention. The non-natural variants of the present invention. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uthaipibull C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to non-natural variants of a C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel variants of the C-terminal fragment of Plasmodium merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface protein-1, useful as vaccines for treating or preventing malaria -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 96;
                                                                                                                                                                                                                                                                                                          Merozoite surface protein; protazoacide; vaccine; malaria.
              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 105; DB 22;
100.0%; Pred. No. 1.3e-07;
iive 0; Mismatches 0;
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            Mismatches
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                                                                                                                                                                 AAB37608 standard; protein; 96
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99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                      Merozoite surface protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2000; 2000WO-GB01558
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                                                             nsgcfrhidereeckcil 33
                                               NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                      27-FEB-2001 (first entry)
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-015762/02
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es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AA;
                                                                                                                                                                                                                                                                                                                                                                             WO200063245-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAY-1999;
25-MAY-1999;
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          18;
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Gaps

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AAB37609 RESULT

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Length 108;

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This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 kD C-terminal fragment (P19), linked to a Glycosylephosophatidylinositol membrane anchoring sequence. P19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the P19 fragment provides a high level of protective immunity since it includes epitopes not presented in the P42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by restriction enzyme sequence used create the chimeric sequence"
                                                                                                                                                                                                                              Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35..127 /note= "derived from P. falciparum C-terminal p19 fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                 Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 105; DB 18;
Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                 Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..19 /rocte= "signal peptide" 20..127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22593 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Plasmodium vivax.
Chimeric - Plasmodium falciparum.
                                                                                                                               Barnwell JW, Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PfMSP1(p19)S protein sequence.
                                                 96FR-0001821.
                 97WO-FR00291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 nsgcfrhidereeckcll 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "m
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                                                                                 PASTEUR.
                                                                                                                                                                                 WPI; 1997-425034/39.
P-PSDB; AAW22592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1998
                                                                                 (INSP ) INST
(UYNY ) UNIV
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                 14-FEB-1997;
                                                 14-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum meroxoite surface protein 1 (MSPI) 19 kD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSPI from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
96..116
/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "amino acids derived from P. falciparum MSPI p19
fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                        Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein purification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium vivax, merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                  Mendis K, Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 105; DB 18;
larity 100.0%; Pred. No. 1.6e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22592 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                     Barnwell JW, Longacre-Andre S,
Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PfMSP1(p19)A protein sequence.
                                                                                                                                                  96FR-0001822.
                                                                                                                                                                                 PASTEUR.
NEW YORK STATE.
                                                                                                                  97WO-FR00290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 nsgcfrhldereeckcll 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96..116
/note= "g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
Synthetic.
                                                                                                                                                                                                                                                                                WPI; 1997-425033/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AA;
                                                                                                                                                                                                                                                                                                 N-PSDB; AAT94550
                                                                                                                                                                                 (INSP ) INST
(UYNY ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9730159-A2
                                                 WO9730158-A2
                                                                                                                14-FEB-1997;
                                                                                                                                                  14-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997
                                                                                 21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Gaps

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This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Aani613-Ser1705 which correspond to the 19 kD c-terminal fragment (p19) of MSP-1 from Plasmodium falciparum. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; treatment; cast extensions (SPF: Sporzacite surface protein: 2.5SP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apteal membrane antigen-1; ANA-1; erychrocyte binding antigen-175; seBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen: PEG-27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                       Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Derived from Honey bee"
23..359
/label- Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                           Barnwell JW, Longacre-Andre S, Mendis K, Nato F;
Roth C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 105; DB 18;
100.0%; Pred. No. 1.7e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70278 standard; Protein; 350 AA.
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                               Disclosure; Fig 1C; 85pp; French.
                                                97WO-FR00290.
                                                                             96FR-0001822.
                                                                                                                         NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 nsgcfrhldereeckcll 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Res 18; Conservative
                                                                                                            PASTEUR
                                                                                                                                                                                           WPI; 1997-425033/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AA;
                                                                                                                                                                                                             N-PSDB; AAT94549
                                                                                                       (INSP ) INST
(UYNY ) UNIV
                                                  14-FEB-1997;
                                                                             14-FEB-1996;
                                                                                                                                                                                                                                                        fragment - ug
purìfication
                      21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by restriction enzyme sequence used create the chimeric sequence"
                                                                                                                                                                                                                     Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35..127
/hote= "derived from P. falciparum C-terminal p19
fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                 Barnwell JW, Longacre-Andre S, Mendis K, Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note- "derived from P. vivax MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 105; DB 18;
100.0%; Pred. No. 1.7e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW36102 standard; Protein; 127 AA.
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Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                         Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PfMSP1(p19)S protein sequence.
                              97WO-FR00291,
                                                                                       PASTEUR.
NEW YORK STATE.
                                                           96FR-0001821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 nsgcfrhldereeckcll 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .127
                                                                                                                                                                           WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 127 AA;
                                                                                                                                                                                           P-PSDB; AAW22592
                                14-FEB-1997;
                                                                                       (INSP ) INST
(UYNY ) UNIV
                                                           14-FEB-1996;
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21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36102;
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                                                                                                                                               Roth C;
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MSP-2;

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(GENZ ) GENZYME TRANSGENICS CORP.
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX25586
                                          WPI; 1999-288313/24
P-PSDB; AAX56008.
                         Chen LH, Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-0CT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9920766-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-0CT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY05832;
                                                                                                                                                                                                                                                                              Sequence
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Matches
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                                                                                                                                                                                                                               The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetranus toxoid and 21 antigenic epitopes from circumsporozoite from tetranus toxoid and 21 antigenic epitopes from circumsporozoite protein (GSP), sporozoite surface protein-2 (SSP-2), liver stage protein (LSA-1), merozoite surface protein (MSP-1), MSP-2, apical membrane antigen (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein (AMA-1) and gamete specific antigen, Pfg77. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALWAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Main-CDC/NIIMALWAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                       Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
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Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSP-1; merozoite surface protein; malaria; vaccine;
protein engineering; protein expression; codon usage;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                               (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY09372 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                          P. falciparum in biological samples
                                                                                                                                                                                                                   Claim 3; Page 43-44; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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97US-0062592.
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                                                                                                                              Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1999 (first entry)
                                                          99WO-US18869.
                                                                             98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                                                                                                                                  WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
                                                                                                                                                             N-PSDB; AAZ51336.
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20-OCT-1997;
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                   WO200011179-A1.
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                                                                               21-AUG-1998;
                                                             19-AUG-1999;
                                         02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY09372;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                 Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an CC malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an CC malaria target for the development of a vaccine against comported to the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 compared to the native sequence (see has been modified (see AAX56008) compared to the native sequence (see nower the AT content (from 76 to 49.7%) and to eliminate IO mRNA cospenite. These alterations allow MSP-1-42 to be expressed in sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell culture and in transgenic mice. Native MSP-1-12 mammalian cell culture systems or in transgenic animals. The mammalian cell culture systems or in transgenic animals. The invention allows expression of MSP-1 protein in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Modified malarial protein for use in anti-malarial vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 105; DB 20;
100.0%; Pred. No. 4.4e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY05832 standard; Protein; 355 AA.
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                                                                               Example; Fig 1; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US22225.
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97US-0062592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Gaps

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This present sequence comprises a 42 kDa C-terminal portion of manaria merozotic surface protein MSP-1 (i.e. MSP-1-42), an impariant enerozotic surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. Nucleic acids (see AAX25586 and AAX25593) encoding MSP-1-42 have been modified according to a method of the invention in order to improve expression in mammallan cells and in transgenic animals. The invention provides modified recombinant nucleic acid sequences and methods for increasing the mRNA levels and protein expression of proteins that are difficult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified recombinant nucleic acid sequences useful for producing malarial DNA vaccine
              This present sequence comprises a 42 kDa C-terminal portion of manaria merozotice surface protein MSP-1 (i.e. MSP-1.42), an important target for the development of a vaccine against Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. A nucleic acid (see AAX56008) encoding MSP-1.42 has been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals by reducing the AT content and removing mRNA instability motifs. The invention allows expression of MSP-1-42 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSP-1; merozoite surface protein; malaria; vaccine;
protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

100.0%; Score 105; DB 20;

Best Local Similarity 100.0%; Pred. No. 4.5e-07;

Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05833 standard; Protein; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 43pp; English.
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97US-0062592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 nsgcfrhldereeckcll 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-302742/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen LH, Meade H;
                                                                                                                                                                                                                                                                                                                                           361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX25587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09920766-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-1998;
20-OCT-1997;
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*0000000000000x8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a 42 kDa C-terminal portion of malaria macrocite surface protein MSP-1 (i.e. MSP-1-42), an analaria macrocite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 compared to the native sequence (see AAX2588) compared to the native sequence (see AAX2587) such that 306 nucleocide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintential manala and sequence. These alterations allow MSP-1-42 to be expressed in provides modified recombinant nucleic acid sequences and methods for increasing the mRNA levels and protein expression of proteins that contein candidates for expression are those derived from lower collure systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower conganisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mNA instability motifs or rare codons relative to the recombinant expression system coding sequences of high AT content or which have mNA instability motifs or rare codons relative to the recombinant expression in the milk of transgenic animals, and also provides a DNA vaccine the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 105; DB 20;
100.0%; Pred. No. 4.4e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY09373 standard; Protein; 361 AA.
                                          Disclosure; Fig 1; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US22226
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97US-0062592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.

Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAX56009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9920774-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-1998;
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20-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sednence
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Gaps 6;

Indels

0;

Pred. No. 4.7e-07; Mismatches 0;

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Search completed: January 29, 2002, 10:21:45 Job time: 421 sec
 Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
                                                                         1 NSGCFRHLDEREECKCLL 18
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                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing malaria vaccine, useful for treatment or prevention of all forms of malaria in humans, by expressing immunogenic merozoite protein fragment in a baculovirus system \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a major merozoite surface protein-1 C-terminal fragment of 42kDa (MSP1-42). This fragment is linked to a malittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a malaria vaccine, which is used to treat or prevent malaria, caused by any of the four species of Plasmodium that infect humans.
                                                                                                                                                                                                                                                            Gaps
to express in cell culture systems, especially mammalian cell culture systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower organisms such as parasites, bacteria and viruses that have DNA conform sequences of high Ar content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Major merozoite surface protein-1; MSP1-42; melittin signal peptide; malaria vaccine.
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                           Length 361;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A major merozoite surface protein-1 fragment of 42kDa.
                                                                                                                                                                                                                        100.0%; Score 105; DB 20;
100.0%; Pred. No. 4.5e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                            AAB83926 standard; Protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYHA-) UNIV HAWAII.
(UYCH-) UNIV CHINESE HONG KONG.
(QUEE-) QUEEN EMMA FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HO WKK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1999; 99US-0165178.
01-DEC-1999; 99US-0168327.
22-AUG-2000; 2000US-0226861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2000; 2000WO-US31064.
                                                                                                                                                                                                                                                                                                               277 nsgcfrhldereckcll 294
                                                                                                                                                                                                                                                                                            1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-2001 (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-335879/35.
N-PSDB; AAF89840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 AA;
                                                                                                                                                                        Sequence 361 AA;
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100.0%; Score 105; DB 22; Length 375;

Query Match

(OT92U) XNAJ8 30A9 SIHT

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US-VOS-VOY-Y-19-1
Sequence 1, Application US/08290919
Patent No. 5720959
GENERAL INFORMATION:
APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: WACCINE
YITLE OF INVENTION: WACCINE
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STREET: 0.COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Z0023518

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBL
COMPUTER: IBM PC COMPATIBL
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
SOFTWARE: PATENTIN ROWATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-CCT-1994
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION NUMBER: PCT/CB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMENT (202) 861-3000
TELECAMENT (202) 861-3000
TELECAMENT (202) 861-3000
TELECAMENT (202) 822-0944
US-08-334-179A-8

US-08-326-110A-55

US-08-465-380-55

US-08-466-397-55

US-08-466-397-55

US-08-461-965-55

US-08-249-471-55

US-09-249-471-55

US-09-249-451-55

US-09-249-461-55

US-09-249-461-55

US-09-249-461-55

US-09-249-461-55

US-09-398-398-32

US-09-398-312

US-09-382-313

US-09-382-313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 48 amino acids TYPE: amino acid
     MOLECULE TYPE: protein FEATURE:
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                                                                                                                                                             January 29, 2002, 10:24:04; Search time 133.18 Seconds (without alignments) 3.041 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-290-919-2
US-08-290-919-2
US-08-290-919-11
PCT-US94-00198-1
US-08-10-284-1
US-08-10-284-1
US-08-10-33-2
US-09-946-049-2
US-09-946-049-2
US-09-946-049-2
US-09-938-2
US-09-382-911-2
US-08-015-985-6
US-08-015-985-6
US-08-015-985-6
US-08-015-985-6
US-08-015-985-6
US-08-015-985-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-981-392-13
US-08-334-179A-4
US-08-334-179A-2
                                                                                                                                                                                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                        US-09-763-397A-11
105
1 NSGCFRHIDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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26188
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Match Length
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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Pred. No. 1.3e-08;
Mismatches 0; Indels
                                                                                                                                                                                  Sequence 12, Application US/08290919

Sequence 12, Application US/08290919

Sequence 12, Application US/08290919

GENERAL INFORMATION:

APPLICANT: HOLDER, ANTHONY A.

APPLICANT: CHAPPEL, JONATHAN A.

APPLICANT: CHAPPEL, JONATHAN A.

TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA

TITLE OF INVENTION: VACCINE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS: 19

STREET: 1100 NEW YORK AVENUE, N.W.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMIT Release #1.0, Version #1.25
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
TILING DATE: 04-07-1994
TILING DATE: 04-07-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 43-55
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
FRICH APPLICATION NUMBER: PCT/GB93/00367
APPLICATION NUMBER: PCT/GB93/00367
ATTORNEY CAGENT INFORMATION:
NAME: KOKULIKS, PAÚL N.
REGISTRATION NUMBER: 16,773
REFERENCÉ/DOCKET NUMBER: 16,773
REFERENCÉ/DOCKET NUMBER: 212242/HCM/MJL/6BC8/TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 861-3000
TELEFAX: (202) 861-3000
TELEFAX: (202) 861-3000
TELEFAX: (202) 802-0944
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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100.0%;
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                                              1 NSGCFRHLDEREECKCLL 18
                                                                         15 NSGCFRHLDEREECKCLL 32
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           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE:
US-08-290-919-12
             18;
                 Matches
                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONNTHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                       Length 48;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REMANDLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER: E09 203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION NUMBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
NAME: KOKULIS, PAUL N.
TELECOMMUNICATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105; DB 1;
Pred. No. 1.3e-08;
                                                                                                                                                     ; Score 105; DB 1;
; Pred. No. 1.3e-08;
0; Mismatches 0;
                                                                         - Mand N, or N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STRRET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /label= X OTHER INFORMATION: /note= "X
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08290919
Patent No. 5720959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
100.0%;
                                              OTHER INFORMATION: /label= X OTHER INFORMATION: /note= "X US-08-290-919-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 861-3000
TELEFAX: (202) 862-944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 amino acids
                                                                                                                                                                                                                                              1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                     15 NSGCFRHLDEREECKCLL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY di
COMPUTER: IBM PC COMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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                                          LOCATION:
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US-08-290-919-2
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Best Local Similarity 53.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
PCT-0594-00198-2
SGUGNEC 2, APD11cation PC/TUS9400198
SGUGNEC 2, APD11cation PC/TUS9400198
SGUGNEC 1 INFORMATION:
APPLICANT SCHELING COLP.
TITLE OF INVENTION: RAS Associated GAP Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: 1 GIRAId Farms
                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUIN, PAUL G.
REGISTRATION NUMBER: 23,743
REFERENCE/DOCKET NUMBER: DX0352 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (201)822-7039
INFORMATION FOR ESQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2485 amino acids
"wrnp. amino acid
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CLASSIFICATION NUMBER: FILINGSAYOLES
CLASSIFICATION N.
PRIOR APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: LUND, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX0352 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)822-7255
TELEPHONE: (201)822-7255
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: NEW SELECT
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 6.0.8
SOFERMIRE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00198
               CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/00198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 564..9380
PCT-US94-00198-1
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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APPLICANT: BLACKMAN, MICHAEL J.

PEPLICANT: CHAPPEL, JONATHAN A.

TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA

TITLE OF INVENTION: VACCINE

TITLE OF INVENTION: VACCINE

CORRESPONDENCE ADDRESS: 19

ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.

STREET: 1100 NEW YORK AVENUE, N.W.

STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.5%; Score 53; DB 1; Length 106; Best Local Similarity 55.6%; Pred No. 0.67; Matches 10; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTR: U.C.
ALP. 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION NUMBER: 212000
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: CONSHITCH SERVICE CHARRACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Schering Corp.
TITLE OF INVENTION: RAS Associated GAP Proteins
VUMBER OF SEQUENCES:
CORRESSONNENCE ADDRESS:
ADDRESSEE: Schering Corp.
STREET: 1 Giraid Farms
CITY: Madison
STRATE: New Jersey
COUNTRY: USA
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: Machinosh
MEDIUM TYPE: Floppy disk
COMPUTER: Machicash
MEDIUM TYPE: Machinosh
MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 NAGCFRDDNGTEEWRCLL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-290-919-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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PCT-US94-00198-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08411389
Patent No. 5605799
GENERAL INFORMATION:
APPLICANT: White, Raymond L.
APPLICANT: Cawthon, Richard M.
APPLICANT: Li, Ying
TITLE OF INVENTION: NEUROFIBROMATOSIS TYPE 1 GENE IN HUMAN TUMORS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Cliviletti
STREE: DC
CITY: Washington
STATE: DC

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                                                                                                                                                   Length 2818;
                                                                                                                                                       Score 45; DB 1; Length 281 pred. No. 2.4e+02; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/411,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19780-107116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: US/08/047,088
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REFERNCE/OOCKET NUMBER: 19780-1071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08449933; Patent No. 58591055
Patent No. 58591055
Patent No. Application: Applicant No. 1010105; Applicant: Collins, Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....rarH: 2818 amino acids
TVPE: amino acid
TOPOLOGY: 11--
                                                                                                                                                            42.9%;
53.8%;
                                                                                                                                                       Query Match 42.9
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2818 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11111 | : : 1
709 CFRHLCEEADIRC 721
                                                                                                                                                                                                                                                                                                                                                                                             709 CFRHLCEEADIRC 721
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Best Local Similarity
Matches 7; Conserv
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US-08-510-284-1
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US-08-411-389-2
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Patent No. 5580355
Patent No. 5580355
Patent No. 5580355
Patent No. TOTALE OF INVENTION:
TITLE OF INVENTION: TO REVERSE ACTIVATED RAS INDUCED MALIGNANT TRANSFORMATION IN TITLE OF INVENTION:
TITLE OF INVENTION: MAMMALIAN CELLS
TITLE OF INVENTION: MAMMALIAN CELLS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
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BUBLICATION INFORMATION:
AUTHORS: Marchik, Douglas A.; Saulino, Ann M.;
AUTHORS: Tavakkol, Roxanne; Swaroop, Manju;
AUTHORS: Wallace, Magaret R.; Andersen, Lone B.;
AUTHORS: Milachell, Anna L.; Gutmann, David H.;
AUTHORS: Boguski, Mark; Collins, Francis S.
TITLE: CDMA Cloning of the Type I Neurofibromatosis Gene:
TITLE: Complete Sequence of the NFI Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                  42.9%; Score 45; DB 5; Length 2485; llarity 53.8%; Pred. No. 2.1e+02; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: GSA
2 IP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPETECT
APPLICATION NUMBER: US/08/510,284
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PRIOR APPLICATION DATA:
APPLICATION UNDBER: 08/071,575
FILING DATE: 1-JUNE-1993
ATTORNEY AGENT INFORMATION:
NAME: Harson, No. 580955man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5319
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAN: (212) 888-384
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 2881 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
LENGIH: 2485 amino acids
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 CFRHLCEEADIRC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CFRHLDEREECKC 16
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GY: linear
                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5580955
JOURNAL: Gen
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                                                                                                                                                                                                                                              ; ORGANISM:
PCT-US94-00198-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-510-284-1
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NAME/KEY: Modified-site

LOCATION: (2771-2772)

LOCATION: (2771-2772)

LOCATION: (2771-2772)

OTHER INFORMATION: Acid insertion of an 18 amino
OTHER INFORMATION: acid insertion(SEQ ID NO:10) representing an alternatively
OTHER INFORMATION: spliced product.

NAME/KEY: Modified-site

LOCATION: (1370-1371)
OTHER INFORMATION: /note= "Position of a 21 amino acid
OTHER INFORMATION: /note= "Position of a 21 amino acid
OTHER INFORMATION: /note= "Position of a 21 amino acid
OTHER INFORMATION: /note= "NEI catalytic domain"

LOCATION: 1125..1537
OTHER INFORMATION: /note= "NEI catalytic domain"

FEATURE:
FEATURE: REPORMATION: /note= "NEI catalytic domain"
                                                                  /note= "At variance with previously published sequence. Shows an CTG leucine codon rather than previously published CTC"
                                                                                                                                                                              FEATURE:
NAME/KEY: Modified-site
LOCATION: 1555
OTHER INFORMATION: //note= "At variance with previously
OTHER INFORMATION: published sequence. Lacks an extra CAT histidine condon af
OTHER INFORMATION: this residue"
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NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NOTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
AUTHORS:
Wallace, M.R. et al.
TITLE: Type 1 Neurofibromatosis Gene: Correction
VOLUME: 250
ISSUE: 12/21/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
LOCATION: 2746..2818
OTHER INFORMATION: /note= "Corresponding amino acids
OTHER INFORMATION: for the PstI-HindIII fragment designated pMAL.B3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
LOCATION: 65:371
OTHER INFORMATION: for the Hpal-Pstl fragment designated pMAL.HF3A.P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.4e+02;
2; Mismatches 4; Indels
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AUTHORS: Wallace, M.R. et al.
TITLE: Type 1 Neurofibromatosis Gene: Identification
TITLE: of a Large Transcript in Three NF1 Patients
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: FROM 1 TO 2818
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; RELEVANT RESIDUES IN SEQ ID NO: US-08-449-933-2
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Best Local Similarity 53.8%;
Matches 7; Conservative
       Modified-site
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709 CFRHLCEEADIRC 721
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                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                OTHER INFORMATION:
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07/13-1990
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                                                                                                                                                                                                                                                                                                                                                                                                     EATURE:
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LOCATION: 1395, 1306, 1400, 1423, 1426, 1430)
LOCATION: 1395, 1306, 1400, 1423, 1426, 1430)
OTHER INFORMATION: /no.t- "Invariant residues within
OTHER INFORMATION: most statistically significant regions of similarity among the OTHER INFORMATION: GAP family of proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "At variance with previously published sequence which shows an ATG methionine codon rather than an ATA isoleucine codon"
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LOCATION: group(1264..1290, 1345..1407, 1415..1430)
OTHER INFORMATION: 'Anote= "Most statistically
OTHER INFORMATION: significant regions of similarity among the GAP family of
OTHER INFORMATION: proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Cleavage-site
LOCATION: group 583..586, 815..818, 2573..2576, 2810..2813)
OTHER INFORMATION: //octe= "Potential CAMP-dependent
OTHER INFORMATION: protein kinase recognition sites"
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,933

FILING DATE: 25-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOORA, AUTOHORIER: 20344-20553.10

TELEPAN: (415) 813-5600

TELEFAN: (415) 813-5600

TELEFAN: (415) 813-5600

TELEFAN: (415) 813-5600

TELEEX: 70614 MRSNEYSENS

TELEFAN: (415) 813-5600

TELEEX: 70614 MRSNEYSENS

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

TURN THE COMMING ACTION AND ACTION A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2549..2556
COTHER INFORMATION: /note- "Potential tyrosine
OTHER INFORMATION: phosphorylation site"
APPLICANT: Wallace, Margaret R.
APPLICANT: Marchuk, Douglas A.
APPLICANT: Anderson, Lone B.
APPLICANT: Guttman, David H.
TITLE OF INVENTION: Neurofibromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: anino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSTITON IN GENOME:
CHROMOSOME/SEGMENT: 17q11.2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
LOCATION: group(1264, 12
LOCATION: 1395, 1396, 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                             STATE:
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/note= "At variance with previously published sequence. Shows an CTG leucine codon rather than previously published CTC"
                   /note= "At variance with previously published sequence which shows an ATG methionine codon rat than an ATA isoleucine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Position of an 18 amino OTHER INFORMATION: acid insertion(SEQ ID NO:10) representing an alternatively OTHER INFORMATION: spliced product" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /hote= "Position of a 21 amino acid OTHER INFORMATION: insertion representing an alternatively spliced product"
                                                                                                                                                                                                                                                                                                                           /note= "At variance with previously published sequence. Lacks an extra CAT histidine condon this residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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LOCATION:
LOCATION: /note= "Corresponding amino acids
OTHER INFORMATION: /note= "Corresponding amino acids
OTHER INFORMATION: /note hpal-xho! fragment designated pMAL.HF3A.X"
PUBLICATION INFORMATION:
AUTHORS: Wallace, M.R. et al.
JUTILE: Type 1 Neurofibromatosis Gene: Correction
JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Corresponding amino acids for the PstI-HindIII fragment designated pMAL.B3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Corresponding amino acids
for the HpaI-PstI fragment designated pMAL.HF3A.P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Wallace, M.R. et al. TITLE: Type I Neurofibromatosis Gene: Identification TITLE: Of a Large Transcript in Three NF1 Patients JOURNAL: Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: FROM 1 TO 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "NF1 catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%; Score 45; DB 4; Ilarity 53.8%; Pred. No. 2.4e+02; Conservative 2; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 12/21-1990
RELEVANT RESIDUES IN SEQ ID NO:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: 1555
OTHER INFORMATION: /note-
OTHER INFORMATION: publish
OTHER INFORMATION: this re
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
LOCATION: 2746..2818
OTHER INFORMATION: /note
OTHER INFORMATION: for t
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site LOCATION: (2771~2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: (1370~1371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site LOCATION: 65..371
                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Domain
LOCATION: 1125..1537
OTHER INFORMATION: /r
                                                                                                                                                      LOCATION: 1183
OTHER INFORMATION: OTHER INFORMATION: FEATURE:
LOCATION: 496
OTHER INFORMATION: OTHER INFORMATION: 1
OTHER INFORMATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 65..371
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CFRHLDEREECKC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
07/13/90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VOLUME: 250
ISSUE: 12/21/90
PAGES: 1749-
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-966-049A-2
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LOCATION: group(1264, 1276, 1358, 1377, 1389, 1390, 1391,
LOCATION: 1395, 1396, 1400, 1423, 1426, 1429, 1430)
OTHER INFORMATION: /note= "Invariant residues within
OTHER INFORMATION: most statistically significant regions of similarity among th
OTHER INFORMATION: GAP family of proteins"
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NAME/KEY: Modified-site
NAME/KEY: Modified-site
LOCATION: group(1264.11290, 1345..1407, 1415..1430)
OTHER INFORMATION: /noce= "Most statistically
OTHER INFORMATION: significant regions of similarity among the GAP family of
OTHER INFORMATION: proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Cleavage-site
LOCATION: group(583.586, 815..818, 2573..2576, 2810..2813)
LOCATION: JOICE "POTENTIAL CAMP-dependent
OTHER INFORMATION: protein kinase recognition sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/07/966,049A
FILING DATE: 02-0405
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 2549..2556
OTHER INFORMATION: /note- "Potential tyrosine
OTHER INFORMATION: phosphorylation site"
                                                                                     APPLICANT: COLLINS, Francis S.
APPLICANT: Wallace, Margaret R.
APPLICANT: Warchuk, Douglas A.
APPLICANT: Marchuk, Douglas A.
APPLICANT: Anderson, Lone B.
APPLICANT: Anderson, Lone B.
APPLICANT: Buttman, David H.
TITLE OF INVENTION: Neurofibromatosis Gene NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster STREET: 755 page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, Antoinette F.
REGISTRATION NUMBER: 34.002
REFERENCE/DOCKET NUMBER: 20344-20553.20
TELEPHONE: (415) 494-0792
TELEFAN: (415) 494-0792
TELEFAN: (415) 494-0792
TELEFX: 766141 MRSNPOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2818 amino acids
                   Sequence 2, Application US/07966049A; Patent No. 6238861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT: 17q11.2 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: anino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Modified-site
LOCATION: 2549..2556
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
  US-07-966-049A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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NAME/KEY: Modified-site LOCATION: 4 LOCATION: 4 LOCATION: 4 COUNTER INFORMATION: /product= "4Hyp" OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-841-483-2
; Sequence 2, 78-pplication US/08841483B
; Patent No. 5976875
; Genence 2, 78-pplication US/08841483B
; Patent No. 5976875
; Genence 2, 78-pplication US/08841483B
; Genence 2, 78-pplication US/08841483B
; APPLICANT: Bunting, Michaeline
; APPLICANT: Tang, Wen
; APPLICANT: Topham, Matthew
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 2037.2.1
; CURRENT PELLANG NUMBER: US/08/841,483B
; CURRENT FILING DATE: 1997-04-22
; EARLIER APPLICATION NUMBER: 60/016,210
; STUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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illarity 46.7%; Pred. No. 67;
Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.9%; Score 44; DB 1; Length 27;
Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-00-382-911-2
; Sequence 2, Application US/09382911
; Patent No. 6221658
                                                                                                         MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus purpurascens
FEATURE:
                                                                                                                                                                                                                                                                                                           Disulfide-bond
1..16
                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
8..20
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| NQKCFQHLDDCCSRKC 20
  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NSGCFRHLDEREECKC 16
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                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQ ID NO 2
| LENGTH: 567
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-08-841-483-2
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Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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US-08-619-936-1
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                                                                                               US-09-542-331-2

Sequence 2, Application US/09542331

SERIEM INFORMATION:

APPLICANT: Chong, VI

TITLE OF INVENTION:

TITLE OF INVENTION: NEI Protein and Its Role in Activation

TITLE OF INVENTION: Adealy! Cyclase by PACAP38-Like Neuropeptides

CURRENT APPLICATION NUMBER: US/09/542,331

CURRENT APPLICATION NUMBER: US 09/046,745

EARLIER FILING DATE: 1998-03-24

SEABLIER FILING DATE: 1998-03-24

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PREASED for Windows Version 4.0

SEQ ID NO 2

LENGTH: 2818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2818;
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Pred. No. 2.4e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREY APPLICATION DATA:
APPLICATION NUMBER: US/08/619,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08619936
Fatent No. 567286
GAREAL INFORMATION:
APPLICANT: Terlau, Heinrich
APPLICANT: Terlau, Heinrich
APPLICANT: Grilley, Michelle
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptide PVIIA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
ATTORNET INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24260-107674-04
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 2
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11111 | ::|
709 CFRHLCEEADIRC 721
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CRGANISM: Human
US-09-542-331-2
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US-08-619-936-1
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US-08-015-985-6
                                    APPLICANT: Bunting, Michaeline
APPLICANT: Bunting, Michaeline
APPLICANT: Bunting, Michaeline
APPLICANT: Tang, Wen
APPLICANT: Tang, Wen
APPLICANT: Topham, Matthew
TITLE OF INVENTION: Diacytglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Methods of Use Thereof
FILE REFERENCE: 2037.2.1a of Use Thereof
CURRENT APPLICATION NUMBER: US/09/382,911
CURRENT APPLICATION NUMBER: 08/841,483
PRIOR PILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/016,210
PRIOR PILING DATE: 1996-04-22
PRIOR PILING DATE: 1996-04-22
SOFTWARE: PatentIn Ver. 2.0
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US-08-015-985-6
Sequence 6, Application US/08015985
Fatent No. 5538886
GENERAL INFORMATION:
APPLICANT: Sap, Jan M.
TITLE OF INVENTION: PHOSPHATASE-ALPHA
NUMBER OF EXQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
COUNTRY: US-N. NORK
COUNTRY: US-N. N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 4; Length 567;
Pred. No. 67;
3; Mismatches 5; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM FC compatible
COMPUTER: LBM FC compatible
COMPUTER: LBM FC compatible
COMPUTER: LBM FC compatible
COMPUTER: LBM FC COMPATION:
COMPUTER: PATENTIN FC COMPATION FTILING DATE: LO FEB 193
CLASSITICATION NUMBER: US/08/015,985
ATTORNEY/AGENT INFORMATION:
APPLICATION 1435
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acid
TYPE: amino acid
TYPE: ANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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95 DEGCLRKADKRFQCK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-382-911-2
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LENGTH: 567
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GenCore version 4.5
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- protein search, using sw model OM protein

January 29, 2002, 10:26:39 ; Search time 144.96 Seconds (Without alignments) 9.459 Million cell updates/sec Run on:

Title: Perfect score:

US-09-763-397A-11 105 1 NSGCFRHLDEREECKCLL 18 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		major merozoite su	merozoite surface	major merozoite su	major merozoite su		major merozoite su	major merozoite su	major merozoite su	probable major sur	major merozoite su	merozoite surface	major blood-stage		major merozoite su	c	kinesin light chai	kinesin light chai	keratin type II, h	keratin type II -		clusterin - quail	neurofibromatosis-	neurofibromin I -	neurofibromin - mo	hypothetical prote		pletotrophic effec	aggrecan precursor	kappa-conotoxin PV
		ID		A40040	S47282	SAZQK1	S05603	A54498	A26868	SAZQGM	A45948	A24594	A45546	A39401	A45604	A28121	A45532	F82532	C41539	153013	A61368	157463	S07714	150131	B55282	JC5196	154352	T16580	S15197	F85921	9	A58997
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		Match Length		400	651	1631	1639	1701	1701	1726	1726	1640	1785	1726	1751	680	1772	298	260	269	479	495	449	451	2818	2820	2825	13055	116	116	2109	27
æ	Ouery	Match		0.00T	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.2	58.1	57.1	57.1	50.5	50.5	•		43.8	•	•	42.9	•	42.9		•	42.9	42.4	42.4	42.4	41.9
		Score		COT	105	105	105	105	105	105	105	100	61	9	9	23	23	46	46	46	S	45.5	45	45	45	45	45	45	44.5	•	44.5	44
	Result	NO.		- + •	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

hypothetical prote prote protein-tyrosine-p	protein-tyrosine-p	hypothetical 8.1K	hypothetical prote	clusterin precurso	Spot 3 protein and	hypothetical prote	hypothetical prote	hypothetical prote	probable membrane	chorismate mutase	clusterin precurso	WD-repeat protein	androgen-regulated
B84809 JC1285	A36065 A47373	J01429	T27079	A42108	T47542	T25804	T19210	T16494	T36724	S26053	A35744	T50211	S28258
7	٦,	7	7	7	7	7	7	7	7	_	7	7	7
1444	802	75	386	446	623	1127	191	278	297	387	439	206	176
41.9	41.0	40.0	40.0	40.0	39.5	39.5	39.0	39.0	39.0	39.0	39.0	39.0	39.0
44443	4 4 3 3	42	42	42	41.5	41.5	41	41	41	41	41	41	41
30 31	333	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	

major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments

C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 17-Feb-1994 #text_change 09-Jun-2000
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000
C; Accession: A45545
R; Blackman, M.J; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
Mol. Blochem. Parasitol. 49, 29-33, 1991
A; Title: Proteolytic processing of the Plasmodium falciparum merozoite surface proteil
A; Reference number: A45545; MuID:92131048
A; Reference number: A45545
A; Accession: A45545
A; Molecule type: DNA
A; Residues: 1-400 < BLA>
A; Residues: 1-400 < BLA>
A; Residues: 1-400 < BLA>
C; Superfamily: major merozoite surface antigen
C; Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Gaps .; 0 Length 400; Indels 100.0%; Score 105; DB 2; 100.0%; Pred. No. 2.3e-08; Live 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 18; Conservative

ö

1 NSGCFRHLDEREECKCLL 18 o. Vo

301 NSGCFRHLDEREECKCLL 318 qq

RESULT 2
847282
merozoite surface antigen 1 - malaria parasite (Plasmodium falciparum) (strain RO-71)
C; Species: Plasmodium falciparum
A; Variety: strain RO-71
C; Species: Ob-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000
C; Accession: 847282
R; Tolle, R.; Bujard, H.; Cooper, J.A.
submitted to the EMBL Data Library, July 1994
A; Description: Plasmodium falciparum: recombination within the C-terminal region of m A; Reference number: 847282
A; Accession: 847282
A; Rocession: 847282
A; Residues: 1-651 < TOL>
A; Reperimental source: Strain RO-71
C; Superfamily: major merozoite surface antigen
C; Reywords: glycoprotein; merozoite; surface antigen

ö Gaps ; Length 651; Indels Query Match 100.0%; Score 105; DB 2; Best Local Similarity 100.0%; Pred. No. 3.5e-08; Matches 18; Conservative 0; Mismatches 0;

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major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (Sypecies: Plasmodium falciparum) (Sypecies: Plasmodium falciparum) (Sypecies: Plasmodium falciparum) (Sybecies: Plasmodium falciparum) (Syaccession: A54498 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 (Syaccession: A54498 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 (Syaccession: A54498 #sequence_revision Principarum Prochem: Parasitol: 27, 291-302, 1988 Principarum Prochem: Parasitol: 27, 291-302, 1988 Principarum Prochem: A54498 #uID:88142999 Ayrelence number: A54498 #uID:88142999 #uID:88142999 Ayrelence number: A54498 #uID:88142999 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:8814299 #uID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAZOGM
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
N:Alternate names: 195K glycoprotein
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000
C;Accession: A2386; 506501
A;Weber, J.L.; Leininger, W.M.; Lyon, J.A.
Nucleic Acids Res. 14, 3311-3323, 1986
A;Title: Variation in the gene encoding a major merozoite surface antigen of the huma
A;Reference number: A23386; MUID:86205236
A;Reference number: A23386; MUID:86205236
A;Residues: 1-1104 <WEB1>
A;Residues: 1-1104 <WEB1>
A;Residues: 1-1104 <WEB1>
A;Cross-references: EMBL:X03831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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Pred. No. 8.2e-08;
Mismatches 0;
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Pred. No. 8.2e-08;
Mismatches 0;
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tive 0;
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Best Local Similarity 100.0%; P. Matches 18; Conservative 0;
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Best Local Similarity 100.
Matches 18; Conservative
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A; Residues: 1-1701 <TAN>
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A26868
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S05603
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
N.Alternate names: gp195 surface antigen
C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jun-2000
R:Wyler, P.J.
Submitted to the EMBL Data Library, April 1989
A:Reference number: S05603
A:Rocession: S05603
A:Roser-references: EMBL:X15063; NID:g9896; PIDN:CAA33163.1; PID:g9897
R:Wyler, P.J.
Nuclectide and deduced amino acid sequence of the gp195 (MSA-1) gene from plasm
A:Reference number: S04850
A:Rocession: S0485
                                                                                                                                                                                                                                            ASALOKI
majorn merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
C; Species: Plasmodium falciparum falciparum) (st
C; Species: Plasmodium falciparum
C; Species: A5120
C; Scession: A5120
R; Mackay, M.; Goman, M.; Bone, N.; Hyde, J.E.; Scaife, J.; Certa, U.; Stunnenberg, H.; E
EMBO J. 4 3813-3819, 1985
A; Title: Polymorphism of the precursor for the major surface antigens of Plasmodium falc
A; Reference number: A91030; MUID:86136024
A; Recession: A5120
A; Residues: 1-1631 <AAC>
C; Comment: The merozoite stages of different strains have strain-specific surface antige
C; Comment: P alciparum has three stages: sporozoite, merozoite, and gametocyte. The merozoite surface antigen; tandem repeat; transmembrane prote
C; Superfamily: major merozoite surface antigen; tandem repeat; transmembrane prote
C; Superfamils: major merozoite surface antigen #status predicted AMT>
F; 1-19/Domain: signal sequence #status predicted AMD>
F; 20-1631/Product: major merozoite surface antigen #status predicted AMD>
F; 67-84/Region: 3-residue repeats (S-G-Ty)
F; 1614-1631/Domain: membrane anchor #status predicted AMD>
F; 97, 259, 755, 759, 835, 911, 955, 1049, 1156, 1165, 1436, 1563/Binding site: carbohydrate (Asn) (
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Pred. No. 8e-08;
Mismatches 0; Indels 0
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Pred. No. 7.9e-08;
Mismatches 0;
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ilarity 100.0%;
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                                             552 NSGCFRHLDEREECKCLL 569
1 NSGCFRHLDEREECKCLL 18
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major merozoite surface antigen precursor - Plasmodium chabaudi chabaudi cispecies: Plasmodium chabaudi chabaudi cispecies: Plasmodium chabaudi chabaudi cispecies: Plasmodium chabaudi di chacession: A4546

R.Deleersnijder, W.; Hendrix, D.; Bendahman, N.; Hanegreefs, J.; Brijs, L.; Hamers-Ca A; Cochem. Parasitol. 43, 231-44, 1990

A; Title: Molecular cloning and sequence analysis of the gene encoding the major meroz A; Reference number: A4556

A; Accession: A4556

A; Status: preliminary

A; Molecule type: mRNA

A; Rossidues: 1-1786 CDEL>

A; Rossidues: 1-1786 CDEL>

A; Cossidues: Caperfamily: major merozoite surface antigen
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Cippecies: Plasmodium vivax
Cippecies: Plasmodium vivax
Cipate: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Nov-1999
Cipate: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Nov-1999
Cipate: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 24-Nov-1999
Cipate: Procession: A39401
Airitle: Primary structure of the merozoite surface antigen 1 of Plasmodium vivax rev
Airitle: Primary structure of the merozoite surface antigen 1 of Plasmodium vivax rev
Airitle: Primary
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major blood-stage surface antigen Pv200 - Plasmodium vivax
C;Species: Plasmodium vivax
C;Species: Plasmodium vivax
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45604
R;Gibson, H.L.; Tucker, J.E.; Kaslow, D.C.; Krettli, A.U.; Collins, W.E.; Kiefer, M.C
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                                               Length 1640;
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                                          Score 100; DB 2; L4
Pred. No. 4.5e-07;
; Mismatches 0;
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55.6%; Pred. No. 0.48;
tive 4; Mismatches
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Pred. No. 0.35;
3; Mismatches
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                                    95.2%;
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Best Local Similarity 61.1%;
Matches 11; Conservative
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                                          Query Match 95.2
Best Local Similarity 94.4
Matches 17; Conservative
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Matches 10; Conserv
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R:Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.

Nucleic Acids Res. 16, 1206, 1988

A;Title: Merozotte surface protein sequence from the Camp strain of the human malaria pa A;Title: Merozotte surface protein sequence from the Camp strain of the human malaria pa A;Teference number: S06361, MUD:88143999

A;Accession: S06361

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1104-1726 <WBE2>

A;Crowment: The merozoite stages of different strains have strain-specific surface antige C;Comment: The merozoite surface antigen c;Comment: The merozoite surface antigen c;Superfamily: major merozoite surface antigen c;Superfamily: major merozoite surface antigen c;Fi2-19/Domain: signal sequence #status predicted <SIG>
F;20-1726/Prodouct: major merozoite surface antigen %status predicted <MAT>
F;20-1726/Prodouct: major merozoite surface antigen %status predicted <MAT>
F;67-19/Domain: signal sequence #status predicted <SIG>
F;20-1766/Prodouct: major merozoite surface antigen %status predicted <MAT>
F;67-19/Domain: signal sequence #status predicted <MAT>
F;77-765/Region: 3-residue repeats (F-E-P)
F;77-765/Region: 3-residue repeats (F-E-P)
F;77-765/Region: 3-residue repeats (F-E-P)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carbohy
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PASSAL

Probable major surface antigen (83K, 19K, 42K) precursor - malaria parasite (Plasmodium

C;Species: Plasmodium falciparum

C;Species: Da-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jun-2000

C;Accession: AA5594

R;Holder, A.A.; Lockyer, M.J.; Odink, K.G.; Sandhu, J.S.; Riveros-Moreno, V.; Nicholls,

Nature 317, 270-273, 1985

A;Title: Primary structure of the precursor to the three major surface antigens of Plasm

A;Reference number: A24594; MuID:86014355

A;Mocession: A24594

A;M
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major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
C;Species: Plasmodium falciparum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C;Accesion: A45948
R;Chang, S;P: Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A;Reference number: A45948; MID:89005525
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Pred. No. 8.4e-08;
; Mismatches 0;
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A Status: preliminary
A Molecule type: DNA
A Residues: 1-1726 <CHA>
A Cross references: GB:M37213
C Superfamily: marozo merozoite surface antigen
C; Keywords: surface antigen
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Length 1772;

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Score 53; DB 2 Pred. No. 5.5; 3; Mismatches

50.5%;

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A;Cross_references: GB:J03975; NID:g160081; PID:g160082
C;Superfamily: major merozoite surface antigen
C;Reywords: surface antigen
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Best Local Similarity
Matches 8; Conserv
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Matches 10; Conserv
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Major merozoite surface antigen precursor - Plasmodium yoelli

C; Species: Plasmodium yoelli
C; Species: Date: Date: Plasmodium yoelli
C; Species: Date: Old-Unu-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999
C; Accession: A4532; A45531
R; Lewis, A. P.
Mol. Blochem. Parasitol. 36, 271-282, 1989
A; Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface A; Reference number: A4532; MUID:90014981
A; Accession: A4533
A; Accession: A4533
A; Accession: A4533
A; Residues: 1-1772 <LEW>A; Long, C.A.
A; Residues: 1-1772 <LEW>A; Long, C.A.
Mol. Blochem. Parasitol. 36, 283-285, 1989
A; Reference number: A45331; MUID:90014982
A; Reference number: A45331; MUID:90014982
A; Reference number: A45331
A; Accession: A45331
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A 20121

A 2
A;Title: Structure and expression of the gene for Pv200, a major blood-stage surface and A;Reference number: A45604; MUID:92158013
A;Accession: A45604
A;Status: preliminary
A;Moteria : preliminary
A;Moteria : preliminary
A;Moteria : 1-1751 - G(1B>
A;Cross-references: GB:M75674; NID:g160608; PID:g457336
A;Otes: sequence extracted from NCBI backbone (NCBIN:83591, NCBIP:83592)
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
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Pred. No. 0.49;
4; Mismatches 4; Indels
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55.68;
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Best Local Similarity 55.6%
Matches 10; Conservative
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isopentenyl monophosphate kinase XF2645 [imported] - Xylella fastidiosa (strain 9a5c) (5pecies: Xylella fastidiosa on 20-Aug-2000 #text_change 02-Sep-2000 (5) decession: R92532 (5) decession: P82532 (5) decession: P82532 (5) decession: P82532 (6) decession: P82532 (6) decession: P82532 (7) decession: Decesi
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Pred. No. 13;
2; Mismatches
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us-09-763-397a-11.rpr

-Mon Eeb 4 15:23:35 2002

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                                 mus musculu
homo sapien
caenorhabdi
             homo sapien
                        homo sapien
                                                                  homo sapien
guillardia
                                                                                        arabidopsis
cyanidium c
                                                                                                           porphyra pu
escherichia
 caenorhabdi
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS, SEQUENCE FROM N.A.
BAD M., TOOLLE K., BUJATCH H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Maded=3004972; Maded=8613604. Scalfe J., Certa U., Mackay M., Goman M., Bone N., Hyde J.E., Scalfe J., Certa U., Stunnenberg H., Bujard H.; Eplymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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PIR; A25120; SAZOKI.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; POlyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                P11862
076013
021974
014246
078461
P49261
09tm25
P51386
P76188
           09y3a5
043903
                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5839;
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MEROZOITE SURFACE PROTEIN:
TRIPEPTIDE SG(TP) REPEAT.
MEMBRANE ANCHOR.
N-LINKED (GLCNAC...) (POT.
                                                                                                                                                                                                              PRT; 1630 AA
                                                                                                                                                        ALIGNMENTS
           YC97_HUMAN
GAS2_HUMAN
GAS2_MOUSE
KIM6_HUMAN
UNC8_CAEEL
EMR1_HUMAN
                                                                                     RS23_ARATH
FTRC_CYACA
FTRC_PORPU
YDHL_ECOLI
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P04932;
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MSP1_PLAFK
  P04933 plasmodium
P1958 plasmodium
P18819 plasmodium
P08569 plasmodium
P50494 plasmodium
P50495 plasmodium
P13828 plasmodium
P50495 xylella fas
O88447 mus musculu
P37285 rattus norv
Q07666 homo sapien
P07789 pence ratus norv
P21359 homo sapien
P07898 gallus gall
P56633 conus purpu
P52429 homo sapien
P07898 gallus gall
P5663 conus purpu
P52429 momo sapien
P07898 gallus gall
P56433 homo sapien
P07898 gallus gall
P5643 momo sapien
P07898 gallus gall
P5645 momo sapien
P07898 gallus gall
P5649 momo sapien
P07898 gallus gall
P5649 momo sapien
P1805 mus musculu
Q00848 strawberry
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8.183 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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PGCA_CHICK
CXK7_CONPU
PTPA_RAT
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BMR2_HUMAN
                                                                           January 29, 2002, 11:13:41
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Gaps

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-i- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE OF 1032-1682 FROM N.A.
MEDLINE-95354793; PubMed=762856;
Tolle R., Bujard H., Cooper J.A.;
"Plasmodium falciparum: variations within the C-terminal region of "Plasmodium falciparum: variations within the C-terminal region of antiqen-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: AFTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSPI_PLAR3 STANDARD; PRT; 1682 AA.
P19558; 025921.
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MERGZOITE SURRACE PROTEIN 1 PRECURSOR (MERGZOITE SURFACE ANTIGENS)
                        (POTENTIAL).
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MEMOZOTE SURFACE PROTEIN 1.

MEMBRANE ANCHOR (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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EMBL; 23525; CAA68280.1; -
EMBL; 23525; CAA6855.1; -
FIR; S06266; S06266;
Fir; S06008; EGF: 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPT anchor.
SIGNAL
                                                                                                                                                                                                                                                    Length 1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate ro-33 / Ghana).
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5834;
                                                                                                                                                                                                                                                                                                        Indels
N-LINKED (GLCNAC...) (F
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N-LINKED (GLCNAC...) (F
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N-LINKED (GLCNAC...) (F
N-LINKED (GLCNAC...) (F
MW; ZCZ5586616C87F6E CRCC
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ilarity 100.0%; Pred. No. 1.7e-08;
Conservative 0; Mismatches 0;
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1058 105
1165 116
1174 117
1445 144
1526 152
1639 AA;
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Matches 18; Conserv
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MSPL_PLAF3

ID AC P1959B

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EN GN MS
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      SOLUTION
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MEDLINE-86014355; PubMed-2995820;
Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V.,
Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
Freeman R.R.;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 31, Last annotation update)
MEROZOITE SURPACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE AWTIGENS)
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MENCOTIE SURFACE PROTEIN 1.

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).
   GGCNAC...) (POTENTIAL).
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GGLCNAC...) (POTENTIAL).
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PIR, A24594; A24594.
InterPro; IPR000561; EGF-like.
Edm; PPR0008. EGF; 1.
Malaria; Merozolite; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                Length 1630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate Wellcome).
Eukaryota: Alveolata; Apicomplexa: Haemosporida; Plasmodium.
NCBL_TaxID=5848;
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                                                                                                                                                 INKED (GLCNAC. . .) (POTI
ADBDEC3CE0A46322 CRC64;
                                                                                                                                                                                                                                             100.0%; Score 105; DB 1;
100.0%; Pred. No. 1.7e-08;
tive 0; Mismatches 0;
   N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC.
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les 18; Conservative
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P04933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-88011243; PubMed=3079521;
Tanabe K., Mackay M., Goman M., Scalfe J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite plasmodium falciparum.";
"Mol. Biol. 195:273-287(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 (Rel. 08, Created)
50 (Rel. 39, Last sequence update)
70 (Rel. 39, Last annotation update)
50 (Rel. 39, Last annotation update)
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MEROZOITE SURPACE PROFEIN 1.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
       1089 N-LINKED (GLCNAC. . .) (POTENTIAL).
1196 N-LINKED (GLCNAC. . .) (POTENTIAL).
1588 N-LINKED (GLCNAC. . .) (POTENTIAL).
AA, 193719 MW; 3920B75E73038552 CRC64;
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PIR; A26868; A26868.
INT: B25120; B25120.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                   Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate mad20 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=70153;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                   Score 105; DB 1;
Pred. No. 1.8e-08;
; Mismatches 0;
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Best Local Similarity 100.(
Matches 18; Conservative
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30-MAY-2000
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P08569;
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       CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-BRI4299): PubMed-2449612;
MEDLINE-BRI4299): PubMed-2449612;
Peterson M.G., Coppel R.L., Kemp D.J.,
Brown G.V., Anders R.E., Kemp D.J.;
"Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum";
Plasmodium falciparum";
MOI. Biochem. Parasitol. 27:291-302(1988).
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PTW: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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POTENTIAL.

MERCOSITE SURFACE PROTEIN 1.

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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                                                                                                                                                                                                                                                                                                                                                        Length 1682;
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Ekkaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium
NCBL_TAXID=9813.
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100.0%; Pred. No. 1.8e-08;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                              Gaps
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PTW. MENOZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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01-0c1-1996 (Rel. 34, Last sequence update)
01-0c1-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEMS)
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-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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InterPro; IPR000561; EGF-like.
Pfam, PF00008; EGF, 1.
Malaria; Merczotle; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                       Length 1726;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-57270;
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MEROKOITE SURFACE PROTEIN 1.
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  N-LINED (GLCNAC...) (F
N-LINED (GLCNAC...) (F
N-LINKED (GLCNAC...) (F
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Pred. No. 1.8e-08;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 18; Conservative
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MEDLINE-68143999; PubMed-9230296;
Webber J.L., Sim B.K.L., Lyon JA., Wolff R.;
"Merozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum";
Nucleic Acids Res. 16:1206-1206(1988).
--- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                             Gaps
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BELLINE-SEG02235, pubmed-331099,
Weber J.L., Leininger W.M., Lyon J.A.;
Weber J.L., Leininger W.M., Lyon J.A.;
"Variation in the gene encoding a major merozoite surface antigen of the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:331-3323(1986).
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1 - PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.AGG-1987 (Rel. 05, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
MEROZOITE_SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

BROZOGIE SURFACE PROTEIN 1.

N-LINKED GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                    Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5835;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                  Query Match 100.0%; Score 105; DB 1; Best Local Similarity 100.0%; Pred. No. 1.8e-08; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1726 AA.
                                                                                                                                                                                              193768 MW;
                                                                                                                                                                                                                                                                                                                                                  1602 NSGCFRHLDEREECKCLL 1619
                                                                                                                                                                                                                                                                                                                               1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
  536
607
607
608
809
809
919
965
991
1089
1198
1198
1701 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PMMSA) (P195).
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
MSP1_PLAFC
ID MSP1_PLAFC
AC P04934;
                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
                                                              CARBOHYD
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-17XL;
MEDLINE-88124889; PubMed-2448778;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
"The 3' portion of the gene for a Plasmodium yoelii merozoite surface "The 3' portion of the gene for a Plasmodium yoelii merozoite surface "The 3' portion of the gene for a Plasmodium yoelii merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).

1 PTH: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major merozoite surface antigens of Plasmodium yoelii.";
Mol. Blochem. Parasitol. 39:285-288(1990).
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 85:602-606(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen encodes the epitope recognized by a protective monoclonal antibody.";
                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(CRC64;
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MEROZOITE SURFACE PROTEIN 1.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                           (POTENTIAL)
        (POTENTIAL)
                                (POTENTIAL)
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                                                                                                                                                                                                                                     Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                           Indels
N-LINKED (GLCNAC...) (
                                                                                                                                                            5B59CEEFA2F9A026
                                                                                                                                                                                                                                     Score 105; DB 1;
Pred. No. 1.8e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90205979; PubMed-2320061;
Lewis A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1093-1772 FROM N.A.
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                                                                                                                                                                                                                                     100.0%;
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1016
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AA; 196174 M
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                                                                                                                                                                                                                                                                                                                                                                         1627 NSGCFRHLDEREECKCLL 1644
                                                                                                                                                                                                                                                                                                                                           1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium berghei yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; GPI-anchor
                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1772
1772
54
406
646
829
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     944
990
1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990
01-JAN-1990
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P13828;
  CARBOHYD
CARBOHYD
CARBOHYD
                                                                              CARBOHYD
CARBOHYD
CARBOHYD
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CARBOHYD
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CARBOHYD
                                                                                                                                                            SEQUENCE
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MSP1_PLAYO
MSP1_PLAYO
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DI O1-JANN
DI O1-OCT-DE
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OX NCB1_TY
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OX NCB1_TY
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Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alvarenga R.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargol L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carler G.M.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca E.C., Eranco M.C., Frohme M., Furlan L.R.,
RA Hoper J.E., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Langret F., Lambais M.R., Late L.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matukuma A.Y.,
Marchae M.V., Martins E.A.L., Martins E.M.F., Matukuma A.Y.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matukuma A.Y.,
Marques M.V., Martins E.A.L., Matuka M.A.,
Marques M.V., Martins E.A.L., Matuka M.A.,
Marques M.V., Martins E.A.L., Matuka M.A.,
Mardues M.V., Matuka R.C., Palmieri D.A., Paris A.,
Mardues M.V., Matuka R.C., Palmieri D.A., Paris A.,
Mardues M.V., Matuka R.C., Palmieri D.A., Paris A.,
Matuka A.G.K., Peredra H.A. Tr., Pesquero J.B.,
A de Silva A.C.K., de Silva A.M., de Souza A.J.M.,
A de Silva A.C.K., de Silva A.M., de Souza A.J.M.,
A de Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
Ra Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RA Lingarion J. Perugion S. L. Meidanis J., Setubal J.C.;
Rado M.A., Zatz M., Meidanis J., Setubal J.C., Satubal J.C., Satubal J.C., Satubal J.C., Satubal J.C., Satubal J.C., Satuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
4-DIPHOSPHOCYIDYL-2-C-METHYL-D-ERYTHRITOL KINASE (EC 2.7.1.-) (CMK)
(4-CYTIDINE-5'-DIPHOSPHO)-2-C-METHYL-D-ERYTHRITOL KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: DEOXYXYLULOSE-5-PHOSPHATE PATHWAY (DXP) OF ISOPRENOID
                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                         (POTENTIAL).
  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bācteria; Proteobacteria; gamma subdivision; Xanthomonas group;
Xylella.
                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                            Score 53; DB 1; Length 1772; Pred. No. 1.9;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                            -> V (IN REF. 2).
; 9A6291658EB0F45D CRC64;
N-LINKED (GLCNAC...) (F
N-LINKED GLCNAC...) (F
N-LINKED (GLCNAC...) (F
N-LINKED (GLCNAC...) (F
N-LINKED GLCNAC...) (I
N-LINKED (GLCNAC...) (I
N-LINKED (GLCNAC...) (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-9A5C;
MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                  1672 NAGCFRDDNGTEEWRCLL 1689
                                                                                                                                                                                                                            50.5%;
55.6%;
                                                                                                                                                                 AA; 197230
                                                                                                                                                                                                                                                                                                           1 NSGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                            Query Match 50.5
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  1018
1090
1408
1446
1541
1629
1680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                        1408
1446
1541
1629
1680
1521
1772
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                                          CARBOHYD
CARBOHYD
                                                                                  CARBOHYD
CARBOHYD
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                         CARBOHYD
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REPEAT
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P37285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BALBAC; TISSUG-Brain;
STRAIN-BALBAC; TISSUG-Brain;
BEDLINE-98288268; PubMed=9624122;
RADMMAN A., Friedman D.S., Goldstein L.S.;
"Two kinesin light chain genes in mice. Identification and characterization of the encoded proteins.";
"Two kinesin light chain genes in Mice. Identification and characterization of the encoded proteins.";
"I Biol. Chem. 273:15395-15403(1998).
"I FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING POTENT THAT MAY PAY PLAY A ROLE IN ORGANELLE TRANSPORT. THE LIGHT CHAIN MAY FUNCTION IN COUPLING OF CARGO TO THE HEAVY CHAIN OR IN THE MODULATION OF ITS ATPASE ACTIVITY.

"IT OLICOMERIC COMPLEX COMPOSED OF TWO HEAVY CHAIN S AND ""..." TITLE TO LICOMERIC COMPLEX COMPOSED OF TWO HEAVY CHAINS AND ""..."
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                           ;
0
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MGD; MGI:107978; KICI.
InterPro; IPR00215; Kinesin_light.
InterPro; IPR001440; TPR.
InterPro; PR001440; TPR.
Ffan; PR00181; TRN:SINLIGHT.
SMART; SM00028; TR; 4.
PROSITE: PS01160; KINESIN_LIGHT; 3.
Motor protein; Microtubules; Coiled coil; Repeat; TPR repeat.
DOMAIN
23 152 COILED COIL.
TPR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWO LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE KINESIN LIGHT CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 6 TPR REPEATS.
                                                                                                                                                                                                                                                                                    Length 298;
                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                  Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                         ATP (POTENTIAL).
972DB2DAF4722AD1 CRC64;
                                                                                                                                                                                                                                                                                  Score 46; DB 1;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KNSS OR KLC1.
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF055665; AAC27740.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                   Complete proteome.
NP_BIND 109 119 A:
SEQUENCE 298 AA; 31800 MW;
                                                                                                                                                                                                                                                                              43.8%;
                                                                                                                                                   EMBL; AE004071; AAF85442.1;
                                                                                                                                                                                                                                                                                                                                                                                         253 SGCFVEFSTRDEAECAL 269
                                                                                                                                                                                                                                                                                                                                                  2 SGCFRHLDEREECKCLL 18
                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLC1_MOUSE
088447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLC1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9205221; PubMed-1946431;
Cyr J.L., Pfister K.K., Bloom G.S., Slaughter C.A., Brady S.T.;
Molecular genetics of kinesin light chains: generation of isoforms
by alternative splicing.".
1- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
PROTEIN THAT MAY PLAY A ROLE IN ORGANELE TRANSPORT. THE LIGHT
CHAIN MAY FUNCTION IN COUPLING OF CARGO TO THE HEAVY CHAIN OR IN
THE MODULATION OF ITS ATPASE ACTIVITY.
1- SUBUNIT: OLICOMERIC COMPLEX COMPOSED OF TWO HEAVY CHAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; A, B AND C (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN
                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHT; 4.
Coiled coil; Repeat; TPR repeat;
                                                                                                                            Score 46; DB 1; Length 537;
Pred. No. 7.1;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE KINESIN LIGHT CHAIN FAMILY.
                                                                             60926 MW; 1EE2E52444F287B5 CRC64;
                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KNSI OF KLCI OR KLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL.
TPR 1.
TPR 2.
TPR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M75148; -; NOT_ANNOTATED_CDS.
EMBL; M75147; -; NOT_ANNOTATED_CDS.
EMBL; M75146; -; NOT_ANNOTATED_CDS.
Interpro; IPR002151; Kinesin_light.
Interpro; IPR001440; TPR.
Pfam; PF00515; TPR; 5.
PR.NTS; PR000381; RTNSINLIGHT.
SMART; SM000281; PR; 4.
PROSITE; PS01160; KINESIN_LIGHT; 4.
PROSITE; PS01160; KINESIN_LIGHT; 4.
TPR 2.
TPR 3.
TPR 4.
TPR 5.
                                                                                                                            43.8%;
                                                                                                                                                         Conservative
                                                                                                                                                                                                         418 NKPIWMHAEEREECK 432
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
 282
324
366
409
492
                                                                                                                                                                                     1 NSGCFRHLDEREECK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWO LIGHT CHAINS.
 249
291
333
376
459
537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing.
                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209
251
293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL DEATH.
                                                                  MIM; 600025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLUS_COTJA
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells.";
                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                              REPEAT
                                        EMBL;
                                                   EMBL;
                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLUS_COTJA
                                                                                                                                                                                                                                                                                                                                           Matches
  ò
                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDDTTDDDDTTDDDDTTDDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN PRODUCT MAY WELL UNDERGO ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES. MOSTLY ABUNDANT IN BRAIN AND SPINE.
-!- SIMILARITY: BELONGS TO THE KINESIN LIGHT CHAIN FAMILY.
-!- SIMILARITY: CONTAINS 6 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94099888; PubMed-8274221;
Cabeza-Arvelaiz Y., Shih L.-C.N., Hardman N., Asselbergs F.,
Bilbe G., Schmitz A., White B., Siciliano M.J., Lachman L.B.;
"Cloning and genetic characterization of the human kinesin light-chain
                                      MISSING (IN ISOFORM B).
VSMSVEWNGMRRMKLGLVK -> A (IN ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT. THE LIGHT CHAIN MAY FUNCTION IN COUPLING OF CARCO TO THE HEAVY CHAIN OR IN THE MODULATION OF ITS ATPASE ACTIVITY.

-1- SUBUNIT: OLIGOMERIC COMPLEX COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT CHAINS.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerber S., Rozet J.M., Perrault I., Ducrog D., Souied E., Munnich A.,
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- ALTERNATIVE PRODUCTS: AS FOR THE RAT KINESIN LIGHT CHAIN, THE
                                                                                                                                 ö
                                                                                                       43.8%; Score 46; DB 1; Length 556, 53.3%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                 1A843B34BCDDB53E CRC64;
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF267530; AAF72543.1; EMBL; AF26718; AAF72543.1; JOINED. BMBL; AF267519; AAF72543.1; JOINED. EMBL; AF267520; AAF72543.1; JOINED. EMBL; AF267521; AAF72543.1; JOINED. EMBL; AF267523; AAF72543.1; JOINED. EMBL; AF267524; AAF72543.1; JOINED. EMBL; AF267524; AAF72543.1; JOINED.
TPR 4.
TPR 5.
TPR 6.
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Cell Biol. 12:881-892(1993).
                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                              KINESIN LIGHT CHAIN 1 (KLC 1).
KNS2 OR KLC1 OR KLC.
                                                                 63247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L04733; AAA16576.1; -.
                                                                                                                                 Conservative
                                                                                                                                                                        STANDARD;
                                                                                                                                                        1 NSGCFRHLDEREECK 15
             377
460
538
538
538
556 AA;
                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606,
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Q07866;
            REPEAT
REPEAT
VARSPLIC
VARSPLIC
SEQUENCE
 REPEAT
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Michel D., Chatelain G., Herault Y., Brun G.;
Michel D., Chatelain G., Herault Y., Brun G.;
Michel D., Chatelain G., Herault Y., Brun G.;

alternative promoters with distinct regulatory elements.";

Eur. J. Blochem. 229:115-223(1995)

-! FUNCTION: NOT YET CLEAR, IT IS KNOWN TO BE EXPRESSED IN A VARIETY
OF TISSUES AND IT SEEMS TO BE ABLE TO BIND TO CELLS, MEMBRANES,

AND HYDROPHOBIC PROTEINS. IT HAS BEEN ASSOCIATED WITH PROGRAMMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Neuroretina;
MEDLINE-89239492; PubMed-2541393;
Michel D., Gillet G., Volovitch M., Pessac B., Calothy G., Brun G.;
Michel D., Gillet G., Volovitch M., Pessac B., Calothy G., Brun G.;
"Expression of a novel gene encoding a 51.5 kD precursor protein is induced by different retroviral oncogenes in quail neuroretinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                     PROSITE; PS01160; KINESIN_LIGHT; 4.
Motor protein; Microtubules; Coiled coil; Repeat; TPR repeat;
Alternative splicing.
23 152 COILED COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5D9376C3EEDD00FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY DIFFERENT RETROVIRAL ONCOGENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE CLUSTERIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 1;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0AN-1990 (Rel. 13, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLUSTERIN PRECURSOR (51.5 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                        TPR 1.
TPR 3.
TPR 4.
TPR 5.
                                                                                                                                          Interpro; IPR002151; Kinesin_light.
Interpro; IPR001440; TPR.
Pfam; PF00515; TPR; 5.
AF267526; AAF72543.1; JOINED.
AF267527; ARF72543.1; JOINED.
AF267528; AAF72543.1; JOINED.
AF267529; AAF72543.1; JOINED.
                                                                                                                                                                                                                            PRINTS; PR00381; KINESINLIGHT.
SMART; SM00028; TPR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncogene Res. 4:127-136(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NSGCFRHLDEREECK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 4
569 AA:
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120:1048-1054(1996).

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NF1_HUMAN
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                                                                                                                                                                                                                                                                           ALPHA-CHAIN (LARGE SUBBNIT) (FOLENHIAL).
INTERCHAIN (BY SIMILARITY).
INTINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                   BETA-CHAIN (SMALL SUBUNIT) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Wistar; TISSUE-Brain;
Kyritsis A.P., Lee P.S., Mochizuki H., Nishi T., Levin V.A., Saya Differential splicing of the neurofibromatosis type 1 (NFI) generats: Homologous splice variants in human are expressed in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Wistar; TISSUE-Brain; MEDLINE=97137538; PubMed=8982875; Suzuki H., Takahashi K., Yasumoto K., Fuse N., Shibahara S.; "Differential tissue-specific expression of neurofibromin isoform mRNAS in rat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                             KQNNTIE -> SRTTP (IN REF. 1).
8CF811225C5B22F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 451;
8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFIBROMIN (NEUROFIBROMATOSIS-RELATED PROTEIN NF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 2820 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45;
Pred. No. 8
                                                                                                                                                                                                                                                       CLUSTERIN
                                                                                                                      PIR; S07714; S07714.
InterPro; IPR000753; Clusterin.
Pfam; PF01093; Clusterin; 1.
SMART; SM00035; CLa; 1.
SMART; SM00300; CLb; 1.
PROSITE; PS00492; CLUSTERIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [nt. J. Oncol. 1:149-152(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                             EMBL; X15825; CAA33823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.98;
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293 SAGCLRMRDECEKCREIL 310
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51800 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                         Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                          CHAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                             DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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P97526;
                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
-!- FUNCTION: STIMULATES THE GTPASE ACTIVITY OF RAS. NF1 SHOWS GREATER AFFINITY FOR RAS GAP, BUT LOWER SPECIFIC ACTIVITY. MAY BE A REGULATOR OF RAS ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-90139792; PubMed=2134734;

Mallace M.R., Marchuk D.A., Andersen L.B., Letcher R., Odeh H.M.,

Saulino A.M., Fountain J.W., Breteton A., Nicholson J., Mitchell A.L.,

Brownstein B.H., Collins F.S.;

"Type 1 neurofibromatosis gene: identification of a large transcript
disrupted in three NT patlents.";

Science 249:181-186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete human NF1 cDNA sequence: two alternatively spliced mRNAs and absence of expression in a neuroblastoma line.";
DNA Cell Biol. 11:727-734(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bernards A., Haase V.H., Murthy A.E., Menon A., Hannigan G.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1354 1357 POLY-SER.
2820 AA; 317080 MW; FC108487E86DA89F CRC64;
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Wallace M.R., Marchuk D.A., Andersen L.B., Collins F.S.;
Science 250:1749-1749(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF1_HUMAN STANDARD; PRT; 2839 AA. P21359, 000662; 014284; 014930; 09UMK3; 01-MAY-1991 (Rel. 18, Created) 01-MAY-1991 (Rel. 29, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) NEUROFIBROMIN (NEUROFIBROMATOSIS-RELATED PROTEIN NF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 1;
Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0509; RAS_GTPASE_ACTIV_1; 1. PROSITE; PS50018; RAS_GTPASE_ACTIV_2; 1. GTPASE activation 1337 1432 RAS-GAP
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MEDLINE=93090270; Pubmed=1457041;
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InterPro; IPR01251; CRAL_TRIO.
InterPro; IPR001936; RasGAP.
Ffam; PF00616; RasGAP; I
SMART; SM00323; RasGAP; I
SMART; SM00516; SEC14; I.
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53.8%;
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711 CFRHLCEEADIRC 723
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SEQUENCE
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Xu G., O'Connell P., Viskochil D., Cawthon R.M., Robertson M.,
Culver M., Dunn D., Stevens J., Gesteland R., White R., Welss R.;
"The neurofibromatosis type 1 gene encodes a protein related to GAP.";
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MEDLINE=97156204; PubMed=9002664;
Regnier V., Meddeb M., Lecointre G., Richard F., Duverger A.,
Nguyen v.C., Dutrillaux B., Bernheim A., Danglot G.,
"Emergence and scattering of multiple neurofibromatosis (NFI)-related
sequences during hominoid evolution suggest a process of
pericentromeric interchromosomal transposition.";
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of the NF1 gene product.";
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                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE-92412152; PubMed-1339276;
Suzuki H., Takahashi K., Kubota Y., Shibahara S.;
"Molecular cloning of a CDNA coding for neurofibromatosis type 1
protein isoform lacking the domain related to ras GTPase-activating
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Andersen L.B., Ballester R., Marchuk D.A., Chang E., Gutmann D.H.,
Saulino A.M., Camonis J., Wigler M., Collins F.S.;

"A conserved alternative splice in the von Recklinghausen
eurofibromatosis (NRI) gene produces two neurofibromin isoforms,
both of which have GTPase-activating protein activity.";

Mol. Cell. Biol. 13:487-495(1993).
SEQUENCE FROM N.A. (ISOFCRM 1).
BEDLINE-92147138; Pubmed-1783401.
Marchuk D.A., Saulino A.M., Tavakkol R., Swaroop M., Wallace M.R., Andersen L.B., Mitchell A.L., Gutmann D.H., Boguski M.S.,
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Li Y., O'Connell P., Breidenbach H.H., Cawthon R.M., Stevens J., Xu G., Neil S., Robertson M., White R., Viskochil D.;
"Genomic organization of the neurofibromatosis 1 gene (NF1).";
Genomics 25:9-18(1995).
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MEDLINE-91029515; PubMed-2121370;
Martin G.A., Viskochil D., Bollag G., McCabe P.C., Crosier W.J.,
Haubruck H., Conroy L., Clark R., O'Connell P., Cawthon R.M.,
Innis M., McCormick F.;
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MEDLINE-92019823; PubMed-1923522;
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                                                                                                                                                                                             of the NF1 gene product.";
Genomics 11:931-940(1991)
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two codons toward the 3' end of the gene.";
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MEDLINE-92109786; PubMed-1662505;
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"Brain tumors predominantly express the neurofibromatosis type 1 gene transcripts containing the 63 base insert in the region coding
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"The NFI locus encodes a protein functionally related to mammalian
"The NFI locus encodes.";
Cell 63:851-859(1990).
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MEDLINE=93258316; PubMed=1302608;
Upadhyaya M., Shen M.H., Cherryson A., Farnham J., Maynard J.,
Huson S.M., Harper P.S.;
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Hum. Mol. Genet. 1:735-740(1992).
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heteroduplex analysis on Hydrolink gels.";
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J. Med. Genet. 33:2-17(1996).
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                                                                                                                                                                                                         for GTPase activating protein-related domain.";
Biochem. Biophys. Res. Commun. 181:955-961(1991).
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RN [23]
RP VARRANT NF1 ALA-2631.

RX MEDLINE-96091873; PubMed-8544190;
RA Upadhyaya M., Maynard J., Osborn M.J., Huson S.M., Ponder M.,
RA Ponder B.A.J., Harper P.S.;
RA Tonder B.A.J., Harper P.S.;
RT "Characterisation of germline mutations in the neurofibromatosis type
RI J. Med. Genet. 32:706-710(1995).
RL J. Med. Genet. 32:706-710(1995).
RN [24]
RP VARRANT NF1 ARG-629.
RX MEDLINE-96431167; PubMed-8834249;
RA Gasparini P. D'Agruma L., de Cillis G.P., Balestrazzi P.,
RA Mingarelli R., Zelante L.;
RT "Scanning the first part of the neurofibromatosis type 1 gene by RNA-
RT SCSC: identification of three novel mutations and of two new
RT SCSC: identification of three novel mutations and of two new
RT POLYMORPHISMS.";
RL Hum Genet. 97:492-495(1996).
RY MEINT NF1 ARG-1035.
RX MEDLINE-96400960; PubMed-8807336;
Query Match
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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EMBL, AF329535; AAK19354.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
Plassmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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iive 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Last sequenc
01-JUN-2001 (TrEMBLrel. 17, Last annotat
MEROZOITE SURRACE PROTEIN 1 (FRAGMENT).
Plasmodium falciparum.
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Best Local Similarity 100.
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                                                     Search time 285.36 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                        fotal number of hits satisfying chosen parameters:
                                                                                                                                          473505 seqs, 146272329 residues
                                                    January 29, 2002, 11:12:12;
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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09BJV5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
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Maximum DB seq length: 200000000
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Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falloiparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329508; AAK19327.1;
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                                         Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.; "Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum."; Bubmitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF329507; AAK19326.1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Last annotation update)
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100.0%; Pred. No. 4.8e-10;
Live 0; Mismatches 0;
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Pred. No. 4.8e-10;
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01-JUN-2001 (TrEMBLrel. 17, Last annotat
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Matches 18; Conserv
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SEQUENCE FROM N.A.

Blacen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329510; AAK19329.1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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isolates of Plasmodium falciparum.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF329509; AAK19328.1; -.
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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100.0%; Pred. No. 4.8e-10;
Live 0; Mismatches 0;
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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SEQUENCE FROM N.A.

Blasen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

"Antiqualic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field sloates of Plasamodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF329513; AAX19332-1; ...
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT)
                  100.0%; Score 105; DB 5;
100.0%; Pred. No. 4.8e-10;
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Baddeley A., Erl R., Saul A.;

Bannigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasamodium falloparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR329517; AAK1936.1; -.
                                                                                                                                                                        SEQUENCE FROM N.A.

Elsen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOTTE SURFACE PROTEIN 1 (FRAGMENT).
Plasmodium falciparum.
ENKARYOTE, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID-5833;
                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Matches 18; Conservative
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Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.; "Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum."; but the CDC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF329518; AAK19337.1;
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in independent field
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                  77 AA; 8587 MW; 4EA799FF4B4E69D4 CRC64;
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100.0%; Pred. No. 4.8e-10;
iive 0; Mismatches 0;
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100.0%; Pred. No. 4.8e-10;
ive 0; Mismatches 0;
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EMBL; AF329520; AAK19339.1; -.
NON_TER 1 1
NON_TER 77 77
SEQUENCE 77 AA; 8587 MW; 4EA799FF4B4E69D4 CRC64;
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Search completed: January 29, 2002, 11:12:12 Job time: $768\ \mathrm{sec}$

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P. yoelii combined Mature xenoxin-3 p Xenoxin-3. Xenopu Human BRCA2 tumour

Modified merozoite Modified merozoite

Sequence of the P1 MSP1EGF2B EGF2-11k

A major merozoite Human pancreatic

P. falciparum synt

Mature xenoxin-1.
Mature xenoxin-1 p

Xenoxin-1. Xenopu Xenoxin-2. Xenopu Pre-xenoxin-1 prot Human protein sequ Human death domain Zea mays protein f Zea mays protein f Amino acid sequenc Merozoite surface

Pre-xenoxin-1.

Searched:

Database

Sednence:

Run on:

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; ANA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen, Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum MSP-1 antigenic epitope, P598.
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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AAR4388
AAR62970
AAR52970
AAR55134
AAW09390
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AAY 09373
AAY 05833
AAY 09374
AAY 05834
AAW 54145
AAP 50777
AAR 41357
AAB 83926
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AAB37611
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AAB01957
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AAR38596
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AAB69602
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WO200011179-A1.
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 RESULT
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Merozoite surface
PfMSP1(p19)A prote
PfMSP1(p19)A prote
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PfMSP1(p19)S prote
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Merozoite surface
Merozoite surface
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MSP1EGF2A EGF2-lik
                                                                                      (without alignments)
4.528 Million cell updates/sec
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          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                         hits satisfying chosen parameters:
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Listing first 45 summaries
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    protein search, using sw model

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WPI; 2000-237654/20

Result No.

Peptide #6926 enco Wild-type Ramos ce High affinity stre Human lambda light Human lambda light

Variable region of Human Ab light cha

Huntingtin minimal

Claim 2; Fig 2a; 35pp; English.

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merozoite surface protein-1 (MSP-1) of the asexual blood stage of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg77. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allelic variants of epidermal growth factor 1- or 2-like domains - of merozoite surface protein 1, produced recombinantly for malaria vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
          Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                               The present sequence is the antigenic epitope P598, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epidermal growth factor 1; merozoite surface protein 1; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from recombinant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106; DB 21;
Pred. No. 8.1e-08;
; Mismatches 0;
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                                                                              Claim 2; Page 16; 52pp; English
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Matches 19; Conservative
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Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteolytic cleavage of Plasmodium MSP-14-2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-14-2, and has the same affinity for at least one third antibody that inhibits the proteolytic cleavage of Plasmodium MSP-14-2, compared to natural MSP-11-2, The present sequence is the wild-type MSP-1 protein. This sequence was used to generate the variants of the present invention. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uthaipibull C;
                     The sequence is that of an allelic variant of a merozoite surface protein-1 epidermal growth factor (EGF) 2-like domain. It may be used alone or as part of a fusion protein of EGF-1-like and EGF-2-like domains in vaccines against malaria. When expressed recombinantly it is produced in a form indistinguishable from that in the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel variants of the C-terminal fragment of Plasmodium merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface protein-1, useful as vaccines for treating or preventing
                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                     Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Syed S,
                                                                                                                                                                                      100.0%; Score 106; DB 14; 100.0%; Pred. No. 2.2e-07;
                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feeney J, Morgan W,
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 48; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                   AAB37608 standard; protein; 96 AA.
                                                                                                                                                                                                                      :
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99US-0311817.
99CA-2271451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merozoite surface protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2000; 2000WO-GB01558
                                                                                                                                                                                                                                                     1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                      23 edsgsngkkitcectkpds 41
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                      19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holder A, Birdsall B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treat malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-015762/02
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 AA;
                                                                                                                                        54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200063245-A2.
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25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                 AAB37608;
                                                                                                                                           Sequence
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Length 96;

DB 22;

100.0%; Score 106;

Query Match

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65

õ g RESULT AAB37609

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/note= "glycosylphosphatidylinositol anchoring sequence"
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                                                                                                                                                                                                             /note= "amino acids derived from P. falciparum MSP1 p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                              Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium vivax; merozoite surface protein; MSP1; p19;
Plasmodium falciparum; malaria; vaccine; immunity; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                              Plasmodium vivax; merozoite surface protein; MSP1; p19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106; DB 18;
Pred. No. 4.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnwell JW, Longacre-Andre S, Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW22592 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                              fragment"
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                                            PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PfMSP1(p19)A protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                             97WO-FR00290.
                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIV NEW YORK STATE.
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             25-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EDSGSNGKKITCECTKPDS
                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                              PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-425033/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT94550
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                                                                                                                                                                                                                                                                                            WO9730158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              INSP ) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment - um
                                                                                                                                                                                                                                                                                                                                                             14-FEB-1997;
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                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to non-natural variants of a C-terminal fragment of a Plasmodium merozoite surface protein-1 (MSP-1). The non-natural variants have reduced affinity for at least 1 antibody capable of blocking a second antibody that inhibits the proteclytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least one third antibody that inhibits the proteclytic cleavage of Plasmodium MSP-1_4_2, and has the same affinity for at least MSP-1_4_2, compared to natural MSP-1_1_9. The non-natural variants of the present invention are useful for immunising a mammal against malaria, and can be used to treat malaria. The present sequence is MSP-119 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uthaipibull C;
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel variants of the C-terminal fragment of Plasmodium merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                surface protein-1, useful as vaccines for treating or preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                            Merozoite surface protein; protazoacide; vaccine; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                              Indels
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4.1e-07;
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            Pred. No. 3.7e-07;
Mismatches 0;
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100.0%; Pred. No. 4.1
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morgan
                                                                                                                                                                           AAB37609 standard; Protein; 108 AA.
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100.08; Fi
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                                                                                                                                                                                                                                                                             Merozoite surface protein-119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99GB-0009072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDICAL RES COUNCIL.
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99CA-2271451
                                                                              edsgsngkkitcectkpds 83
                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000; 2000WO-GB01558
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                                                                                                                                                                                                                                              (first entry)
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             Best Local Similarity 100.
Matches 19; Conservative
                                                            1 EDSGSNGKKITCECTKPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holder A, Birdsall B,
                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-015762/02.
N-PSDB; AAC68977.
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25-MAY-1999;
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Best Local Sim
Matches 19;
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malaria

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AAW36103 RESULT

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Gaps

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This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 kD c-terminal fragment (P19) of MSP-1 from Plasmodium falciparum. P19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recomblant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high level of protective immunity since it includes epitopes not presented in the P42 fragment.
                                                                                      33..34 /note= "encoded by restriction enzyme sequence used to create the chimeric sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment – useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                      35..127 // Anote= "derived from P. falciparum C-terminal p19 fragment of MSP1"
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                                                                   /note= "derived from P. vivax MSP1"
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100.0%; Pred. No. 4.8e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mendis K, Nato
                                 /note= "mature protein"
"signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1C; 85pp; French.
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Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                    Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PfMSP1(p19)S protein sequence.
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                                                                                                                                                                                                                                                                                                                                                               (INSP ) INST PASTEUR.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                          97WO-FR00291.
                                                                                                                                                                                                                                                                                                                              96FR-0001821.
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Matches 19; Conservative
 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                  Barnwell JW,
                                                                                                                                                                                                                   WO9730159-A2
                                                                                                                                                                                                                                                                                          14-FEB-1997;
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                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      Roth C;
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                                                                                                                                        96..116
/note= "glycosylphosphatidylinositol anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a recombinant protein comprising amino acids 1613-1705 of the Plasmodium falciparum merozoite surface protein 1 (MSP1) 19 KD C-terminal fragment (p19), linked to a glycosylphosphatidylinositol membrane anchoring sequence. p19 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the p19 fragment provides a high lavel of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                      /note= "amino acids derived from P. falciparum MSP1 p19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant protein containing Plasmodium merozoite surface protein-1 p42 fragment - useful in antimalarial vaccines, also new antibodies for diagnosis and protein purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric; Plasmodium vivax; merozoite surface protein; MSP1; p19; Plasmodium falciparum; malaria; vaccine; immunity; epitope.
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100.0%; Pred. No. 4.4e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               Mendis K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW22593 standard; Protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric - Plasmodium vivax.
Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1B; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                 Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PfMSP1(p19)S protein sequence.
                                                                                                                                                                                                                                                                                                         96FR-0001821
                                                                                                                                                                                                                                                                                                                                           PASTEUR.
NEW YORK STATE.
                                                                                                                                                                                                                                                                      97WO-FR00291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
              Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-425034/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW22592
                                                                                                                                                                                                                                                                                                                                           (INSP ) INST
                                                                                                                                                                                                                                                                                                                                                            (UYNY ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                               Barnwell JW,
                                                                                                                                                                                              W09730159-A2
                                                                                                                                                                                                                                                                      14-FEB-1997;
                                                                                                                                                                                                                                                                                                         14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1998
                                                                                                                                                                                                                                  21-AUG-1997
                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22593;
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Roth C;

Query Match

67

g ò

Key Peptide

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Gaps

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Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA;
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ51336
                                                                                                                                                               WO200011179-A1.
                                                                                                                                                                                                          19-AUG-1999;
                                                                                                                                                                                                                                21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1999
                                                                                                                                                                                     02-MAR-2000.
                                                                                                                                                                                                                                                     (NAIM-) NAT
           honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY09372;
                                                                                    Peptide
                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY 09372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of a chimeric protein comprising amino acids 1-32 of the Plasmodium vivax merozoite surface protein 1 (MSP1) linked to amino acids Asn1613-Ser1705 which correspond to the 19 KD C-terminal fragment (pl9) of MSP-1 from Plasmodium falciparum. pl9 is the C-terminal fragment of the 42 kD MSP1 from Plasmodium species. The recombinant protein can be used for the production of anti-malarial vaccines, where the pl9 fragment provides a high level of protective immunity since it includes epitopes not presented in the p42 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; treal epicope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein:2; SSP-2; liver stage antigen-1; LSA-1; marcoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
                                                                       /note- "encoded by restriction enzyme sequence used to create the chimeric sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                              Recombinant protein containing the merozoite surface protein-1 p19 fragment - useful in anti-malarial vaccines, diagnosis and protein
                                                                                                        /note= "derived from P. falciparum C-terminal p19
fragment of MSP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                  'note- "derived from P. vivax MSP1"
                                                                                                                                                                                                                                                              Nato F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 106; DB 18;
100.0%; Pred. No. 4.8e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                              Mendis K,
                   20.127
/note= "mature protein"
1..19
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1C; 85pp; French.
                                                                                                                                                                                                                                                               Longacre-Andre S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 edsgsngkkitcectkpds 117
                                                                                                                                                                                  97WO-FR00290
                                                                                                                                                                                                        96FR-0001822
                                                                                                                                                                                                                                          (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Conservative
                                                                                              35..127
                                                                                                                                                                                                                               (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                              WPI; 1997-425033/39.
N-PSDB; AAT94549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AA;
                                                                                                                                                                                                                                                              Barnwell JW,
                                                                                                                                         WO9730158-A2
                                                                                                                                                                                    14-FEB-1997;
                                                                                                                                                                                                        14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                  purification
                                                                                                                                                              21-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                    Protein
Peptide
                                                                                                                                                                                                                                                                          Roth C;
                                         Reg ton
                                                               Reg ton
                                                                                              Region
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag. T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                            23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 106; DB 21;
; Pred. No. 1.2e-06;
0; Mismatches 0;
                                                                                                                                                                      1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY09372 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozoite surface protein MSP-1-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmodium falciparum life cycle
                                                                 Chimeric - Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
Chimeric - Apis sp.
Chimeric - Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lal AA, Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 edsgsngkkitcectkpds 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INST IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
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98WO-US22225.
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                                                                                                                                                                                                                   malarial DNA vaccine
                                                                                                                                                    WPI; 1999-302742/25
                                                                                                                         Chen LH, Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animal.
                                                                                                                                                                       N-PSDB; AAX25586
                  20-OCT-1998;
                                                15-MAY-1998;
                                                                20-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09920774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY09373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY09373
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      QΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 has been modified (see AAX56008) compared to the native sequence (see AAX56009) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence. These alterations allow MSP-1-42 to be expressed in mammallan cell culture and in transgenic mice. Native MSP-1-12 is known to be difficult to express in cell culture systems, mammalian cell culture systems or in transgenic animals. The invention allows expression of MSP-1 protein in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 355;
                                                                                                                                                                                                                                                                                                                                Modified malarial protein for use in anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
MSP-1; merozoite surface protein; malaria; vaccine;
protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSP-1; merozoite surface protein; malaria; vaccine;
protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106; DB 20;
Pred. No. 1.3e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY05832 standard; Protein; 355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                          (GENZ ) GENZYME TRANSGENICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                               Example; Fig 1; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 edsgsngkkitcectkpds 345
                                                                                                                                                    98WO-US22226.
                                                                                                                                                                                                97us-0062592.
                                                                                                                                                                                98US-0085649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                            Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                      WPI; 1999-288313/24.
                                                                                                                                                                                                                                                          Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic animal.
                               transgenic animal,
                                                                                                                                                                                                                                                                                                    P-PSDB; AAX56008
                                                                                                                                                    20-0CT-1998;
                                                                                                                                                                                15-MAY-1998;
                                                                                                                                                                                              20-OCT-1997;
                                                                                         W09920774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09920766-A2
                                                                                                                      29-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05832;
                                                                                                                                                                                                                                                          Chen LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY 05832
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The present sequence represents a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The nucleic acid sequence encoding MSP-1-42 has been modified (see AAX2586) compared to the native sequence (see AAX2587) such that 306 nucleotide positions have been replaced to lower the AT content (from 76 to 49.7%) and to eliminate 10 mRNA instability motifs while maintaining the same protein amino acid sequence. These alterations allow MSP-1-42 to be expressed in mammalian cell culture and in transgenic mice. The invention provides modified recombinant nucleic acid sequences and methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified recombinant nucleic acid sequences useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 protein in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increasing the mRNA levels and protein expression of proteins that are difficult to express in cell culture systems, mammalian cell culture systems or in transgenic animals. The preferred difficult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein candidates for expression are those derived from lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 106; DB 20; Local Similarity 100.0%; Pred. No. 1.3e-06; les 19; Conservative 0; Mismatchee 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merozoite surface protein MSP-1-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY09373 standard; Protein; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 43pp; English.
                                                                                                                            (GENZ ) GENZYME TRANSGENICS CORP
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98US-0085649.
97US-0062592.
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(GENZ ) GENZYME TRANSGENICS CORP.
 malarial DNA vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                       AAY09374;
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                           AAY09374
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                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                       This present sequence comprises a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. A nucleic acid (see AAX56008) encoding MSP-1-42 has been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals by reducing the AT content and removing mRNA instability moutls. The invention allows expression of MSP-1-42 in the milk of transgenic animals, and also provides a DNA vaccine comprising a vector containing the altered MSP-1-42 nucleic
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                  Length 361;
                                                                                                      protein for use in anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein engineering; protein expression; codon usage;
transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSP-1; merozoite surface protein; malaria; vaccine;
                                                                                                                                                                                                                                                                                               Score 106; DB 20;
Pred. No. 1.3e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        AAY05833 standard; Protein; 361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merozoite surface protein MSP-1-42.
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                                     GENZ ) GENZYME TRANSGENICS CORP.
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                                                                                                                        Example; Fig 2; 35pp; English.
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1 Similarity 100.0%;
19; Conservative 0
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         98US-0085649.
97US-0062592.
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97US-0062592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-302742/25
                                                                         WPI; 1999-288313/24
                                                        Chen LH, Meade H;
                                                                                                      Modified malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen LH, Meade H;
                                                                                                                                                                                                                                                                     361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX25587
                                                                                   P-PSDB; AAX56009
         15-MAY-1998;
20-OCT-1997;
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20-OCT-1997;
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                                                                                                                                                                                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY05833;
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This present sequence comprises a 42 kDa C-terminal portion of malaria merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against plasmodium falciparum. The C-terminal end of the sequence is modified to include a 6xHis tag. Nucleic acids (see AAX2556 and AAX2559) encoding MSP-1-42 have been modified according to a method of the invention in order to improve expression in mammalian cells and in transgenic animals. The invention provides modified a method of the invention protein expression of proteins that are difficult recombinant nucleic acid sequences and methods for increasing the minka levels and protein expression of proteins that are difficult to express in cell culture systems, especially mammalian cells culture systems or in transgenic animals. The preferred difficult protein candidates for expression are those derived from lower corporaisms such as parasites, bacteria and viruses that have DNA coding sequences of high AT content or which have mRNA instability motifs or rare codons relative to the recombinant expression system to be used. The invention allows expression of MSP-1 in the milk vector containing the altered MSP-1-42 nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Asn in native MSP-1-42 (N262Q mutation)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "beta-casein signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 106; DB 20;
Pred. No. 1.3e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified merozoite surface protein MSP-1-42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY09374 standard; Protein; 376 AA.
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/note= "6xHis tag"
Disclosure; Fig 2; 43pp; English.
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97US-0062592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 197
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                                                                                                                                                                                                                                 The present sequence represents a 42 kDa C-terminal portion of malazia merozoite surface protein MSP-1 (i.e. MSP-1-42), an important target for the development of a vaccine against Plasmodium falciparum. The sequence has been modified to include an N-terminal beta-casein signal peptide and an N-terminal 6xHis tag. In addition, N181Q and N782Q mutations have been introduced to eliminate 2 N-glycosylation sites. These modifications allow the MSP-1-42 protein to be expressed in the milk of transgenic mice.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Asn in native MSP-1-42 (N181Q mutation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Asn in native MSP-1-42 (N262Q mutation)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376;
                                                                                                                                             protein for use in anti-malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSP-1; merozoite surface protein; malaria; vaccine; protein engineering; protein expression; codon usage; transgenic animal; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "beta-casein signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 106; DB 20;
Pred. No. 1.3e-06;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified merozoite surface protein MSP-1-42.
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/note= "6xHis tag"
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                                                                                                                                                                                         Example; Fig 11; 35pp; English.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Synthetic.
                                                                  1999-288313/24.
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                          Modified malarial
                        Meade H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 AA;
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                                                                                           P-PSDB; AAX56008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
New modified recombinant nucleic acid sequences useful for producing
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Job time: 422 sec
                                                                                                          Example; Fig 11; 43pp; English.
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                                       malarial DNA vaccine
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553, 2 112, 1 110, 1 110, 1 158, 1 158, 1 158, 1 158, 1 158, 1 158, 1 158, 1

Sequence:

Run on:

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Database

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Sequence Seq
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                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUCASSILILARIA 4.5
PUCASSILILARIA 4.5
PURIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/290,919
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
                           US-09-136-389-153
US-09-025-769B-33
US-09-025-769B-33
US-08-958-201-12
US-08-958-201-14
US-09-025-769B-19
US-09-049-672A-10
US-08-40-159-10
US-08-40-159-10
US-08-40-1729A-10
US-08-47-1729A-10
US-08-47-1729A-10
US-08-47-1729A-10
US-08-47-1729A-10
US-08-47-551B-22
US-08-472-78BA-22
US-08-472-78BA-22
US-08-472-78BA-22
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US-08-472-78BA-22
US-08-472-78BA-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING:
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08290919
Patent No. 5720959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: MA._
STATE: D.C.
COUNTRY: U.S.A.
TO: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-290-919-3
   Sequence 11, Appl Sequence 12, Appl Sequence 22, Appl Sequence 5, Appl Sequence 189, Appl Sequence 21, Appl Sequence 16, Appl Sequence 6, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 2, Appl Sequence 153, Appl Sequence 154, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Appli
                                                                                                                                                                                                                                                      (without alignments)
3.210 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153
Sequence 17,
                                                                                                                                                                                                                        Search time 133.18 Seconds
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Sequence 17
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                              4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-290-919-4

US-08-290-919-11

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US-09-498-346-23

US-09-498-346-21

US-09-498-346-6

US-09-498-346-6

US-09-498-346-6

US-09-498-346-6

US-09-498-346-1

US-09-498-346-3

US-08-378-674-2

US-08-378-674-2

US-09-498-346-3

US-08-378-674-2

US-08-488-113B-153

US-08-472-788A-17

US-08-472-788A-17

US-08-472-788A-17

US-08-472-788A-17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212252 seqs, 22503292 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                        January 29, 2002, 10:24:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 US-09-763-397A-12
106
1 EDSGSNGKKITCECTKPDS 19
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Gapop 10.0 , Gapext 0.5
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Match Length
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                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Maximum DB s
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Gaps

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0
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APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA
TITLE OF INVENTION: VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 106;
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               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212242/HCM/MJL/6BC8/
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Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION UNBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-578-674-22
Sequence 22, Application US/08578674
Patent No. 6077827
GENERAL INFORMATION:
APPLICANT: KOLBE, Hanno V.J.
                                                                                                                                                       RESULT 3
10x-08-200-919-11
Sequence 11, Application US/08290919
Patent No. 5720959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 16,773
REFRENCE/DOCKET NUMBER: 2122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELERA: (202) 822-0944
INFORMATION FOR SEQ ID NO: 11:
               ij
                                                                           22 EDSGSSRKKITCECTKPDS 40
                                                      1 EDSGSNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 1
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.3
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 DSGSNGKKITCECTKP 17
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76_ESTENSKKIICTCKEP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-290-919-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: STATE:
                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
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                                                                                                                                                                               Gaps
                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08290919
Patent No. 5720959
GENERAL INFORMATION:
APPLICANT: HOLDER, ANTHONY A.
APPLICANT: BLACKMAN, MICHAEL J.
APPLICANT: CHAPPEL, JONATHAN A.
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO MALARIA TITLE OF INVENTION: VACCINE
                                                                                                                                    Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 1; Length 53; Pred. No. 9.1e-07;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDION TYPE: FIDEPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,919
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9203821.5
FILING DATE: 22-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00367
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 110,773
REFERENCE/DOCKET NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGENT NUMBER: 212242/HCM/MJL/6BC8/
TELECOMMUNICATION INFORMATION:
                              /label= X
/note= "X = M and N, or N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= X
/note= "X = M and N, or N"
                                                                                                                                 100.0%; Score 106; DB 1; 100.0%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                               Query Match 100.0%; Score 106; D
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 19; Conservative · 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%;
89.5%;
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                              ; OTHER INFORMATION:
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US-08-290-919-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                           US-08-290-919-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-290-919-4
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Gaps

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APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: REIL, Gunthern
APPLICANT: ACHSTETTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 20;
Pred. No. 2.9;
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  BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAME/KEY: Peptide

LOCATION: 1..20
CTHER INFORMATION: /note= "analysed portion of
CTHER INFORMATION: xenoxin-3, alkylated (3)"
US-09-498-346-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                          CURRENT APPLICATION DAYA:

APPLICATION NUMBER: US/09/498,346
FILING DATE: 04-FEB-2000
CLASSIFICATION DATE: 08/578,674
FRICA APPLICATION DATE: 28-DEC-1995
PRIOR APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1994
PRIOR APPLICATION DATE: 4940062.9
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00002
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
FELEPHONE: (703) 836-6620
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             017753-071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-578-674-5; Sequence 5, Application US/08578674; Patent No. 6077827; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.5%;
                                                                 STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.5
Best Local Similarity 53.3
Matches 8; Conservative
                          P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| |:| || | | 6 ANGVKMTQECAKEDT 20
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                          STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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            APPLICANT: KREIL, Gunthern
APPLICANT: ACHSTETTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
STREST: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-498-346-22
Sequence 22, Application US/09498346
Patent No. 6277822
GENERAL INFORMATION:
APPLICANT: ROLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RREIL, Gunthern
APPLICANT: ACHSTETTER, Tilman
TITLE OF INPENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 3; Length 20;
Pred. No. 2.9;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,674
FLING DATE: 29-DEC-1995
CLASSIFICATION NUMBER: FR 90 07901
FLING APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 000202
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,607
REERERNCE/DOCKET NUMBER: 36,607
RELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEBERAX: (703) 836-6620
TELEBERAX: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..20
COTHER INFORMATION: /note= "analysed portion of offer information: xenoxin-3, alkylated (3)"
US-08-578-674-22
APPLICANT: RASMUSSEN, Ulla B.
                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 SNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| |:| || |:
6 ANGVKMTQECAKEDT 20
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Sequence 189, Application US/0875587
Patent No. 604597
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wooster, Richard F
APPLICANT: Wooster, Richard F
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the
TITLE OF INVENTION: identification and sequencing of the BRCA2 cancer:
TITLE OF INVENTION: susceptibility gene and uses thereof.
NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/755,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 4
Pred. No. 9.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                               NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION NUMBER: GB 952555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION NUMBER: GB 952555.0
           PRICRA APPLICATION DATA:

APPLICATION NUMBER: US 08/578,674
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90.07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 0062.9
FILING DATE: 11-JAN-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide US-09-498-346-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ANGVKMTQECAKEDT 22
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US-08-755-587-189
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APPLICANT: KOLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RREIL, Gunthern
APPLICANT: ACHSETTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STRET: P.O. BOX 1404
CITY: Alexandia
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 3; Length 66;
Pred. No. 9.9;
3; Mismatches 4; Indels
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,674
FILING DATE: 28-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/498,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 017753-071 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 9400062.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09498346 Patent No. 6277822
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.5%;
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COUNTRY: United States
ZIP: 22313-1404
Virginia
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.5
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SNGKKITCECTKPDS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| |:| || |:
8 ANGVKMTQECAKEDT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                             22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-578-674-5
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APPLICANT: KOLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RELL, Gunthern
APPLICANT: ACHSTETTER, Tilman
APPLICANT
A
                                                                                                                                                                                                                                                                                       DB 3; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
CITY: Alexandria STATE: Viginia
STATE: Viginia
CUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,346
FILING DATE: 04-FEB-2000
CLASSIFICATION:
                                                                                                         /note= "analysed portion of
xenoxin-3, alkylated (2)"
                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSILLCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/578,674
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
RESISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
RELEPHONE: (703) 836-6620
: TELECHONE: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 21:
SEQUENCE: CHARACTERISTICS:
. SEQUENCE: 30 and 100 acids
                                                                                                                                                                                                                                                                                   Query Match 40.6%; Score 43; Best Local Similarity 57.1%; Pred. No. Matches 8; Conservative 2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09498346 Patent No. 6277822 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             5 SNGKKITCECTKPD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: 1..20
CTHER INFORMATION:
COTHER INFORMATION:
US-08-578-674-21
                                               Peptide
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LOCATION:
                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-498-346-21
          FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08578674
Patent No. 6077827
CENERAL INFORMATION:
APPLICANT: KOLBE, Hanno V.J.
APPLICANT: KREIL, Gunthern
APPLICANT: KREIL, Gunthern
APPLICANT: KREIL, Gunthern
APPLICANT: KREIL, Gunthern
APPLICANT: ACHSTETTER, Tilman
TITLE OF INVENTION: FAMILX OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
219: 2313:1404
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,674
FILING DATE: 28-DEC-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-00UN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
ATTONNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:
TELEPANCE (703) 836-6201
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                  NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 1589 amino acids
APPLICATION NUMBER: GB 9617961.9 FILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 DSGNNFAFQVTNKCNKPD 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DSGSN-GKKITCECTKPD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-755-587-189
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US-08-578-674-21
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Gaps
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APPLICANT: KOLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RELL, Gutthern
APPLICANT: ACHSTETTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.6%; Score 43; DB 4; Length 37; 53.3%; Pred. No. 7.6; 1:ve 3; Mismatches 4; Indels
                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
CUMTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,346
FILING DATE: 04-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "analysed portion of
xenoxine-1, alkylated"
              Pred. No. 7.6;
                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: U4-FED 2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/578,674
FILING DATE: 28-DEC-1995
PRIOR APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 9400062.9
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: R 9400062.9
FILING DATE: 11-JAN-1994
ATTORNEY-AGENT INFORMATION:
NAME: Meuth, Donna M.
FREFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
FENDINGER CHARACTERISTICS:
                                                                                                                                                                                                RESULT 12
US-09-498-346-6
Sequence 6, Application US/09498346
Patent No. 6277822
           53.3%;
           Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                5 SNGKKITCECTKPDS 19
                                                                                                        :|| |:| || |:
8 ANGIKMTQECAKEDT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : NAME/KEY: Peptide
: LOCATION: 1.37
OTHER INFORMATION:
: OTHER INFORMATION:
US-09-498-346-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                           Gaps
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GENERAL INFORMATION:
APPLICANT: KOLEB. Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RASIL, Gunthern
APPLICANT: ACHSTETER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: ALEXANDIA
STATE: VIFGINIA
COUNTRY: United States
CONNERY: United States
                                                                                                                         Length 20;
                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC-1995
CLASSIFICATION NUMBER: PR 90 07901
FILING DATE: 29-JUN 1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING BAPLICATION NUMBER: FR 94 00202
FILING BAPLICATION NUMBER: FR 94 00202
FILING RAPLICATION NUMBER: FR 94 00202
FILING BAPLICATION NUMBER: PR 94 00202
FILING BAPLICATION NUMBER: PR 94 00503
FILING BAPLICATION NUMBER: RR 94 00503
FILING BAPLICATION NUMBER: O17753-071
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-650
INFORMATION FROM SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FRANCEH. 37 AMINO acids
    /note= "analysed portion of
xenoxin-3, alkylated (2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "analysed portion of
xenoxine-1, alkylated"
                                                                                                                         DB 4;
                                                                                                                                                                 2; Mismatches
                                                                                                                         Score 43; DI
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08578674
Patent No. 6077827
                                                                                                                    40.68;
57.18;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                              5 SNGKKITCECTKPD 18
                                                                                                                                                                                                                                             7 ANGVKMTQECAKED 20
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-498-346-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: 1.37
CTHER INFORMATION:
CTHER INFORMATION:
US-08-578-674-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Gaps

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DB 3; Length 37;

40.6%; Score 43;

Query Match

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                                                                                GENERAL INFORMATION:
APPLICANT: KOLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: RESIL, Gunthern
APPLICANT: ACHSTETER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 4; Length 56;
Pred. No. 12;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                          ADDRESSES: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
STATE: United States
LIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.56; OTHER INFORMATION: /note= "analysed portion of CHER INFORMATION: xenoxin-2, alkylated" US-09-498-346-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/578,674
FILING DATE: 28-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
PRIOR APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE DOCKET NUMBER: 01753-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                омы В Сородо 198, 346
04-FEB-2000
                             Sequence 16, Application US/09498346 Patent No. 6277822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-578-674-3
; Sequence 3, Application US/08578674
; Patent No. 6077827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 56 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ANGIKMTOECAKEDN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0. CLASSIFICATION:
US-09-498-346-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
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                                                                                                                                                                          Score 43; DB 3; Length 56;
Pred. No. 12;
3; Mismatches 4; Indels
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LOCATION: 1..56

OTHER INFORMATION: /note= "analysed portion of

CTHER INFORMATION: xenoxin-2, alkylated"
US-08-578-674-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
APTICATION NUMBER: FR 94 00062.9
FILING DATE: 11-JAN-1994
APTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:
TELECAX: (703) 836-620
TELECAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 56 amino acids TYPE: amino acid
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Best Local Similarity 53.3.
Best Local 8; Conservative
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5 SNGKKITCECTKPDS 19
                                :|| |:| || || 8 ANGIKMTQECAKEDT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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ANGIKMTQECAKEDN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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APPLICANT: RESMUSSEN, Ulla B.
APPLICANT: REAL GONTHERN
TITLE GONTENERS:
BOUNDERSEE: BURNES, DOANE, SWECKER & MATHIS, L.L.P.
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNES, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
CITY: Alexandria
STREET: P.O. BOX 1404
CITY: Alexandria
STREET: P.O. BOX 1404
COMPUTER: Lababale FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: 223-1-1404
COMPUTER: 28-DEC-1995
SOFTWARE: PER 90 07901
FLING DATE: 28-DEC-1995
SOFTWARE: 28-DEC-1995
SOFTWARE: 28-DEC-1995
SOFTWARE: 11-JAN-1994
APPLICATION NUMBER: FR 90 07202
FLING DATE: 11-JAN-1994
APPLICATION NUMBER: FR 90 0062.9
FLING DATE: 11-JAN-1994
APPLICATION NUMBER: 36,607
FLING DATE: 11-JAN-1994
APTORNEY AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 01703 36-620
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEBROTH: 66 amino acids
TTELE TIMES: SINGle-
CONDOLICKY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.6%; Score 43; DB 3; Length 66;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-578-674-3
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5 SNGKKITCECTKPDS 19 :|| |:| || |: 8 ANGIKMTQECAKEDT 22 Óγ

0;

0;

Search completed: January 29, 2002, 10:24:05 Job time: 511 sec

Copyright

GenCore version 4.5 (c) 1993 - 2000 Comp

Compugen Ltd

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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length: 2000000000
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2: pir2:*
3: pir3:*
4: pir4:*
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pir3:*
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GNNYTM
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T49799
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S47282
SAZQK1
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CSRP
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9.984 Million cell updates/sec
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ALIGNMENTS

R: Fiolle, R: Bujard, H.; Cooper, J.A.
R: Folle, R: Bujard, H.; Cooper, J.A.
R: Folle, R: Bujard, H.; Cooper, July 1994
A: Description: Plasmodium falciparum: recombination within the C-terminal region of m A: Reference number: S47282
A: A: Accession: S47282
A: A: Accession: S47282
A: Molecule type: DNA
A: Residues: 1-651 <TOL>
A: Residues: 1-651 <TOL>
A: Cross-references: EMBL: Z35329; NID: g535257; PIDN: CAA84558.1; PID: g535258
A: Cross-references: EMBL: Z35329; NID: g535257; PIDN: CAA84558.1; PID: g535258
A: Experimental source: strain RO-71
C: Superfamily: major merozoite surface antigen
C: Keywords: glycoprotein; merozoite; surface antigen major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments C;Species: Plasmodium falciparum C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jun-2000 C;Accession: A45545 R;Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A. Mol. Blochem. Parasitol. 49, 29-33, 1991 A;Reference number: A45545; MUID:92131048 A;Accession: A45545; MUID:92131048 merozoite surface antigen 1 - malaria parasite (Plasmodium falciparum) (strain RO-71) C;Species: Plasmodium falciparum A;Variety: strain RO-71 A;Variety: strain RO-71 C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jun-2000 C;Rocession: S47282 A; Note: sequence extracted from NCBI backbone (NCBIN:77612, NCBIP:77621) C; Superfamily: major merozoite surface antigen C; Keywords: glycoprotein; merozoite; surface antigen; tandem repeat RESULT A45545 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-400 <BLA> В Ş Query Match Best Local Similarity Best Local Similarity 100 Matches 19; Conservative Query Match Best Local 351 100.0%; 100.0%; 19 0; Score 106; DB 2; Pred. No. 5.9e-08; Score 106; DB 2; Pred. No. 8.7e-08; Length 651; Length 400; Indels 0; Gaps 0

Matches

Conservative

0;

Mismatches

Indels

0,;

Gaps

0;

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A; Molecule type: DNA
A; Residues: 1-1631 <MAC>
A; Residues: 1-1631 <MAC>
C; Comment: The merozoite stages of different strains have strain-specific surface
C; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte.
C; Superfamily: major merozoite surface antigen tandem repeat; transmembrane
C; Keywords: glycoprotein; merozoite; surface antigen; tandem repeat; transmembrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 4, 3823-3829, 1985
A;Title: Polymorphism of the precursor for
A;Reference number: A91030; MUID:86136024
† B
                                                                                                                                                                                                                                                                                                                                                       R;Myler, P.J.
Nucleic Acids Res. 17, 5401, 1989
A;Title: Nucleotide and deduced amino acid sequence of the gp195 (MSA-1) gene from Plasm A;Reference number: S04850; MUID:89345116
A;Accession: S04850
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F;67-84/Region: 3-residue repeats (S-G-T/P)
F;1614-1631/Domain: membrane anchor #status predicted <MBN>
F;97,259,755,759,835,911,955,1049,1156,1165,1436,1563/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Mackay, M.;
EMBO J. 4, 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Plasmodium falciparum
C;Date: 30-Sep-1987 #sequence_revision.30-Sep-1987 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
C; Species: Plasmodium falciparum
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                                                      Q
                                                                                                                                                                                                                           C;Keywords: glycoprotein; merozoite; surface antigen F;1-19/Domain; signal sequence #status predicted <SI
                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1504-1639 < MYL2>
A; Cross references: EMBL:X15063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: S05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: S05603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993
C;Accession: S05603; S04850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      major merozoite surface antigen precursor - malaria
N;Alternate names: gp195 surface antigen
C;Species: Plasmodium falciparum
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                                                                                                                                                                                                                                                                      C; Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: X15063; NID: g9896; PIDN: CAA33163.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-1639 <MYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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                                                                                                                                                                                                           F;20-1639/Product:
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                                             EDSGSNGKKITCECTKPDS
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                                                                                                    Conservative
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Pred. No. 1.8e-07;
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Pred. No. 1.8e-07;
; Mismatches 0;
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C;Comment: The merozoite stages of different strains have strain-specific s C;Comment: P. falciparum has three stages: sporozoite, merozoite, and gamet C;Comment: P. falciparum has three stages: sporozoite, merozoite, and gamet C;Superfamily: major merozoite surface antigen; tandem repeat F;1-19/Domain: signal sequence #status predicted <SIG> F;20-1726/Product: major merozoite surface antigen #status predicted <MAT> F;21-19/SOM = 100-105/109-120/Region: 3-residue repeats (S-G-T) F;757-765/Region: 3-residue repeats (T-E-E) F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding
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C;Date: 30-Sep-1987 #sequence_revision 31-Mar-1991
C;Accession: A23386; S03561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Weber, J.L.; Leininger, W.M.; Lyon, J.A. Nucleic Acids Res. 14, 3311-3323, 1986 A; Title: Variation in the gene encoding a A; Reference number: A23386; MUID:86205236
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1726 < CHA>
A; Cross-references: GB: M37213
A; Cross-references: GB: M37213
C; Superfamily: major merozoite
                                                                                                                                                                                                                                            A; Reference number: A
A; Accession: A45948
A; Status: preliminary
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: A45948
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A; Residues: 1104-1726 <WEB2>
A; Cross-references: EMBL: X03831
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R;Weber, J.L.; Sim, B.K.L.; Lyon,
Nucleic Acids Res. 16, 1206, 1988
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N;Alternate names: 195K glycoprotein
                                                                                                                                                                                                                                                                                         A; Title: Plasmodium falciparum: A; Reference number: A45948; MUII
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Exp. Parasitol. 67, 1-11, 198
                                                                                                                                                                                                                                                                                                                                                                                                              major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
C; Species: Plasmodium falciparum
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Res. 14, 3311-3323,
                                          Conservative
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MUID:89005525
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Pred. No. 1
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Pred. No. 1.8e-07;
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1.8e-07;
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EDSGSNGKKITCECTKPDS

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A; Molecule type: DNA
A; Residues: 1-1701 <TAN>
A; Residues: 1-1701 <TAN>
C; Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-1701/Product: major merozoite surface antigen #status predicted <MAT>
                                                                                                                                R:Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J. Mol. Biol. 195, 273-287, 1987
A:Title: Allelic dimorphism in a surface antigen
A:Reference number: A26868; MUID:88011243
A:Accession: A26868
                                                                                                                                                                                                                                                   major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st C;Species: Plasmodium falciparum C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000 C;Accession: A26868
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1701 <PET>
A:Cross-references: GB:M19143; NID:g160412; PIDN:AAA29653.1; PID:g160413
C:Superfamily: major merozoite surface antigen
C:Keywords: surface antigen
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R;Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.; Mol. Biochem. Parasitol. 27, 291-302, 1988
A;Title: Variation in the precursor to the major merozoite surface antigens of Plasmodin A;Reference number: A54498; MUID:88142999
A;Accession: A54498
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A;ResIdues: 1-1640 <HOL>
C;Superfamily: major merozoite
C;Keywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                         A26868
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Best Local S
Matches 18
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Best Local Similarity
Matches 17; Conserv
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89.5%;
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Pred. No. 6.7e-07;
0; Mismatches 0;
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1.4e-05;
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major merozoite surface antigen precursor - Plasmodium yoelii C;Species: Plasmodium yoelii C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change C;Accession: A45532; A45531
R;Lewis, A.P.
                                                                                    RESULT
A45532
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submitted to the EMBL Data
submitted to number: S50349
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R;Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 602-606, 1988
A;Title: The 3' portion of the gene for a Plasmodium yoelii merozoite surface antigen A;Reference number: A28121; MUID:88124889
A;Accession: A28121
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C; Species: Plasmodium yoelii
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A; Map position: 9L
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C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change
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                                                                                                                                                                                                                                                                                                                                            A; Note: the authors translated the codon GTA for residue
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J03612; NID:g160678; A;Experimental source: strain 17XL
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-680 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-995 <LYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S50358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YIL169c - yeast (Saccharomyces N;Alternate names: hypothetical protein YI9402.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 17; Conserv
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9; Conserv
                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                            antigen
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47.48;
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89.5%;
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Pred. No.
                                                                                                                                                                                                                                       Score 47;
Pred. No.
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Pred. No. 1.4e-05;
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11;
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32;
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26-Aug-1999

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hypothetical protein [imported] - Methanobacterium thermoautotrophicum (fragment) C;Species: Methanobacterium thermoautotrophicum C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000 C;Accession: T45261 R;Harms, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: pace...
A;Status: pace...
A;Molecule type: DNA
A;Residues: 1-167 <HAR>
A;Cross-references: EMBL:x97589; PIDN:CAA66200.1
A;Cross-imantal source: strain Marburg; DSM 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J04668; NID:g160492; PID:g160493
R;Daly, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Biochem. Parasitol. 36, 283-285, 1989
A;Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: cloning A;Reference number: A45531; MUID:90014982
A;Accession: A45531
A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13820.1; PID:g695205 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, C;Superfamily: Epstein-Barr virus BGLF2 protein
                                                                     A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-341 <TEL>
                                                                                                                                                                                  R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
                                                                                                                                                                                                                                                             C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999
C;Accession: S55627
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A;Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface A;Reference number: A45532; MUID:90014981
A;Accession: A45532
                                                                                                                                           A; Reference number: S55594; MUID: 95302501 A; Accession: S55627
                                                                                                                                                                                                                                                                                                           hypothetical protein 33 - equine herpesvirus 2 C; Species: equine herpesvirus 2
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S55627
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A; Residues: 454-1094 <DAL>
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A; Residues: 1-1772 <LEW>
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8; Conserv
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46.7%;
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50.0%;
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Pred. No.
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67;
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                                                                                                                      translation not shown
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Search completed: January 29, Job time: 652 sec
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A; Molecule type: DNA
A; Residues: 1-468 <KAW>
                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1999 A; Description: Pyrococcus abyssi genome sequence: A; Reference number: A75001 A; Accession: B75053
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date:
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                                                                                                                                                                                                                      C; Superfamily: Methanococcus jannaschii conserved hypothetical
                                                                                                                                                                                                                                          A; Gene:
                                                                                                                                                                                                                                                                       A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50319.1; PID:g545
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                      R; anonymous, Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Pyrococcus abyssi
;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
;Accession: B75053
                                                                                                                                                                                                                                                          Genetics:
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Best Local Similarity
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Best Local Similarity 57.1%;
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                                                                                221 SGKAGLKITLEDLKPD 236
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                                                                                                              SGSNGKKITCECTKPD 18
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Pred. No.
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GenCore version 4.5
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OM protein - protein search, using sw model

January 29, 2002, 11:13:42; Search time 80.65 Seconds (without alignments) 8.638 Million cell updates/sec Run on:

US-09-763-397A-12 106 1 EDSGSNGKKITCECTKPDS 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	۵,	m	_	_		_			P13828 plasmodium	Q9y5e5 homo sapien	P97370 mus musculu	017482 drosophila	P38952 xenopus lae		_	t genome	t genome	mus musca	P38951 xenopus lae	Q94550 dreissena p	xenopus la		P24525 brassica na		P26291 pisum sativ		mus m	P20948 trypanosoma		homod	homo	P01710 homo sapien	l homo
SUMMARIES	. OI s	MSP1_PLAF	MSP1_				MSP1	MSP1_PLAFM	YIQ9_YEAST	. MSP1_PLAYO	. CDB4_HUMAN	. ATND_MOUSE	TIM_DROVI	XEN3_XENLA	VE1_HPV70	POLG_TMEVD	POLG_TMEVB .	POLG_TMEVG	BRC2_MOUSE	XEN2_XENLA	MT_DREPO	XEN1_XENLA	BAP2_YEAST	CYPH_BRANA	. CDAD_HUMAN	. UCRI_PEA	RAG2_HUMAN	RAG2_MOUSE	VSY1_TRYCO	MTCD_HELPO	LV2B_HUMAN	LV2D_HUMAN	LV2G_HUMAN	LV2H_HUMAN
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P04209 homo sapien O52250 halomonas e	P01871 homo sapien P26613 salmonella	P34089 oryctolagus	088799 mus musculu	008773 rattus norv	P05160 homo sapien	O9y512 homo sapten	P01703 homo sapien	P01709 homo sapien
LV2K_HUMAN ECB2_HALEL	MUC_HUMAN AMY2_SALTY	RAG2_RABIT	ZAN_MOUSE	RGSE_RAT	F13B_HUMAN	CDAA_HUMAN	LV1E_HUMAN	LV2F_HUMAN
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112	454	1328	5376	544	661	948	103	111
38.7	38.7	38.7	38.7	38.2	38.2	38.2	37.7	37.7
41	41	41	41	40.5	40.5	40.5	40	40
34 35	36 37	38	40	41.	42	43	44	45

ALIGNMENTS

	MSP1_PLAFK P04932:	STA	STANDARD;			1630	4			
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	01-0CT-1996		34, L	ast an	34. Last annotation update)	on a	date)			
	MEROZOITE SU	CE	PROTE	IN 1 P	PROTEIN 1 PRECURSOR (MEROZOITE	R.	EROZÓI	TE SUR	SURFACE ANTIGENS)	FIGENS)
	MSP-1.									
		alcipa	rum (isolat	(isolate K1 / Thailand)	Thai	land).			
	Eukaryota; A	Alveolata;		picomp	Apicomplexa; Haemosporida;	аето	sporid		Plasmodium.	
	NCBI_TaxID=5839;	839;								
		:								
	SEQUENCE FROM N.A.	Μ. A.	:							
	MEDLINE-86136024; PubMed-30049/2;	6024;	Pubme	d=3004	17;					
	Mackay M., Goman M., Bone N., Hyde J.E.,	oman M	.∵ .∵	ne N.,	Hyde J	Э.	Scaife J	:	Certa U	::
	nnenberg	H., Bu	jard	H.;						
	"Polymorphism of the precursor for	m of t	he pr	ecurso	r for t	the major	jor	surface	antigens	ns of
	Plasmodium falciparum merozoites: studies at	alcipa	rum m	erozoi	tes: st	ndie		he gen	the genetic level.";	vel.";
		4:3823-3829(1985).	9 (I 9 B	. (
RN [2]										
	REVISIONS, S	SEQUENCE FROM	E FRO	M N.A.						
RA Pan	W., Toll	е В.,	Bujar	d H.;						
	Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases	UN-199	5) to	the E	MBL/Ger	Bank	/DDBJ	databa	ises.	
	SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR	LAR LO	CATIO	N: ATT	ACHED I	O TH	E MEMB	RANE B	3Y A GPI	-ANCHOR
ပ္ပ	(POTENTIAL)	AL).								
		OZOITE	SURF	ACE AN	TIGEN C	ONTA	IN THE	SEOUE	INCE OF	PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42
U	KDA AND	19 KDA	ANTI	GENS W	HICH AF	E TH	E MAJO	R SURF	ACE ANT	IGENS OF
U	MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.	ES. TH	E MAT	URATIO	N TAKE	PLAC	E DURI	NG SCH	IIZONT.	
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	European	Bioin	forma	tics I	nstitut			are no	restr	the European Bioinformatics Institute. There are no restrictions on its
	non yd	-profi	t in	stitut	ions as	Jon		its co	ntent	is in no
	modified and this statement is not removed.	this	state	ment i	s not r	ещом		sage	by and	Usage by and for commercial
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	EMBL: X03371: CAA27070.1:	CAA2	7070.	1						
	PIR: A25120:	SAZOKI	1	ì						
	InterPro: IPR000561: EGF-like	2000g	1: EG	F-like						
	Pfam: PF00008: EGF:	B: EGF	1.							
	Malaria: Merozoite: Polvprotein: Repeat:	ozoite	Pol	vorote	in: Rer	eat:	Signal:	1: Glv	Glycoprotein:	in:
	nsmembran	e: GPI	-anch	or.					1 1 1 1 1 1 1 1	
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	CARBOHYD	729	259		N-LINKED		(GLCNAC.	·	(POTENTIAL)	IAL).
FT CAR	CARBOHYD	755	755		N-LINKED		(GLCNAC.	·	(POTENTIAL)	IAL).
_	CARBOHYD	759	759		N-LINKED	_	GLCNAC.	·	(POTENTIAL)	IAL).
FT CAR	CARBOHYD	774	774		N-LINKED	_	GLCNAC.	·	(POTENTIAL)	IAL).
FT CAR	CARBOHYD	835	832		N-LINKED	_	GLCNAC.	·	(POTENTIAL)	IAL).
	CARROHYD	111	61		N-1.TNXED	_	CICNAC	-	/ DOTFNTTAL	TAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-86014355; PubMed-2995820; Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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     N-LINKED (GLCNAC...) (POTENTTAL).
N-LINKED (GLCNAC...) (POTENTIAL).
MW; ADBDEC3CE0A46322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A24594; A24594.
InterPro; IPR00561; EGF-like.
Pfam; PF000008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
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                                                                                                                                                                         Length 1630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                Indels
                                                                                                                                                                         100.0%; Score 106; DB 1;
100.0%; Pred. No. 1.2e-08;
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0
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                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate Wellcome).
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Matches 19; Conserv
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MSP1_PLAFW
ID MSP1_PLAFW
AC P04933;
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REVISIONS.
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                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE-88166657; PubMed=3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen precursor pl90 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: MEROZÓTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBPACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
  LINKED (GLCNAC. .) (POTENTIAL).
2C255B6616C87F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSP1_PLAF3 STANDARD; PRT; 1682 AA.
P19598; 025921;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MEROZOLIE SURFACE PROTEIN 1 PRECURSOR (MEROZOLIE SURFACE ANTIGENS)
(PPMMSA) (P190).
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MEROZOITE SURFACE PROTEIN 1.
MEMBRANE ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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EMBL; 200087; CAA68280.1; -.
EMBL; 235326; CAA84555.1; -.
PIR; S06286; S06286.
Interpro; IPRO00561; EGF-like.
Pfam; PF00008; EGF; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                 Length 1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmodium falciparum (isolate ro-33 / Ghana).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5834;
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                                                                                                                                                                                                                                                    Score 106; DB 1;
Pred. No. 1.2e-08;
        N-LINKED (GLCNAC. .
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Best Local Similarity
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SEQUENCE FROM N.A.
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MSP1_PLAFP
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SEQUENCE OF 1104-1726 FROM N.A.
MEDLINE-8814399; Pubmed-3278296;
Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
"Merozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 16:1206-1206(1988).
                                                                                                                                                                                                                                Gaps
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MEDLINE-86205236; PubMed-3517809;
Webber J.L., Leininger W.M., Lyon J.A.;
"Variation in the gene encoding a major merozoite surface antigen of the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA AWTIGENS WHICH ARE THE MAJOR SUBFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEROZOTTE SURFACE PROTEIN 1.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                    (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
1 19 POTENTIAL.
                                                                                                                                                                                             Length 1682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5835;
                                                                                                                                          C82A1E159948CAD6 CRC64;
                                      (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
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100.0%; Pred. No. 1.2e-08;
ive 0; Mismatches 0;
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                                                                                                                                          AA; 192462
                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exp. Parasitol. 67:1-11(1988).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS MEROZOITES. THE MATURATION FAKE PLACE DURING SCHIZONT.
                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Pfam; PF00008; EGF; 1.
Malaria: Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                        Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (isolate Palo Alto / Uganda).
Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                       Indels
              N-LINKED (GLCNAC...) (F
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N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                          Score 106; DB 1;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1726 AA
                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                        100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                       1677 EDSGSNGKKITCECTKPDS 1695
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Best Local Similarity 100.
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Eukaryota; Alveolata;
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                                                                                                                                  Gaps
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-!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.; "Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOI. Biochem. Parasitol. 27:291-302(1988).
                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
1-JAN-1990 (Rel. 13, Last sequence update)
01-027-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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MEGOZOTTE SURRACE PROTEIN 1.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MW; 5B59CEEFA2F9A026 CRC64;
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Pfam, PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                  Length 1726;
                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3920B75E73D38552 CRC64;
                                                                                                  Score 106; DB 1;
Pred. No. 1.3e-08;
; Mismatches 0;
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                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
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1016
1114
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1726
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ID MSP1_PLAFF
AC P13819;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                            parasite
                                               Gaps
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURRACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-115 FROM N.A. MEDLINE-86136024; PubMed=3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunenberg H., Bujard H.; Prolymorphism of the precursor for the major surface antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88011243; Pubmed-3079521; MEDLINE-88011243; Pubmed-3079521; Tanabe K., Mackay M., Goman M., Scaife J.G.,; Malchay M., Goman M., Scaife J.G.,; Mallelic dimorphism in a surface antigen gene of the malaria plasmodium falciparum."; J. Mol. Biol. 195:273-287(1987).
                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate mad20 / Papua New Guinea).
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=70153;
                Length 1701;
Score 93; DB 1; Length 1/v
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanabe K.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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                                             1; Mismatches
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Pfam; PF00008; EGF; 1.
                                                                                              1652 EDSGSSRKKITCECTKPDS 1670
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                                                                              1 EDSGSNGKKITCECTKPDS 19
                                               17; Conservative
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PIR; B25120; B25120.
                Query Match
Best Local Similarity
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1110
2339
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P08569;
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MSP1_PLAFM
                                               Matches
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STRAIN=17XL;
                      MSP1_PLAYO
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  RESULT 9
MSP1_PLAYO
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                             Gaps
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HYPOTHETICAL PROTEIN YIL169C.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Barrell Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones I.
Couls E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
              (POTENTIAL).
                                             INKED (GLCNAC. . .) (POTENTIAL).
INKED (GLCNAC. . .) (POTENTIAL).
3FC2EC59AF96EA98 CRC64;
                                                                                                                           ;
                                                                                                     Length 1701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.1%; Score 51; DB 1; Length 995; 47.4%; Pred. No. 2.5;
                                                                                                                           1; Indels
                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 99.7 RAP PROTEIN IN SDL1 5'REGION PRECURSOR YILL169C OR Y19402.07C.
                       (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
                                                                                                     87.7%; Score 93; DB 1; 1
89.5%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; S0001431; YIL169C.
InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR000727; T_SNARE.
Hypothetical protein; Signal POTENTIAL.
SIGNAL
                                                                                                                                                                                                                            995 AA
                                                                                                                           Mismatches
  N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
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919 919 N
965 965 N
991 991 N
1089 1089 N
1196 1196 N
1588 1588 N
                                                                                                                                                                                                                                                   31, Created)
                                                                                                                                                            1652 EDSGSSRKKITCECTKPDS 1670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99735 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 246921; CAA87023.1; -.
                                                                                                                                                  1 EDSGSNGKKITCECTKPDS 19
                                                                                                                           Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                         Query Match
Best Local Similarity
-hes 17; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                 01-FEB-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                            YIQ9_YEAST
P40442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
CARBOHYD
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SEQUENCE
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                                 CARBOHYD
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Matches
                                                                                                                                                                                                                    YIQ9_YEAST
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                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.; "The 3' portion of the gene for a Plasmodium yoelli merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ģ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen encodes the epitope recognized by a protective monoclonal antibody. Natl. Acad. Sci. U.S.A. 85:602-606(1988).
-i- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-0CT-1996 (Rel. 34, Last annoctation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis upstream of the gene encoding the precursor to major merozoite surface antigens of Plasmodium yoelii."; Mol. Biochem. Parasitol. 39:285-288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURPACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROZOITE SURFACE PROTEIN 1.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                              Plasmodium berghei yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Length 1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . V (IN REF. 2).
9A6291658EB0F45D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1
1772 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     > ^-
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-90205979; Pubmed-2320061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88124889; PubMed=2448778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1093-1772 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03612; AAA29762.1; -. EMBL; J04668; AAA29702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 197230
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50.0%;
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1724 ESTENSKKIICTCKEP 1739
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
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PIR; A45532; A45532.
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Best Local Similarity
                                                                                                                                           (PMMSA) (230 KDA)
                                                                                                                                                                                                                                               NCBI_TaxID=5862;
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Gaps

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4; Mismatches

Conservative

1 EDSGSNGKKITCECTKPDS 19

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us-09-763-397a-12.rsp

278 AA.

STANDARD;

(Mouse)

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                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.

IISSUE SPECIFICITY: WIDELY EXPRESSED.

INSCELLANDEUS: THE BETA SUBUNIT SEEMS TO BE ENCODED BY A MULTIGENE PARILY: EACH DIFFERRY SUBUNIT MAY HAVE SPECIALIZED FUNCTIONS.

SIMILARITY: BELONGS TO THE NA+/K+ AND H+ ATPASES BETA CHAIN
                                     15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (SODIUM/POTASSIUM-
DEPENDENT ATPASE BETA-3 SUBUNIT) (ATPB-3).
                                                                                                                                                                                                                                                                             retina.";
Biochim. Biophys. Acta 1350:21-26(1997).
Biochim. Biochim. BIST THE NON-CATALYTIC COMPONENT OF THE ACTIVE
-I- FUNCTION: THIS IS THE NON-CATALYZIS OF ATP COUPLED WITH THE
ENZYME, WHICH CATALYZES THE HUDROLYSIS OF ATP COUPLED WITH THE
EXCHANGE OF NA AND K IONS ACROSS THE PLASMA MEMBRANE. THE EXACT
FUNCTION OF THIS GLYCOPROTEIN IS NOT KNOWN.
                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                Besirli C.G., Gong T.-W.L., Lomax M.I.; "Novel beta 3 isoform of the Na, K-ATPase beta subunit from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00287; Na_K-ATPase; 1.
PROSITE; PS00390, ATPASE.Na_K-BETA_1; 1.
Sodium/potassium transport; Transmembrane; Glycoprotein;
Multigene family; Signal-anchor.
                                                                                                                                                                                                                   STRAIN-BALB/C; TISSUE-Retina;
MEDLINE-97157071; PubMed-9003452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U59761; AAC00019.1; -.
MGD; MGI:107788; Atplb3.
InterPro; IPR000402; Na_K_beta.
                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                          Mus musculus
ATND_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                MEDLINE=99308636; PubMed=10380929; Wu Q., Maniatis T.; "A striking organization of a large family of human neural cadherin-like cell adhesion genes."; Cell 97:779-790(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CADHERIN 1.
CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 6.
CADHERIN 5.
CADHERIN 6.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: POTEWIAL CALCIUM-DEPENDENT CELL-ADHESION PROTEIN.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00112; CA; 5. PROSITE; PS00232; CADHERIN_1; 5. PROSITE; PS00232; CADHERIN_1; 5. PROSITE; PS50268; CADHERIN_2; 5. Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 795;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                            20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTOCADHERIN BETA 4 PRECURSOR (PCDH-BETA4).
                                                              795 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.5; i
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002126; Cadherin.
Pfam; PF00028; Cadherin; 5.
PRINTS; PR00205; CADHERIN.
                                                                                           (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF152497; AAD43758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
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55.6%;
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                                                                STANDARD;
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                                                                                                                                                                           Homo sapiens (Human)
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Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566
795 A
                                                                                                                                                                                                                    NCBI_TaxID=9606;
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28
690
711
34
137
351
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                                                                                             20-AUG-2001
                                                                CDB4_HUMAN
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DOMAIN
CARBOHYD
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TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                         PCDHB4
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                                                  CDB4_HUMAN
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                        Gaps
                        ö
42.5%; Score 45; DB 1; Length 278; 61.5%; Pred. No. 6.5;
                        Indels
                                                                                                                                       1343 AA.
                          2; Mismatches
                                                                                                                                       PRT;
                          Conservative
                                                                                                                                       STANDARD;
                                                                                                                                       TIM_DROVI STANDARD 017482; 044430; 044785;
                                                                 ||| | |::| ||
237 DSGLNKKEVTVEC 249
                                                 14
                                                  2 DSGSNGKKITCEC
              Best_Local Similarity
Matches 8; Conser
                                                                                                              RESULT 12
TIM_DROVI
                                                                                                                                       AC P
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373 DSGENGKMI --- CSIPDN 387 2 DSGSNGKKITCECTKPDS 19

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RESULT 11 ATND_MOUSE

CYTOPLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
EXTRACELLULAR (POTENTIAL)

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

57 128 154 191 124 197 278 AA;

N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

98A46FF6EDA85AAC CRC64;

31775 MW;

us-09-763-397a-12.rsp

288 DNGSGGKKESCE 299

g

2 DSGSNGKKITCE 13

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CHIEFOLICAL CYCLE DEPENDS ON THE RHYTHMIC FORMATION AND NUCLEAR
LOCALIZATION OF THE THAPER COMPLEX. LIGHT INDUCES THE DEGRADATION
C LOCALIZATION OF THE THAPER COMPLEX. LIGHT INDUCES THE DEGRADATION
OF TIM, WHICH PROMOTES ELIMINATION OF PER. NUCLEAR ACTIVITY OF THE
HETERODIMER COORDINATIVELY REGULATES PER AND TIM TRANSCRIPTION
THROUGH A NEGATIVE FEBBBACK LOOP. BEHNAVES AS A NEGATIVE ELEMENT
IN CIRCADIAN TRANSCRIPTIONAL LOOP. DEES NOT APPEAR TO BIND DNA,
SUGGESTING INDIRECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).
CHOROLOGY A COMPLEX AND THE NUCLEAR AT SPECIFIC PERIODS OF THE DAY.
TRANSLOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY.
TRANSLOCATION INTO THE PRINCICEAR REGION ABOUT ONE HOUR BEFORE
TRANSLOCATION INTO THE NUCLEAR. SIMILARITY).
CHOR NUCLEAR LOCALIZATION (BY SIMILARIZATION DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE-9803379; PubMed-9365248;
MEDILINE-9803379; PubMed-9365248;
Myers M.P., Rothenfluh A., Chang M.W. Young M.W.;
"Comparison of chromosomal DNA composing timeless in Drosophila melanogaster and D. virilis suggests a new conserved structure for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NECESSARY FOR NORMAL CIRCADIAN RHYTHM (BY
                                                                                  Drosophila virilis (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sehgal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98186271; PubMed-9504927;
Ousley A., Zafarullah K., Chen Y., Emerson M., Hickman L., Sehgal Conserved regions of the timeless (tim) clock gene in Drosophila analyzed through phylogenetic and functional studies.";
Genetics 148:815-825(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein; Repeat; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> H (IN REF. 2).
-> S (IN REF. 2).
-> A (IN REF. 2).
; 3FCZF286AC5355F5 CRC64;
                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-1194 AND 1196-1343 FROM N.A.
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POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 25:4710-4714(1997).
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EMBL; AF032402; AAB94891.1; JOINED.
EMBL; AF038502; AAB94930.1; -.
EMBL; AF040096; AAB94942.1; -.
Flybase; FBgn0022834; Dvir\tim.
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15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
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Biological rhythms;
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                                                                 FIMELESS PROTEIN.
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Kolbe H.V.J., Huber A., Cordier P., Rasmussen U.B., Bouchon B., Jaquinod M., Vlasar R., Delott E.C., Krell G.;
Jaquinod M., Vlasar R., Delott E.C., Krell G.;
Xenoxins, a family of peptides from dorsal gland secretion of Xenopus laevis related to snake venom cytotoxins and neurotoxins.";
J. Biol. Chem. 268:16458-16464(1993).
-!- FUNCTION: LACKS ALPHA-NEUROTOXIC ACTIVITY, HAS APPARENTLY NO ANTIBACTERIAL ACTIVITY, NOR ANTI-COAGULANT POTENCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forslund O., Hansson B.G.; 70 "Human papillomavirus type 70 genome cloned from overlapping PCR products: complete nucleotide sequence and genomic organization."; J. Clin. Microbiol. 34:802-809(1996).
                                                                                              Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
REPLICATION PROTEIN E1.
              66 AA.
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MEDLINE-96249586; PubMed-8815087;
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8 ANGVKMTQECAKEDT 22
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                                                                                                                                         Xenopodinae; Xenopus.
NCBL_TaxID=8355;
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Best Local Similarity
Matches 8; Conserv
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Mismatches

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Best Local Similarity

Matches

Query Match

42.5%; 66.7%;

Score 45; DB 1; Length 1343; Pred. No. 28;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLG_TWEVD STANDARD; PRT; 2301 AA. P0LG_TWEVD STANDARD; P0.856; Q88567; Q88569; Q88569; Q88570; P13899; Q88564; Q88565; Q88567; Q88567; Q88569; Q88570; Q88571; Q88572; Q88573; Q88574; Q89580; Q1-1AN-1990 (Rel. 13, Created) Q1-1AN-1990 (Rel. 13, Last sequence update) Q1-3AN-1990 (Rel. 13, Last sequence update) Q20-AUG-2001 (Rel. 40, Last annotation update) Q20-AUG-2001 (Rel. 40, Last annotation update) P2A TO P2C, P3A; GENOME-LINKED PROTEINS VP1 TO VP4; CORE PROTEINS P2A TO P2C, P3A; GENOME-LINKED PROTEIN VPG; PICORNAIN 3C (EC 2.7, 7.48)] Theiler's murine encephalomyelitis virus (strain DA) (TMEV). Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
         VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROPER. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS. SUBCELLULAR LOCATION: NUCLEAR.
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  FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
                                                                                                                                                                      InterPro; IPR001177; Papillom_El.
Pfam; PF00519; El; 1.
Pfam; PF00524; El_N; 1.
Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
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MEDLINE-88206072; PubMed-2834872;
Ohara Y., Stein S., Fu J., Stillman L., Klaman L., Roos R.P.;
"Molecular cloning and sequence determination of DA strain of
"Theiler's murine encephalomyelitis viruses.";
Virology 164:245-255(1988).
                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 652; Pred. No. 21;
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                                                                                                                                                                                                                                ATP (POTENTIAL).
35B34BE9555739AB CRC64;
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ilarity 47.4%;
Conservative
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Best Local Similarity
Matches 9; Conserv
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POLG_TMEVD
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PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
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InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; Rhv.
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PDB; 1TME; 31-JAN-94.
MEROPS; C03.009; -.
MEROPS; U29.001; -.
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FT STRAND 869 874
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SQ SEQUENCE 2301 AA; 256159 MW; 0B6095DF153DBFDF CRC64;
Query Match
Best Local Similarity 70.0%; Pred. No. 67;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps
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01-JUN-2001 (TrEMBLrel. 17, Created)
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Mismatches 0; Indels
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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"Antigenic drift and immune selection acting on merozoite surface
protein 1.9 and merozoite surface protein 2 in independent field
isolates of Plasmodium falciparum.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A., "Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EMBL; AF329508; AAK19327.1; ...
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SEQUENCE 77 AA: 8542 MW; 4EBC8D8B8AA169D4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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"Antigenic drift and immune selection acting on merozoite surface

protein 1-19 and merozoite surface protein 2 in independent field

isolates of Plasmodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Blacen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";

submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR329511; AAK19330.1; -.
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF329510; AAK19329.1; -.
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.; "Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329523; AAK19342.1; ...
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Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Antigenic drift and immune selection acting on merozolte surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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54 EDSGSNGKKITCECTKPDS 72
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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tive 0; Mismatches 0; Indels
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SEQUENCE 77 AA; 8542 MW; 4EBC8D8B8AA169D4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Baddeley A., Eri R., Saul A.;

Bandisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasamodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329526; AAK1915.1;
                                                                                                  Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.; Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum."; bubuitted (DEC 2000) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2011 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
Plassmodium falciparum.
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plassmodium.
NCBI_TAXID-5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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NCBL_TaxID=5833;
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MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).
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Matches 19; Conservative
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EMBL, AF329528; AAK19347.1;
Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.; "Antigenic drift and immune selection acting on merozoite surface protein 1:19 and merozoite surface protein 2 in independent field solates of plasmodium falcinarium":
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EMBL; AF329527; AAK19346.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOTIE SURFACE PROTEIN 1 (FRAGMENT).
Plasmodium falciparum.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                US-09-763-397A-13
88
1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                      Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB s
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                                                                       OM protein
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                          Run on:
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A_Geneseq_1101:*

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
| SIDS8/gcgdata/geneseq/geneseqg/geneseqp/AA1992.DAT:*
| SIDS8/gcgdata/geneseq/geneseqg/AB1992.DAT:*
| SIDS8/gcgdata/geneseq/geneseqg/geneseqg Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Plasmodium falcipa	Recombinant vaccin	A major merozoite	Protein associated	RAS-related protei	Human qlioblastoma	pML5 human qliobla	Amino acid sequenc	Zif protein with z	Thermococcus chito	Thermococcus GC74-
SUMMARIES	ID	AAY70289	AAY70278	AAB83926	AAR14845	-	-	AAB20623	-		-	-
	Query Match Length DB	17 21	350 21	375 22	513 12			688 21				
д₽	Query Match I	100.0	100.0	100.0	51.1	51.1	51.1	51.1	50.0	50.0	50.0	50.0
	Score	88	88	88	45	45	45	45	44	44	44	44
	Result No.	-	7	m	4	S	9	7	80	6	10	11

Zea mays protein f Gamma-IFN/glucagon Gamma-IFN/glucagon Gamma-IFN/glucagon Zea mays protein f Luman protein sequ Zea mays protein f Human polypeptide Human polypeptide	Amino acid sequenc Merozolte surface Merozolte surface Merozolte surface Merozolte surface Merozolte surface Merozolte surface Modified merozolte Modified merozolte LCMV cost glycopro P. falciparum synt Sequence of the Pl Arabidopsis thalia Arabidopsis thalia		c epitope, P599. ; multivalent; malaria; vaccine; ;genic epitope; treatment; zoite surface protein-1; MSP-1; MSP-2; ythrocyte binding antigen-175; 1; RAP-1; gamete specific antigen; iti-CDC/NIIMALVAC-1 antibody.		
587 311 132 132 130 543 544	100 100 100 100 100 100 100 100 100 100	ALIGNMENT AA.	yP.1 antigenic epito) Z/NIMALVAC.1; multi- toxoid; antigenic e i; CSP; sporozoite sur LSA-1; merozoite sur 1; AMA-1; erythrocy ated protein-1; RAP- revention; anti-CDC/		SERVICES
AG222 AR728 AR728 AG331 AG331 AM253 AR796 AM399	AAY 0 5 6 8 1 AAY 0 3 7 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ALIC	MSP-1 antiger CDC/NIIMALVAC us toxoid; antien; CSP; spoi : LSA-1; mero: en-1; AMA-1; colated protein		SER
		17	/NIMA toxoid ; CSP; ; CSP; 1, AMA 1; AMA ted pr		69. 03. GY. HUMAN SE;
222122222222222222222222222222222222222	777077777777777777777777777777777777777	de;	Y-I tox tox SA- SA- 11, ted		8869 7703 LOGY & HUI In Si
107 172 172 172 280 293 296 306 1566 693	2229 32529 32529 22529 22529 22539 22539 22539 22539 22539 22539 22539 22539 22539	. It it	CD CDC CDC CDC CDC CDC CDC CDC CDC CDC	rum.	-US1 -009 4UNO LTH asna
		rd; irst	Lpar tetr tet lger ant	pa .	0 0 I
	44444444444444444444444444444444444444	ndan (f)	alcı prot pe; oite anti ane ptry	alci Al.	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
44444444		ta o	n re	n fa 79-1 00.	999; 998; NAT OUS DI Shi
44 44 44 44 44 44 44 44 44 44 44 44 44	444444444444444444444444444444444444444	1 70289 70289; JUN-20	Plasmodium falciparum Recombinant protein; T-cell epitope; tetar Circumsporozoite proi liver stage antigen- apical membrane antig EBA-175; rhoptry asso Pfg27; antiparasitic	asmo 2000 -MAR	AUG-19 AUG-19 IM-) N SH) U AA,
113 114 117 118 118	00000000000000000000000000000000000000	ULT 70289 AAY AAY 06	CC TRE	P1 WO 02	19-21-721-721-721-721-721-721-721-721-721-
		RES AAY ID XX AC XX XX XX	X X X X X X X X X X X X X X X X X X X	XX OX XX OY XX OY X	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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The present sequence is the antigenic epitope P599, derived from merozoite surface protein-1 (MSP-1) of the asexual blood stage of plasmodium falciparum. It is used in the construction of recombinant protein Construction of recombinant protein comprises, melittin signal peptide, carcine. The recombinant protein comprises, melittin signal peptide, carcine. The recombinant protein comprises, melittin signal peptide, carcine protein protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (SSP-2), apical membrane antigen-1 (AAA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, PGZ7. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antipartal infections. Anti-CDC/NIIMALVAC-1 varcine has maintal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxold; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-2; apical membrane antigen-1; AAA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; pf927; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
       Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 88; DB 21; Length 17; 100.0%; Pred. No. 4e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         detecting P. falciparum in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                  Page 17; 52pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200011179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (RAP-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 waccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                   Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Major merozoite surface protein-1; MSP1-42; melittin signal peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A major merozoite surface protein-1 fragment of 42kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 88; DB 21; 100.0%; Pred. No. 9.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
             (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB83926 standard; Protein; 375 AA
                                                                                                                                                                                                    Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                     plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HONG KONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HO WKK;
                                                            Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1999; 99US-0165178.
01-DEC-1999; 99US-0168327.
22-AUG-2000; 2000US-0226861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-2000; 2000WO-US31064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 gisyyekvlakykddle 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUEEN EMMA FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYHA-) UNIV HAWAII.
(UYCH-) UNIV CHINESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hui GSN, Lap-Yin P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-335879/35
                                                                                      WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malaria vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB83926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                              Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB83926
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caution is advised in accepting that this sequence is indeed an S6-like protein kinase !
                                                                                                   Score 45;
Pred. No.
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                                                                                                                                                                                                                                                AAW00087 standard; Protein; 688 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COLD-) COLD SPRING HARBOR LAB
                                                                                                   51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900S-0511715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0688352
90US-0511715
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                     80 gidyydrnlalfeeeld 96
                                                                                                                                                       1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wigler MH;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-299902/30.
                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                              513 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colicelli JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1990;
                                                                                                                                                                                                                                                                                                    09-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5527896-A.
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                                                                                                                                                                                                                                                                        AAW00087;
                                                                Sequence
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                                                                                                                                                                                                                       RESULT
AAW00087
            8×8888
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                                   Producing malaria vaccine, useful for treatment or prevention of all forms of malaria in humans, by expressing immunogenic merozoite protein fragment in a baculovirus system
                                                                                                              The present sequence represents a major merozoite surface protein-1 C-terminal fragment of 42kDa (MSP1-42). This fragment is linked to a melittin signal peptide, and then expressed in a in a silkworm/baculovirus system. The protein is used to prepare a malaria vaccine, which is used to treat or prevent malaria, caused by any of the four species of Plasmodium that infect humans.
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In the specification this sequence is given the SEQ ID NO. 26 and is encoded by the nucleotide sequence having SEQ ID NO.25. References to SEQ ID NO. 25 in the text give the clone as $46 which was selected by complementation in S.cerevisiae strain RS60.15B. The yeast strain carries a mutant RAS2 allele such that cells are unable to grow at 36 deg.C. There are two open reading frames and the two corresponding amino acid sequences are printed as SEQ ID NO. 3 & and 27, although only NO.26 is actually mentioned in the text. It is described as being homologous to the S6 protein kinase of Xenopus laevis. N.B. many of the references in the text of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementary screening for genes and prods. • e.g. RAS protein and cAMP, that modify, complement or suppress genetic defect and correct associated phenotypic alteration
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncogene; cancer; cyclic nucleotide phosphodiesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein associated with biochemical pathway involving cAMP.
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                             100.0%; Score 88; DB 22;
100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0;
                                                                                     Example 3; Page 87-88; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 104; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              AAR14845 standard; Protein; 513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US02714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0511715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COLD-) COLD SPRING HARBOR.
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                  1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colicelli JJ;
                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                         375 AA;
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          N-PSDB; AAF89840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wigler MH,
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR14845;
                                                                                                                                                                                                         Sequence
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complementation of two genetically altered S. cerevisiae and S. pombe strains. Clone 546 was selected by complementation in S. cerevisiae and S. pombe strains. Clone 546 was selected by complementation in S. cerevisiae at strain S. Clone 546 was selected by complementation in S. cerevisiae strain RSG0 15B. This strain contains a mutant allele of RAS2, RAS2(vall9ala15), which renders cells unable to grow at 36 deg. C, because such cells are defective in RAS function at elevated temperatures. Human cDNA's from a human glioblastoma cell library were selected that could complement this defect. The deduced sequence of 546 is homologous to a Xenopus laevis gene that encodes a known protein kinase, the 56 protein kinase. Plasmid pML5 was selected by complementation in S. cerevisiae strain SKN37 Tails strain contains a secciated protein of undetermined function. As a consequence of this gene disruption, SKN37 fails to grow in medium rich in amino acids. Human cDNA's were chosen which could complement this defect. Plasmids pATG16 and pATG29 were selected by complementation in the S. pombe cityloid strain SP565. This strain is homozygous for disruptions of ras1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAW00087-89 and AAW00101 are encoded by plasmid fragments which contain human glioblastoma cell cDNA inserts which do
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; glioblastoma; complementation; S. cerevisiae; S. pombe;
Clone S46; strain RS60.15B; RAS2; RAS2(Vall19ala15); Xenopus laevis;
S6 protein kinase; Plasmid PML5; strain SKN37; CAP; adenylyl cyclase;
diploid; strain SPS65; ras1; ras1::LBU2; mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA mols. isolated from human glioblastoma cells – encode RAS-related or cyclic nucleotide phosphodiesterase proteins
DB 12; Length 513; 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAS-related protein encoded by plasmid pML5 (ATCC 68593).
                                                                                                                         Indels
                                                                                                                         3;
                                                                                                                   7; Mismatches
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Length 688;

Score 45;

688 AA;

Sequence

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The present invention describes new isolated RAS-related polypeptides and mammalian cyclic nucleotide phosphodiesterases (PDES). RAS-related polypeptides are capable of complementing a defective RAS function in yeast. The products can be used for screening for agents which can modify, complement or suppress a genetic defect in a biochemical pathway which can proteins affecting cell growth and maintenance. Developing agents that will selectively act upon PDEs is directed toward reproducing the causing the undesirable effects of cyclic nucleotides, e.g. bronchodilation, increased myocardial contractility, anti-inflammation, yet without causing the undesirable effects, e.g. increased heart rate or enhanced lipolysis. The products can also be used for therapeutic, diagnostic and prognostic uses. AAZ32229 to AAZ32285, and AAY9803 to AAX49830, content of the present
                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide
(ras1::LEU2). As a result of this mutation, this strain fails to sporulate, and human cDNA's were selected which could complement this defect. These genes have unknown function.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated RAS-related polypeptides and mammalian cyclic nucleot. phosphodiesterases, used for screening for agents which can modify complement or suppress genetic defects
                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphodiesterase; dunce-like phosphodiesterase; PDE; DPD; cAMP, RAS-related protein; immunoreactive; detection; genetic defect; bronchodilation; increased myocardial contractility;
                                                                                                                                               0;
                                                                                                                  Length 688;
                                                                                                                                                Indels
                                                                                                                                                .;
;
                                                                                                                                                                                                                                                                                                                                                                                        Human glioblastoma cell RAS-related pML5 protein.
                                                                                                               Score 45; DB 17;
Pred. No. 79;
7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 107-112; 145pp; English.
                                                                                                                                                                                                                                                                                              AAY49812 standard; Protein; 688 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-0206188.
90US-0511715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91US-0688352.
                                                                                                                  51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0474379.
                                                                                                                                                                                                                                                                                                                                                            19-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wigler MH;
                                                                                                                                                                                1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                              96
                                                                                                                    Query Match 51.1
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                 80 gidyydrnlalfeeeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-619709/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammation.
                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ32244.
                                                                     688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colicelli JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1990;
19-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5977305-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1999
                                                                                                                                                                                                                                                                                                                              AAY49812;
                                                                         Sequence
                                           defect.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a purified and isolated DNA (I) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert present in the plasmids pPDE46 (ATCC 69522), pPDE43 (ATCC 6951) or pPDE39 (ATCC 69551) or pPDE39 (ATCC 69551) or pPDE39 (ATCC 69551) or pPDE39 (ATCC 69551) or pppE39 (ATCC 69551) or pppE39 (ATCC 69551) or popentic defect in a biochemical pathway in which camplement participates and are also used as hybridisation probes. The present proteins which can function in microorganisms, particularly yeast, to modify, complement, or suppress a genetic defect associated with an indentification or characteristic in the microorganism. AAA88162 to AAA88218 and AAA82614 to AAB20640 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pPDE339 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated DNA encoding a mammalian cyclic nucleotide phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 an is used to modify a genetic defect in a biochemical pathway in which cAMP participates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                     Gaps
                                                                                                                                                                                                                                                           pML5 human glioblastoma cell insert protein sequence SEQ ID NO:28.
                                                                                                                                                                                                                                                                                       Detection; mammalian gene; yeast; microorganism; identification; phenotype; characteristic; dunce-like phosphodiesterase; PDE; RAS-related protein; genetic defect; hybridisation; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                      Indels
                                      3;
       DB 20;
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.1%; Score 45; DB 41.2%; Pred. No. 79; Live 7; Mismatches
                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Column 113-118; 145pp; English.
                          Pred. No.
                                                                                                                                                                           AAB20623 standard; Protein; 688 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0511715.
91US-0688352.
          51.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0206188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.2%
                                                                                                                                                                                                                                      14-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colicelli JJ, Wigler MH;
                                                                    1 GISYYEKVLAKYKDDLE 17
                                                                                     || ||:: || :::|:
80 gidyydrnlalfeeeld 96
                                                                                                                                                                                                                                                                                                                                                                       cerevisiae.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-531664/48.
N-PSDB; AAA88179.
Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 AA;
                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                   US6100025-A.
                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                        AAB20623;
                                                                                                                                                              AAB20623
                                                                                                                                                RESULT
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1 GISYYEKVLAKYKDDLE 17

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invėntion.

80

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Vaccine;

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The present sequence is a zif (zoocin A immunity factor) protein.

The DNA molecule or vector for expressing zif is used to protect organisms susceptible to the bacteriolytic activity of zoocin A.

Non-pathogenic organisms expressing zif can be genetically modified to express zoocin A activity without being at risk from the bacteriolytic activity of zoocin A. The organisms are therefore reasistant to zoocin A. The non-pathogenic organisms that are zoocin A resistant are especially food grade bacteria, such as Streptococcus gordoni. The transformed non-pathogenic organisms that are zoocin A resistant are especially food grade bacteria, such as Streptococcus gordoni. The transformed non-pathogenic organisms are useful as antibacterial compositions, suitable for human ingestion as part of a foodstuff, nutriceutical, a composition are useful for preventing or inhibiting the growth of undesirable organisms susceptible to zoocin A. Additionally the antibacterial composition can be used to treat or prevent Streptococcal sore throat or dental caries. The antibacterials can also be used to treat animals, particularly horses that are infected with group C streptococci. GRAS (generally recognized as safe) organisms transformed with the zif encoding polynucleotides produce zoocin A without organisms then have a wide range of applicability in antibacterials, particularly foodstuffs.
                                       2if: zooA: zoocin A activity; immunity factor; protection;
bacteriolytic enzyme; antibacterial; Streptococcal; sore throat;
dental caries; food; nutriceutical; dairy product; confectionery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zoocin A immunity factor useful in the treatment or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2
Pred. No. 65;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcal sore throat or dental caries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermococcus chitonophagus glycosidase.
  Zif protein with zoocin A activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 34-35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW34560 standard; Protein; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
47.1%;
                                                                                                                                                                                                                                                                            98WO-NZ00171.
                                                                                                                                                                                                                                                                                                                      97NZ-0329227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Simmonds RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-347690/29.
                                                                                                                                                 Streptococcus equi.
                                                                                                                                                                                                                                                                                                                                                                                  UNIV OTAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX76141
                                                                                                                                                                                           WO9926969-A1.
                                                                                                                                                                                                                                                                                                                    21-NOV-1997;
                                                                                                                                                                                                                                                                            23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              Beatson SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1998
                                                                                                           chewing gum
                                                                                                                                                                                                                                     03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW34560;
                                                                                                                                                                                                                                                                                                                                                                                      UYOT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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  a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY36754-Y37949 are encoded by open reading frames (ORPS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against chlamydia trachomatis. Antisenses and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                    paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                eye disease; conventional trachoma; nonendemic trachoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                    Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 44;
64.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 933; 1755pp; English.
                                                                                                                      AAY37149 standard; Protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY17497 standard; Protein; 410 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0107077.
97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                            (first entry)
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gidyydrnlalfeeeld 96
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GISYYEKVLAKYKD 14
                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||: || || :||
|86 gisflekklamhkd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                            07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-1998;
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17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04 - NOV - 1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffais R;
                                                                                                                                                                AAY37149;
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Gaps

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Sequence

Query Match

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AAY17497

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97WO-US22623
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                                                                                                                                                                                                                                  baking industries
                                                                                                                                                          N-PSDB; AAV36913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-2000
            08-DEC-1997;
                                         10-0CT-1997;
                                                        06-DEC-1996;
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ó;
                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents glycosidase isolated from Thermococcus chitonophagus. The enzyme or its encoding nucleic acid sequence is used for generating glucose from soluble oligosaccharides. The enzyme can be used in the food processing, pharmaceutical, textile, detergent and baking industries. The enzyme is also used to treat lactose intolerance, as a diagnostic reporter molecule, in corn wet milling or in the fruit juice industry. The enzymes can be used to hydrolyse guar gum to remove non-reducing terminal mannose residues. The nucleic acids encoding the enzyme may be used to generate probes to identify similar sequences.
                                                                                                                                                                                                                                                                                                                                 New thermostable glycosidase(s) - from Thermococcus, Staphylothermus and Pyrococcus, used in the textile, food processing, pharmaceutical, detergent and baking industries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
             Glycosidase; thermostable; textile; food processing; pharmaceutical; detergent; baking; industry; Thermococcus; Staphylothermus; Pyrococcus; glucose; soluble oligosaccharide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosidase, GC74-22G; thermostable enzyme; oligosaccharide; glucose; sugar; baking; textile; detergent; beta-galactosidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 18; Length 511; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ;
                                                                                                                                                                                                                                                               Swanson RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermococcus chitonophagus strain GC74-22G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by TTG"
                                                                                                                                                                                                                                   (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW49864 standard; Protein; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermococcus GC74-22G glycosidase.
                                                                                                                                                                                                                                                                Mathur EJ,
                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 7; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                       96US-0712612.
96US-0583787.
                                                                                                                                                            97WO-US00092
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                                                                          Thermococcus chitonophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::|| : :||:| : 338 gvnyytrevvkyqdpm 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GISYYEKVLAKYKDDL 16
                                                                                                                                                                                                                                                                                          WPI; 1997-372858/34.
N-PSDB; AAT93684.
                                                                                                                                                                                                                                                                Lam DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 6; Conserv
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11-JAN-1996;
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                                                                                                                                  17-JUL-1997
                                                                                                                                                                                                                                                                Bylina EJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of glycosidase GC74-22G deduced from a polynucleotide (see AAV36913) of Thermococcus chitonophagus GC74 clone (22G) that grows optimally at 85 degC. The sequence shows 46% amino acid identity to a beta-galactosidase of sulfolobus sulfataricus ATCC 49255/MT4. The invention provides 18 polynucleotides (see AAV36907-24) coding for thermostable glycosidases (see AAW49888-75) having glucosidase, alpha-galactosidase, beta-mannasidase, beta-mannase, endoglucanase or pullulanase activity. Vectors and host cells are also claimed. A method is provided for producing the enzymes by recombinant techniques. A claimed method for generating glucose from soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell oligosaccharides comprises contacting a sample (selected from dairy products, fruit juice, detergent, textile, quar quim, animal feed, plant blomass or waste product) containing oligosaccharides (selected from maltose, cellobiose, lactose, sucrose, raffinose,
                                                                                                                                                                                                                                                                                                                               Glycosidase enzymes from organisms of the genera Staphlothermus, Pyrococcus and Thermococcus - for deriving sugar from oligosaccharides, useful in the e.g. food processing, textile or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 511;
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Pred. No. 82;
6; Mismatches 4;
                                                                                                                                                                      Swanson RV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 7a-b; 92pp; English.
                                                                                                                                                                      Mathur EJ,
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37.5%;
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97US-0949026.
96US-0056916.
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Best Local Similarity
6; Conserve
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                                                                                                                                                                      Bylina EJ, Lam DE,
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990x - 0143542. 990x - 0144665. 990x - 0144005. 990x - 0144006. 990x - 0144331. 990x - 0144333. 990x - 0144884. 990x - 0144884. 990x - 0145086. 990x - 0145087. 990x - 0145087. 990x - 0145087. 990x - 0145088. 990x - 0146388. 990x - 0146389. 990x - 014972. 990x - 014972. 990x - 014992. 990x - 0150884. 990x - 0150884.	990S-015378. 990S-015378. 990S-0154018. 990S-0154039. 990S-0155139. 990S-0155486. 990S-0156486. 990S-0156486.
13 - JUL - 1999; 14 - JUL - 1999; 15 - JUL - 1999; 16 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 19 - JUL - 1999; 20 - JUL - 1999; 21 - JUL - 1999; 22 - JUL - 1999; 23 - JUL - 1999; 23 - JUL - 1999; 24 - JUL - 1999; 25 - JUL - 1999; 26 - JUL - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 29 - JUL - 1999; 20 - JUL - 1999; 21 - JUL - 1999; 22 - JUL - 1999; 23 - JUL - 1999; 24 - JUL - 1999; 25 - JUL - 1999; 26 - AUG - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 29 - JUL - 1999; 20 - AUG - 1999; 21 - JUL - 1999; 22 - JUL - 1999; 23 - JUL - 1999; 24 - JUL - 1999; 25 - JUL - 1999; 26 - AUG - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 29 - JUL - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 21 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1	0.7.5EP-1999; 13.5EP-1999; 15.5EP-1999; 16.5EP-1999; 20.5EP-1999; 23.5EP-1999; 24.5EP-1999; 24.5EP-1999; 28.5EP-1999; 29.5EP-1999;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72812 is a gamma-IFN/glucagon/BNP fusion protein, it was used to demonstrate a new method for the isolation of peptides. The fusion protein is recombinantly produced in transformed E. coli, the glucagon/BNP is then cleaved from the granule forming protein gamma-IFN, using a protease. The glucagon can now be isolated from the cell culture.
peptide to a granule forming protein and cleaving the peptide from the resulting fusion protein using a protease
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gamma-IFN/glucagon/BNP; fusion protein; peptide isolation method; granule forming protein; protease cleavage; E. coli; B-type natriuretic peptide; gamma-interferon; recombinant production.
                                                             AAR72811 is a gamma-IFN/glucagon fusion protein, it was used to demonstrate a new method for the isolation of peptides. The fusion protein is recombinantly produced in transformed E. coli, the glucagon is then cleaved from the granule forming protein gamma-IFN, using a protease. The glucagon can now be isolated from the cell culture.
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Mismatches
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Pred. No.
                                                                                                                                                                                                Score 42;
Pred. No.
                                         Example 1; Pages 11-12; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gamma-IFN/glucagon/BNP fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 12; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             AAR72812 standard; protein; 175 AA.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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granule forming protein; protease cleavage; E. coli;
gamma-interferon; recombinant production.
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Pred. No.
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99US-0161404.
99US-0161405.
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
      99US-0157117.
99US-015753.
99US-015865.
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99US-0158332.
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58.3%;
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eqikakfkddld 103
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      04-OCT-1999;
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99US-0148684
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05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                    Zea mays protein fragment SEQ ID NO: 40099.
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99US-0137222
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99US-0137502
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2 ISYYEKVLAKYKDDLE 17
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16-JUN-1999;
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Job time: 422 sec

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Search completed: January 29, 2002, 10:21:46

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Sequence 8, Appli
Sequence 1, Appli
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Patent No. 5278286
Patent No. 5278286
Sequence 8, Appli
Sequence 14, Appl
Sequence 24, Appl
Sequence 37, Appl
                   Sequence Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Treet
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 5; Length 513;
Pred. No. 19;
7; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: BOTON: MICHAEL F. S5447
REFERENCE/DOCKET.NUMBER: 25447
TELECOMMUNICATION NUMBER: 27805/30197
TELECOMMUNICATION NUMBER: 27805/30197
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US-08-657-3098-37
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US-08-436-748-3
US-08-483-857-4
US-08-961-083-20
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application PC/TUS9102714 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: AMINO ACID
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Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) MOLECULE TYPE: protein PCT-US91-02714-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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PCT-US91-02714-26
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    Sequence 26, Appl
Sequence 28, Appl
Sequence 28, Appl
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Sequence 28, Appl
Sequence 23, Appl
Sequence 23, Appl
Patent No. 5182210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238, App
Sequence 248, App
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Patent No. 5168
                                                                                                             ; Search time 133.18 Seconds
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Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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US-07-688-352C-28
US-09-146-249A-28
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5182364-14
52.08-354-456A-9
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US-08-449-639-8
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Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             January 29, 2002, 10:24:05

    protein search, using sw model

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                                                                                                                                                                   US-09-763-397A-13
88
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Result

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Gaps

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US-09-146-249A-28

US-09-146-249A-28

Sequence 28, Application US/09146249A

Patent No. 60693-00

CENERAL INFORMATION:

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 688;
3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                              COMPUTER KEADABLE FORM disk
MEDIUM TYPE: FILOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: US/08/474,379C
FILING DATE: US/08/474,379C
FILING DATE: US/08/11,715
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: US-APR-1994
PRIOR APPLICATION DAMBER: US 07/688,352
FILING DATE: US-ARR-1994
PRIOR APPLICATION DAVIBER: US 07/688,352
FILING DATE: US-ARR-1991
REGISTRATION NUMBER: US-MS-1991
REGISTRATION NUMBER: 286,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INPORMATION:
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7; Mismatches
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STATE: Illinois
SCOUTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                           STATE: Illinois
COUNTRY: United States of America
21P: 60606-6402
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TELERAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
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41.28;
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80 GIDYYDRNLALFEEELD 96
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Best Local Similarity 41.2
Matches 7; Conservative
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                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                Chicago STATE: T11
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APPLICANT: Wigler, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                              US-01-688-352C-28
Sequence 28, Application US/07688352C
Sequence 28, Application Sequence Application Sequence Application Sequence Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 688; 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCH RPC-DOS/MS-DOS
SOFTWARE: PATCHIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
TILING DATE: 19910419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chlosgo
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 26;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27805/30197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-ARR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/08474379C Patent No. 5977305 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELES: (312)
TELENEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
"VPE: AMINO ACID
'THE SECOND ACID
'THE SECOND ACID
'THE SECOND ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.1%;
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Best Local Similarity 41.2*
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GISYYEKVLAKYKDDLE 17
                                                                               1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-474-379C-28
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Gaps

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APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Min-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Hulzhong
TUTLE Chen, Hulzhong
TITLE OF INVENTION: Beta-glucosidase Coding Sequences and Protein from
TITLE OF INVENTION: Orpinomyces PC-2
TITLE OF INVENTION: Orpinomyces PC-2
CURRENT APPLICATION NUMBER: US/09/306,593
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: US 60/084,494
EARLIER FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 13
LENGTH: 450
                                                                                                                      Gaps
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Sequence 23, Application US/08687956A
Sequence 23, Application US/08687956A
Sequence 23, Application US/08687956A
GENERAL INFORMATION:
APPLICANT: BURNIE, JAMES P
APPLICANT: MATHEWS, RUTH C
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
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Pred. No. 24;
5; Mismatches 4; Indels
                                                                     DB 3; Length 688;
26;
                                                                                                                   Indels
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ALUNESSEE: PILLSBURY, MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
STREET: PLOOR
CITY: WASHINGTON
STATE: DC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,956A
FILING DATE: 29-JUL-1996
CLASSIFICATION: 536
                                                                                                                 7; Mismatches
                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ; ORGANISM: Thermoanaerobacter brockii US-09-306-593-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: READABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 US-09-306-593-13
; Sequence 13, Application US/09306593
; Patent No. 6184018
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%;
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                            1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                       80 GIDYYDRNLALFEEELD 96
                                                                   Query Match 51.1
Best Local Similarity 41.2
Matches 7; Conservative
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295 GVNYYTRSIVKYDED 309
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  US-08-206-188B-28
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Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 3;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago States Tower, 233 SOUTH VITY: Chicago STATE: Illinois COUNTRY: United States of America LOW TRY: United States of America LOW TRY: United States of America COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vers CURRENT APPLICATION NUMBER: US/08/206,188B FLING DATE: 01 WAR-1994
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTATION NUMBER: 36107
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-ARR-1990
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/09/146,249A
                                                                                                                                                  NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,474-6300
TELEFRAX: 312-474-0448
                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID. 00: 28:
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amino acid
GY: linear
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 51.1
Best Local Similarity 41.2
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 688 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-146-249A-28
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: SOURNEY
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
APPLICANT: Sekulbroken
APPLICANT: S
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Pred. No. 5.5;
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                                                                                                                                                                                                                                                                                                                                                CORRENT APPLICATION DUBRE: US/08/940,095
PILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RECENENCE/DOCKET NUMBER: 009196-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-4935
TELEPAX: 66141 PENNIE
TELEPAX: 66141 PENNIE
SEQUENCE CHARACTER STICS:
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 248, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                      COMPOTER: IBM Compatible
COMPOTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.
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MEDIUM TYPE: Diskette
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Matches 7; Conservative
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-940-095-238
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                  STREET: LLC.
                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
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      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-940-095-248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sexul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2; Length loopered. No. 1.7e+02; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARCELLY NO. 5182210

PAPLICANT: BINNS, MATTHEW M.; BOURSNELL, MICHAEL E.G.;

CAMPBELL, JOAN I.A.; TOMLEY, FIONA M.

TITLE OF INVENTION: FOWLPOX VIRUS PROMOTERS

NUMBER OF SEQUENCES: 22

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,608

FILING DATE: 21-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                             50885/222892
                                     APPLICATION NUMBER: GB 9401689.6
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16,773
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202/861.3000
TELEFAX: 202/861.3000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE GIRARACTERISTICS:
LENGTH: 1566 amino acids
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Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus sobrinus
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ESS: single
unknown
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455 LSKYQEELAQYKKDL 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ISYYEKVLAKYKDDL 16
                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 EKVLAKYKDDLE 17
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49 EKIEQRYKEDLE 60
                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
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5182210-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-687-956A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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Sequence 248, Application US/08940093
Sequence 248, Application US/08940093
Sequence 248, Application US/08940093
Settent No. 6037323
GENERAL INFORMATION:
APPLICANT: Beatine, Riaus
APPLICANT: Cornut, Isabelle
APPLICANT: ON THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
SCORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: DATE: 25-5EP-1997
CLASSIFICATION NUMBER: 30,742
RECIENCALON UNMBER: 30,742
RECIENCALON UNMBER: 30,742
RECIENCALON UNMBER: 30,742
RECIENCALON UNMBER: 30,743
TELECOMMUNICATION UNMBER: 650-67-67-67
TELECOMMUNICATION UNMBER: 670-67-67-67
TELECOMMUNICAT
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Pred. No. 5.5;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal acetylated and C-terminal amidated
   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
TOPOLOGY: linear
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERICATICS:
LENGTH: 18 amino acids
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Best Local Similarity 58.3
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION:
CTHER INFORMATION:
CG-08-940-093-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SYYEKVLAKYKD 14
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5 AFYEKVLEKLKE 16
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Fatent No. 6037323
GENERAL INFORMATION:
APPLICANT: BEASEUX, Jean-Louis
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Cornut, Isabelle
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITTLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & Edmonds LLP
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                                                                                                                                                                                                                                                                                                                                                                            NAME: COCUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFENCE/COCKET NUBBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEFAX: 65149 ENNIE
TELERAX: 66149 ENNIE
TELERAX: 661-893-6556
TELERAXION FOR SEO ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIERCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: EstsEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: NO. 6004925e
US-08-940-095-248
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SYYEKVLAKYKD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|||||| | :
5 AFYEKVLEKLKE 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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Gaps
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APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA.
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/COKET NUMBER: 009196-0005-999
TELECOMMUNICATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.3%; Score 39;
58.3%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-1997
                                                                                                   RESULT 14
US-08-940-096-248
; Sequence 248, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238, Application US/09465719
Patent No. 6265377
PAPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/940,
                                                                                                                                                                                             Dasseux, Jean-Louis
Sekul, Renate
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 18 amino acids
amino acid
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Matches 7; Conservative
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ZIP: 10036-2811
COMPUTER READABLE FORM:
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5 AFYEKVLEKLKE 16
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5 AFYEKVLEKLKE 16
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US-08-940-096-248
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US-09-465-719-238
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STATE:
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                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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                                                                                               Length 18;
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                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal acetylated and C-terminal amidated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A
REGIGSTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
                                                                                                             Pred. No. 5.5;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PSSTEM: DOS
SOFTWARE: PSSTESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                               Sequence 238, Application US/08940096
Patent No. 6046166
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATER:
OPERATING SYSTEM: DOS
; TOPOLOGY: linear
; MOLEGULE TYPE: No. 6037323e
US-08-940-093-248
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
                                                                                         Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: NO. 6046166e
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION:

CTHER INFORMATION:

CS-08-940-096-238
                                                                                                                                                                                         ::||||| | |:
5 AFYEKVLEKLKE 16
                                                                                                                                                                     3 SYYEKVLAKYKD 14
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TITLE OF INVESTION ADOLIPOPROFEIN A-1 AGONISTS
TOTAL OF INVESTION ADOLIPOPROFEES 359
CORRESPONDENCE ADORESS:
TOTAL OF A TOTAL TOTAL ADOLE A TOTAL OF A TOTAL
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Search completed: January 29, 2002, 10:24:06 Job time: 512 sec THIS PAGE BLANK (USPTO)

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4.5
Compugen Ltd.
   GenCore version
Copyright (c) 1993 - 2000
                                                                          OM protein - protein search, using sw model
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January 29, 2002, 10:26:41 ; Search time 144.96 Seconds (without alignments) 8.933 Million cell updates/sec Run on:

US-09-763-397A-13 88

1 GISYYEKVLAKYKDDLE 17 Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	merozoite surface		merozoite	major merozoite su	major merozoite su	hypothetical prote		Φ	histidinol dehydro	probable integral	conserved hypothet	hypothetical prote	hypothetical prote	ъ	UDP-n-acetylmuramo	zinc metalloprotei	probable AMP-bindi	DNA topoisomerase	hypothetical prote		hypothetical prote		hetical		thiamin biosynthes	probable minor cap	minor capsid prote		
SUMMARIES		S47282	A54498	A26868	SAZQGM	A45948	F86311	T25614	E45734	A86776	671561	A82083	S49942	T51532	3890	A71699	2938	T07943	3767	T17935	3875	T25031	T19415	F83602	G64771	T46944	T13090	VHBPBL	885690	270031
	ΩI	S4.	A5	AZ	SA	A4	F.8	12	E4	A8	67	A8	S4	T5	80	A7	B8.	T0	Τ4	11	A8	T	11	F.8	ġ9	T4	11	ΛH	B8	C2
	BB	7	~	7					7	7	~																			
	Length		1701	1701	1726	1726	815	806	431	431	451	540	587	1755	447	445	909	701	878	176	308	401	425	459	482	482	530	533	533	636
d	Query Match	100.0	100.0	100.0	100.0	100.0	56.8	53.4	9.05	50.6	50.0	50.0	50.0	50.0	49.4	48.9	48.9	48.9	48.9	47.7	47.7	47.7	47.7	47.7	47.7	47.7	•	٠	47.7	47.7
	Score	88	88	88	88	88	20	47	44.5	44.5	44	44	44	₹*	43.5	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42
	Result No.	П	7	3	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

nitrate reductase		surface antigen A	cell surface antig	probable reverse g	hypothetical prote	major merozoite su	hypothetical prote	surface glycoprote	surface glycoprote	cytovillin homolog				
T08105	H75034	A60338	A43607	C71129	S38011	876079	G82504	A75020	E71206	A45545	T03118	VGXPLM	VGXPLA	A45620
77	7	~	7	7	7	~	~	~	7	7	~	-	-	7
911	1214	1528	1566	1624	619	152	155	307	307	400	401	498	498	559
47.7	47.7	47.7	47.7	47.7	47.2	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6	46.6
42	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Description: Plasmodium falciparum A; variety: Species: Plasmodium falciparum) (strain RO-71) C; Species: Plasmodium falciparum A; variety: Strain RO-71 C; Deccies: Plasmodium falciparum C; Deccies: Plasmodium falciparum C; Davision: S47282 C; Accession: S47282 A; Prolle, R.; Bujard, H.; Cooper, J.A. Submitted to the EMBL Data Library, July 1994 A; Description: Plasmodium falciparum: recombination within the C-terminal region of m A; Reference number: S47282 A; Accession: S47282 A; Accession: S47282 A; Molecule type: DNA A; Residues: 1-651 <TOL>
A; Residues: 1-651 <TOL>
A; Residues: 1-651 <TOL>
A; Residues: 1-651 <TOL>
C; Superfamental source: strain RO-71 C; Superfamental source: strain RO-71 C; Superfamily: major merozoite surface antigen C; Keywords: glycoprotein; merozoite; surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 88; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 17; Conservative 0; Mismatches 0;
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RESULT 2 A54498 madys marvanite enrfane antinen preminent - majaría paraeite (Djaemodium falniparim)	major microsico ourseo university processor major microsico (resumble description) C;Species: Plasmodium falciparum	C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000	; Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V	Mol. Biochem. Parasitol. 27, 291-302, 1988	A; Title: Variation in the precursor to the major merozoite surface antigens of Plasmo	A; Reference number: A54498; MUID:88142999	A; Accession: A54498	A; Status: preliminary	A; Molecule type: DNA	A; Residues: 1-1701 <pet></pet>	A; Cross-references: GB:M19143; NID:g160412; PIDN:AAA29653.1; PID:g160413	C; Superfamily: major merozoite surface antigen	C;Keywords: surface antigen
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Gaps

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Indels

Length 1701;

Query Match 100.0%; Score 88; DB 2; Lo Best Local Similarity 100.0%; Pred. No. 1.8e-05; Matches 17; Conservative 0; Mismatches 0;

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reobles Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Arcession: F66311
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hudzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; WUID:21016719
                                                                                                                                major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) C.Species: Plasmodium falciparum C.Species: Plasmodium falciparum C.Species: Plasmodium falciparum 30-Sep-1993 #text_change 09-Jun-2000 C.Specession: A45948 #Sequence_revision 30-Sep-1993 #text_change 09-Jun-2000 C.Specession: A45948 #Sequence_revision 30-Sep-1993 #text_change 09-Jun-2000 R.Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A. Exp. Parasicol. 67, 1-11, 1988 #A71file: Plasmodium falciparum: gene structure and hydropathy profile of the major me A.Reference number: A45948; MuID:89005525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:AE005172; NID:99802741; PIDN:AAF99810.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88; DB 2; Length 17
Pred. No. 1.8e-05;
Mismatches 0; Indels
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Pred. No. 7.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-1726 <CHA>
A; Cross-references: GB:M37213
C; Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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100.0%;
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1450 GISYYEKVLAKYKDDLE 1466
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
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A; Molecule type: DNA
A; Residues: 1-815 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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A45948
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N.Alternate names: 195K glycoprotein

C;Species: Plasmodium falciparum

C;Species: Plasmodium falciparum

C;Date: 30.Sep-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000

C;Accession: A23386; S06361

R;Weber, J.L.; Leininger, M.M.; Lyon, J.A.

Nucleic Acids Res. 14, 3311-3323, 1986

Natitle: Variation in the gene encoding a major merozoite surface antigen of the human manacession: A23386; MUID:86205236

A;Accession: A23386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
F;1-19/Domain: signal sequence #status predicted <SIS>
F;20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
F;757-765/Region: 3-residue repeats (T-E-E)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carbohy
                                                                                                                                                                                                                                                                                                       C; Accession: A26868
R; Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
A; Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium A; Reference number: A26868; MUID:88011243
A; Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium A; Reference number: A26868
A; Molecule type: DMA
A; Residues: 1-1701 < TAN>
C; Superfamily: major merozoite surface antigen
C; Superfamily: major merozoite surface antigen
C; Reywords: surface antigen
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 1-1701/Product: major merozoite surface antigen #status predicted <MAT>
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                                                                                                                                                                                                                  major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
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R;Weber, J.L.; Slm, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A;Title: Merozoite surface protein sequence from the Camp strain of the human malaria B;Reference number: S06361; MUID:88143999
A;Accession: S06361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
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                                                                                                                                                                                                                                                  C;Species: Plasmodium falciperum
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1701;
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ilarity 100.0%;
Conservative 0
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Best Local Similarity luv..
Local 17; Conservative
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A; Residues: 1104-1726 <WEB2>
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A; Residues: 1-1104 <WEB1>
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Best Local Similarity
Matches 17; Conserv
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probable integral membrane protein - Chlamydia trachomatis (serotype D, strain UW3/Cx C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Species: 33-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C; Accession: G71561
R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A; Reference number: A71570; MUID:99000809
A; Reference reliminary
A; Accession: G71561
A; Accession: G71561
A; Residues: preliminary
A; Residues: 1-451 < ARN>
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                                                          A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-431 <<270>
A; Residues: 1-431 <<270>
A; Construction: CSTOSS-references: GB:AD005176; NID:g12724178; PIDN:AAK05307.1; GSPDB:GN00146
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: hisD
C; Superfamily: histidinol dehydrogenase; histidinol dehydrogenase homology
C; Keywords: oxidoreductase
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Pred. No. 34;
2; Mismatches
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Best Local Similarity 62.5%;
Matches 10; Conservative
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394 SYYPKEVLAAFKEDVE 409
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Best Local Similarity 64.3
Matches 9; Conservative
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86 GISFLEKKLAMHKD 99
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A; Status: preliminary
A; Molecule type: DNA
      A; Accession: A86776
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A; Residues: 1-37, E'. 39-42, 'S', 44-68, 'P', 70-73, 'T', 75-163, 'T', 165-244, 'E', 246-247, 'N', 24
A; Experimental source: strain IL1403 (auxotrophic for histidine)
C; Superfamily: histidinol dehydrogenase; histidinol dehydrogenase homology
C; Keywords: histidine biosynthesis; oxidoreductase
F; 35-429/Domain: histidinol dehydrogenase homology <HID>
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                                                                                                                                                    A:Accession: T25614
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-806 < DAV>
A:Cross-references: EMBL:U88315; PIDN:AAB42369.1; GSPDB:GN00023; CESP:C37H5.5
A:Experimental source: strain Bristol N2; clone C37H5
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A Status: preliminary
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A Molecule Lype: DNA
A Mole: sequence extracted from NCB1 backbone (NCB1R:115814, NCB1P:115826)
A Mole: sequence extracted from NCB1 backbone (NCB1R:115814, NCB1P:115826)
B Mole: Godon, J.J.: Bhilph, S.D.; Renault, P.
J. Bacteriol. 175, 4391-4399, Blips
A Molecular Mol
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A;Map position: 5
A;Introns: 95/3; 141/1; 254/3; 342/1; 365/3; 672/3; 750/2
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C37H5.
A;Reference number: 220058
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Pred. No. 27;
3; Mismatches
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Pred. No. 21;
2; Mismatches
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62.5%;
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Best Local Similarity 62.5
Matches 10; Conservative
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767 YDKVESKYLDDLE 779
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: A7169
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71639
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C;Accession: C83890
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MuID:20263314
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A;Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14867.1; PID:g386
A;Experimental source: strain Madrid E
C;Genetics:
                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosldues: 1-447 <STO>
A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05642.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
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Pred. No. 48;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: murD; RP410
C;Superfamily: UDP-N-acetylmuramate--alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43.5;
Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: bglA
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GINYYTGSVARYKENEGLFDLE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GISYYEKVLAKYKD-----DLE 17
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52.4%;
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Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 49.4%
Best Local Similarity 45.5%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A71699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763310; GSPDB:GN00009; MIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 90/2; 127/1; 209/3; 239/1; 323/3; 359/3; 397/1; 430/2; 452/3; 574/3; 634/3; 3; 1637/3; 1679/3
A; Note: T20K14_150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein YIL036w - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein X19905.12
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: S49942
R;Odell, C; Bowman, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: S49931
A;Reference number: S49931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C83890
beta-glucosidase bglA [imported] - Bacillus halodurans (strain C-125)
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                                          Score 44; DB 2; Length 540;
Pred. No. 41;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 9L
C;Superfamily: fos/jun DNA-binding domain homology
F;420-460/Domain: fos/jun DNA-binding domain homology <FJD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1755 <SAT>
A; Cross-references: EMBL:AL391143
A; Experimental source: cultivar Columbia; BAC clone T20K14
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2;
Pred. No. 45;
5; Mismatches
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50.0%;
                                             Query Match 50.0%;
Best Local Similarity 50.0%;
Matches 8; Conservative
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216 VKYYERKKAKYSDKSE 231
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850 GIKYFEKVAERIKD 863
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471 LNYYEKLISKFK 482
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Best Local Similarity
6, Conserve
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-587 <ODE>
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Gaps

4;

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4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
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sw model - protein search, using OM protein

January 29, 2002, 11:13:43; Search time 80.65 Seconds (Without alignments) 7.728 Million cell updates/sec Run on:

1 GISYYEKVLAKYKDDLE 17 US-09-763-397A-13 88 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length DB Query Match 1 1000.0 11000.0 Score Result

P1959B plasmodium P0856 plasmodium P0856 plasmodium P04934 plasmodium P04936 plasmodium P04936 plasmodium P04935 cacharomyc P40535 saccharomyc P55913 salmonella P39867 brassica na P3793 schizophyll P3427 saccharomyc P42540 bacteriopha P04931 lymphocytic P5767 homo sapien P04932 plasmodium P04933 plasmodium P04933 plasmodium P04933 plasmodium P64934 brancomyc Q44044 salcaligenes P54296 homo sapien P54 MET3_CANAL YKR9_YEAST VKR9_YEAST VGLY_LYCVA EVC_HUMAN MSP1_PLAFW MSP1_PLAFW IF3A_YEAST NIF5_ALCFA MYM2_HUMAN RYM2_HUMAN MSP1_PLAF3
MSP1_PLAFF
MSP1_PLAFF
MSP1_PLAFF
MSP1_PLAFC
MSP1_PLAFC
HISX_LACLA
Y106_YEAST
WURD_RICPR
YMP9_CAEEL THII_ECOLI THII_SALTY VMCB_LAMBD NIA1_BRANA MAY4_SCHCO SPAA_STRDO CAB1_CAEEL 1528 5728 5728 5727 6727 1639 1465 1102 1102 1102 1102 1102 1102 1105 41.5 41.5 41.5 40.5

POTENTIAL.
MEMBRANE ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).

1682 1682 1682 233 462 528 528

20 1666 233 462 528 599

TRANSMEM CARBOHYD CARBOHYD CARBOHYD CARBOHYD

CHAIN

aeropyrum p sulfolobus cercocebus

macaca mula homo sapien aquifex aeo

PFDA_SULSO ING_CERTO ING_MACMU ING_HUMAN Y678_AQUAE

P12593 influenza b Q58208 methanococc	P40942 clostridium Q58282 methanococc	Q55318 synechocyst Q92ms6 helicobacte	P48285 helicobacte P42848 thermotoga	P07399 lymphocytic Q66001 canine dist	066000 canine dist	Ol3681 schizosacch
VNS1_INBGL Y798_METJA	CEXY_CLOSR Y872_METJA	FENR_SYNY3 ENO_HELPJ	ENO_HELPY ENO_THEMA	VGLY_LYCVW HEMA_CDVA4	HEMA_CDVA6	YJ13_SCHPO
пп					٦,	-
281	387	413	426 429	498	607	615
44 .3 44 .3	44.3	44.3	44.3	44.3	44.3	44.3
3 3 3	6 6 6 6 6 6 6	33	8 6 8 8	6 6 8	36	36
34 35	36	38	40 41	42	44	45

ALIGNMENTS

RESULT	
MSP	
Ω	MSP1_PLAF3 STANDARD; PRT; 1682 AA.
AC	P19598; Q25921;
DT	
DT	
DŢ	(Rel.
DE	MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
DE	•
GN	MSP-1.
SO	Plasmodium falciparum (isolate ro-33 / Ghana).
ဗ	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
×o	
RN	[1]
RP	SEQUENCE OF 1-1061 FROM N.A.
RX	MEDLINE-88166657; PubMed-3327688;
RA	Certa U., Rotmann D., Matile H., Reber-Liske R.;
RT	"A naturally occurring gene encoding the major surface antigen
RT	precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
RL	EMBO J. 6:4137-4142(1987).
RN	[2]
RP	SECUENCE OF 1032-1682 FROM N.A.
XX	MEDI.TNE=95354793: PubMed=7528566:
DA	Holle B Buyard H Cooper I A
E C	JOINTY NOT BELLEVILLED TO COORDER OF THE CAMPINAL FOR THE CAMPINAL FOR THE PROPERTY OF
- E	monotopies any factor and income a continuo de continu
I I	merozoite suriace antigener:
R.	Exp. Parasitol. 81:4/-54(1995).
ပ္ပ	-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
ပ္ပ	(POTENTIAL).
ខ	-!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42
႘	KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF
ខ្ល	MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
ပ္ပ	
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ນ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
SS	or send an email to license@isb-sib.ch)
) [
DR	EMBL: M35727; AAA29715.1;
DR	EMBL: Y00087: CAA68280.1:
DR	Z35326; CAA84555.1;
DR	806286;
DR	InterPro; IPR000561; EGF-1ike.
DR	Pfam; PF00008; EGF; 1.
ΚW	Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
KW	Transmembrane; GPI-anchor.
FT	
F	20 1682

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(PMMSA) (P190).
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                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988
30-MAY-2000
30-MAY-2000
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P08569;
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                   CARBOHYD
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CARBOHYD
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ID MSP1_
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BELLINE-88142999; PubMed-2449612;

Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G.,

Brown G.V., Anders R.F., Kemp D.J.;

Brown G.V., Mondrow G.V., Woodrow G.V.,

Brown G.V., Woodrow G.V., Woodrow G.V.,

Brown G.V., Mondrow G.V., Woodrow G.V.,

Brown G.V., Woodrow G.V., Woodrow G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                             (POTENTIAL)
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                       Length 1682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                    LINKED (GLCNAC. . .) (POTEN
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LINKED (GLCNAC. . . ) (POTEN
LINKED (GLCNAC. . . ) (POTEN
C82A1E159948CAD6 CRC64;
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    (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
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                                                                                                                                                                                                                                            100.0%; Score 88; DB 1; 1 100.0%; Pred. No. 6.8e-06;
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                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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InterPro; IPR000561;
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P13819;
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MSP1_PLAFF
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            SOLUTION
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDILIDE-88011243; Pubmed-3079521;
Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite
                                                                                                                                                                                                                       Gaps
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-: SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
PTM: MEROZOITE SUREACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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MEROZOITE SURFACE PROTEIN 1.
N-LINKED (GLCNAC. ..) (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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PIR: B25120; B25120.
Interpro; IPCF-11ke.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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0
                                                                                                                                                      Query Match
100.0%; Score 88; DB 1; Length 1701;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate mad20 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70153;
                                   N-LINKED (GLCNAC. . .) (POTI
MW; 3920B75E73D38552 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.";
J. Mol. Biol. 195:273-287(1987).
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39, Last sequ
39, Last anno
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1588 1588
1701 AA; 193719
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SEQUENCE FROM N.A.
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P50495;
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KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBFACE ANTIGENS OF
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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10-MAR-1989 (Rel. 10, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-1103 FROM N.A.
MEDLINE-86205236; PubMed-3517809;
Weber J.L., Leininger W.M., Lyon J.A.;
Variation in the gene encoding a major merozoite surface antigen the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
                 (POTENTIAL)
(POTENTIAL)
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MENOZOITE SURFACE PROTEIN 1.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                     100.0%; Score 88; DB 1; Length 1701; 100.0%; Pred. No. 6.9e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                         3FC2EC59AF96EA98 CRC64;
        N-LINKED (GLCNAC...)
                                                                                         AA; 193768
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                                                                                                                                                                       1425 GISYYEKVLAKYKDDLE 1441
                                                                                                                   Ouery Match 100.0
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                             1 GISYYEKVLAKYKDDLE 17
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1196
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P04934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
-!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
(PMMSA) (GP195).
                                                                                                                                                                          (POTENTIAL).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Pred. No. 7e-06;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
Siddiqui W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                              INKED (GLCNAC. . .) (POTI DD8AD45FA352BCF3 CRC64;
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MEROZOITE SURFACE PROTEIN 1
N-LINKED (GLCNAC...) (INTINEED (GLCNAC...)) (INTINEED (GLCNAC...) 
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Best Local Similarity 100.
Matches 17; Conservative
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EMBL; AE006353; AAK05307.1; -

PIN; E45734, E45734.

PIN; E45734, E45734.

PIN E4574.

PRO01692; Histidinol_dh. 1.

PRINTS; PRO0083; HOLDHDRGNASE.

PROSTITE; PS00611; HISTIDIOL_dh. 1.

PROSTITE; PS00611; HISTIDIOL_dh. 1.

PRINTS; PS00611; HISTIDIOL_dh. 1.

PRINTS; PS00611; HISTIDIOLHUPROGENASE; 1.

Histidine biosynthesis; Multifunctional enzyme; Oxidoreductase; NAD;
                                                                                                                                                                                                                                                                                                                                                 STRAIN-NCDO 2118;
MEDLINE-3015709; PubMed-1400209;
Delocime C., Ehrlich S.D., Renault P.;
Histidine biosynthesis genes in Lactococcus lactis subsp. lactis.";
J. Bacteriol. 174:6571-6579(1992).
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 INKED (GLCNAC. . .) (POTENTIAL).
5B59CEEFA2F9A026 CRC64;
                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PATHWAY: TENTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: TO OTHER PROKARYOTIC, FUNGAL AND PLANTS HDH.
                                                                                     100.0%; Score 88; DB 1; Length 1726; 100.0%; Pred. No. 7e-06;
                                                                                                          0; Indels
 N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
40-AUG-2001 (Rel. 40, Last annotation update)
HISTIDINOL DEHYDROGENASE (EC 1.11.23) (HDH).
                                                                                                                                                                                                        431 AA.
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                          PRT;
                                                                                                           ;
0
   990 990
1016 1016
1114 1114
1221 1221
1613 1613
1726 AA; 196174 M
                                                                                                                                            1450 GISYYEKVLAKYKDDLE 1466
                                                                                                                                GISYYEKVLAKYKDDLE 17
                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 174:65
[2]
SEQUENCE FROM N.A.
STRAIN=IL1403;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                           Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH
                                                                                                                                                                                                          HISX_LACLA
Q02136;
              CARBOHYD
                                             CARBOHYD
     CARBOHYD
                                     CARBOHYD
                                                                                                                                                                                     RESULT 6
HISX_LACLA
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                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
-CT067/CT068/CT069/CT070 FOR A METAL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i - SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                    Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE METAL TRANSPORT SYSTEM MEMBRANE PROTEIN CT069.
L -> V (IN REF. 1).
E -> A (IN REF. 1).
P -> R (IN REF. 1).
T -> A (IN REF. 1).
T -> B (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                  Score 44.5; DB 1;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01325; Fe_dep_repress; 1.
SMART; SM00529; HTH_DTXR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001281; AAC67660.1; -.
InterPro; IPR001367; HTH_DtxR.
InterPro; IPR001626; ABC-3.
Ffam; PF00950; ABC-3; 1.
         E S K S Z E H H P S E E
                                                                                                                                                                                                                                                                                                        MM:
                                                                                                                                                                                                                                                                                                                                                                       50.6%;
62.5%;
                                                                                                                                                                                                                                                                             403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 SYYPKEVLAAFKEDVE 409
                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SYYEK-VLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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58
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38
43
69
74
74
245
245
248
301
303
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TRANSMEM 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                        431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y069_CHLTR
O84072;
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                                                                                                                                                                 CONFLICT
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445 AA;
                                                                                                                     SEQUENCE FROM N.A.
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                                            ADDING ENZYME).
                                                                                               NCBI_TaxID=782;
                                                       MURD OR RP410.
                                                                                                                                                                                              mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMP9_CAEEL
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SEQUENCE
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                         Churcher C.M., Connor R., Copsey T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsenla T.S., Jaqqals K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC.1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-RVO-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 65.3 KDA PROTEIN IN NOT3-CKA1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 587;
                                                                                   Length 451;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                           POTENTIAL.
925F4BD18C473C5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 389 ATP (POTENTIAL).
587 AA; 65264 MW; 1B98DC38BC8CAE94 CRC64;
                                                                                   Score 44; DB 1;
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
           POTENTIAL.
POTENTIAL.
POTENTIAL.
  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD; SG001298; CST6.
Pfam; PF00170; bZIP; 1.
SMART; SM00338; BRL2; 1.
Mpychetical protein; ATP-binding.
NP BIND
SEQUENCE 587 AA; 65264 MW; 1B96
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURD_RICPR
ID MURD_RICPR STANDARD; F
AC 092DC2;
DT 30-MAY-2000 (Rel. 39, Created)
                                                     51231 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 246861; CAA86915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                   Query Match 50.0%;
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                        STANDARD;
                                                                                                                              1 GISYYEKVLAKYKD 14
                                                                                                                                          |||: || || :||
86 GISFLEKKLAMHKD 99
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ISYYEKVLAKYK 13
100
145
192
233
269
451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                       YID6_YEAST
P40535;
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                         TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                  RESULT 8
YID6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson S.G.E., Zomorodipour A., Andersson J.O., Scheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 22.0 KDA PROTEIN B0361.9 IN CHROMOSOME III PRECURSOR.
B0361.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 396:133-140(1998).

-!- FUNCTION: CELL WALL FORMATION. CATALYZES THE ADDITION OF D-GLUTAMATE TO THE NUCLEOTIDE PRECURSOR UDP-N-ACETYLMURAMOYL-L-ALANINE (UMA) (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE + D-GLUTAMATE = ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-
                            20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (EC 6.3.2.9) (UDE
ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE) (D-GLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                 Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase; ATP-binding; Complete proteome.
NP_BIND 111 117 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
B9CCCF7437FB7AA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-ALANYL-D-GLUTAMATE.
-! PATHWAY: BEPTIDOGLYCAN BIOSYNTHESIS.
-! SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMII-: SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AA
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.9%; Score 43; DB Best Local Similarity 52.4%; Pred. No. 19; Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MADRID E;
MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50129 MW;
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us-09-763-397a-13.rsp

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THII OR B0423
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                                                                          DOMAIN
SEQUENCE
                                                                                                                             Query Match
                                                               TRANSMEM
                                                                                                                                                                                                                                             RESULT 12
THII_ECOLI
δy
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                             Gaps
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NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iwasaki K., Toyonaga R.;
"The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
in synaptic transmission.";
EMBO J. 19:4806-4816(2000).
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
--- SUBUNIT: BINDS TO THE RAB3 GDP/GPT EXCHANGE FACTOR AEX-3.
--- TISSUB SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
--- SIMILARITY: BELONGS TO THE NPDC1 / CAB-1 FAMILY.
                                                                                                                                                                                                                                                                                 Score 42; DB 1; Length 194;
Pred. No. 12;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                 HYPOTHETICAL PROTEIN B0361.9. 79C9F7A2570AAF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND INTERACTION WITH AEX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                        CABI_CAEEL STANDARD; PRT; 425 AA. 093249; P90751; 15-JUL-1998 (Rel. 36, Created) 20-MAY-2000 (Rel. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20428446; PubMed-10970871;
                                                                                                                                         MormPep; B0361.9; CE00838.
InterPro: IPR003014; PAN.
InterPro: IPR003609; Pan_app.
Pfam; PF00024; PAN; 1.
SMART; SM00473; PAN_AP; 1.
Hypothetical protein; Signal.
SIGNAL
                                                                                                                                                                                                                                              SEQUENCE 194 AA; 22017 MW;
                                                                                                                                                                                                                                                                                   47.78;
46.78;
                                                                                                                             EMBL; U00031; AAK18868.1; -.
                                                                                                                                                                                                                                                                                              Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                            127 TYYEKIRCRELDDVE 141
                                                                                                                                                                                                                                                                                                                                    3 SYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAB-1 OR C23H4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN CAB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durbin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                               CAB1_CAEEL
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                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINHEALZ / MG1655;
MEDLINE-97426617; Pubmed-9278503;
MEDLINE-97426617; Pubmed-9278503;
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                 Length 425;
                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                   6CC2C50AEEB7A1FA CRC64;
                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Sequence update)
01-AUG-2001 (Rel. 40, Last annotation update)
THIAMINE BIOSYNTHESIS PROTEIN THII.
                                                                                                                                                                                                                                                 Score 42; DB 1
Pred. No. 27;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 AA
                                                                                                                                             AEX-3-BINDING.
                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000148; AAC73526.1; -.
EMBL; U82664; AAB40179.1; -.
EMBL; U34923; -; NOT_ANNOTATED_CDS.
ECOGENE; EG13273; thiI.
InterPro; IPR003720; ThiI.
Pf02568; ThiI; 1.
                                                                                                               320 PO
424 AE
47224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 253-482 FROM N.A.
                                                                                                                                                                                                                                                    47.7%;
50.0%;
EMBL; AF293976; AAG17881.1;
EMBL; Z78416; CAB01682.1; -.
WormPep; C23H4.1; CE17435.
                                                                                                                                                                                                                                                                                Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               : || | : :||||
97 LKYYGKEVEQYKDD 110
                                                                                                                                                                                                                                                                                                                                                             2 ISYYEKVLAKYKDD 15
                                                                                                            300
205
425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                      Transmembrane.
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                                                                                                                                                                                                                                                                      -i- SUBUNIT: DODECAMER OF PROTEIN B AND PROTEIN B*.
-i- PTM: PROTEIN B* IS A CLEAVAGE PRODUCT OF PROTEIN B.
-i- SIMILARITY: TO BACTERIOPHAGE 21 HEAD PROTEIN 674.
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-15 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN B.
PROTEIN B*.
H-T-H MOTIF (POTENTIAL).
4E8E25B30A9144A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
NITRATE REDUCTASE, CLONE PBNBR1405 (EC 1.6.6.1) (NR).
                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-JUL-1984 (Rel. 29, Last annotation update)
PORTAL PROTEIN (GPB) (MINOR CAPSID PROTEIN B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J02459; AAA96536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.78;
52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A04332; VHBPBL.
Coat protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.7
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica napus (Rape).
                                                                                                                                                  Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3708
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P39867;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 482;
                                                                                                 Length 482;
                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
.s; Complete proteome.
54973 MW; 72AF449459E45762 CRC64;
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41CC9EE3740CE5D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1;
Pred. No. 30;
                                                                                                 Score 42; DB 1;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) THIAMINE BIOSYNTHESIS PROTEIN THII.
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                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-LT2;
MEDLINE-97352701; PubMed-9209060;
                                                                                                                                                                                                                                                                                                                                                                THII_SALTY STANDARD; IP P55913, 006955, 01-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequent AUG-2001 (Rel. 40, Last annument annument
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 AA; 54831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 365-482 FROM N.A.
                                                                                                 47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           StyGene; SG10723; thiI.
InterPro; IPR003720; ThiI.
Pfam; PF02568; ThiI; 1.
                                                                                                 Query Match 47.7
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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  Thiamine biosynthesis;
SEQUENCE 482 AA; 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| ||:|: ||
91 FEKALAQYREQLE 103
                                                                                                                                                                                                                             :|| | :|:| ||
91 FEKALVOYRDOLE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thiamine blosynthesis.
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                                                                                                                                                                                                   5 YEKVLAKYKDDLE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=602;
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RESULT 14 VMCB_LAMBD

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Gaps

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Indels

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CC -- CYMALYTC ACTIVITY: NAME - NUTTABLE - NAME (1) - THERITA,

CC -- COMPATOR ACTIVITY: NAME - NUTTABLE - NAME (1) - THERITA - NAME -
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Search completed: January 29, 2002, 11:13:44 Job time: 820 sec

2 ISYYEKVLAKYKDDLE 17 :|||::::||||| 74 VSYYKEMVLKSNSDLE 89

QY Db

OM protein

Run on:

Searched:

Database

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025977 plasmodium 025978 plasmodium 025978 plasmodium 02598 plasmodium 0259812 plasmodium 02598 plasmodium 02598 plasmodium 02594 plasmodium 025921 plasmodium 025921 plasmodium 025522 plasmodium 025522 plasmodium 025522 plasmodium 025552 plasmodium 02555 arabioopsis 991136 caenorhabdi
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homo sapien
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drosophila
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branchiosto
plasmodium
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Oari S.H., Shi Y.P., Goldman I., Nahlen B., Tibayrenc M., Lal A.A.;
Mol. Biochem. Parasitol. 0:0-0(1998).
EMBL; AF040569; AAC13999-1; -.
InterPro; IPR0000561; EGF-like.
Pfam; PF00008; EGF; 1.
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                                                                                                                                                     09up95
060632
013953
09vk45
056526
056528
09651f1
                                                                                                                                             09agr4
                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 88; DB 5; Length 372;
100.0%; Pred. No. 3.1e-05;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42768 MW; 3ACD3AFA6C047D53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                    372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 AA
                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                   Q25922
Q9FZ65
P91136
                                                                                                                                                                              Q9VK45
Q56526
Q56528
Q9S1F1
               Q25978
Q25979
Q25980
                                        Q25983
Q25983
Q25968
Q9TYG2
Q25924
Q25923
Q9TZT5
Q9TZT5
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                                                                                                                                                                       013953
                                                                                                                                              09AGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                025717;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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372 AA;
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Merozoite.
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                                                          Search time 285.36 Seconds
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        GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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sp_invertebrate:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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SEQUENCE FROM N.A.
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW
Shi Y.P., Albers M.B., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U20730; AAA62221.1; -
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
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STRUCTE FROM N.A.
STRUCTB HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
STRAIN-INFECTED HUMAN BLOOD A.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/Genbank/DDBJ databases.
EMBL, 1020731, AAA62222.1;
InterPro; IPR000561; EGF-11ke.
PF000008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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372 372
372 AA; 42711 MW; E3DBB33F282CD5FC CRC64;
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100.0%; Pred. No. 3.1e-05;
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100.0%; Pred. No. 3.1e-05;
iive 0; Mismatches 0;
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Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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372 AA;
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STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FBE-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U20654; AAA62214 1; ...
InterPro; IPR000561; EGF-like.
Pfam, PF00008; EGF; 1.
                                                                                                                             SEQUENCE FROM N.A.
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20653; AAA62213.1; -.
InterPro; IPR000561; EGF-like.
Pfam; PF00088; EGF; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-TIN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
                   MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                  Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                     Length 372;
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372 372
372 AA; 42660 MW; E9F088252598FB0B CRC64;
                                                                                                                                                                                                                                                                                                               42687 MW; 3F2BF1152598FB10 CRC64;
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100.0%; Pred. No. 3.1e-05;
Mismafches 0;
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 88; DB 5; 100.0%; Pred. No. 3.1e-05;
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Plasmodium falciparum
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372
372 AA;
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Matches 17; Conserv
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SEQUENCE FROM N.A.
STRAIN-INECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB.1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20726; AAA62217.1; -.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
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STRAIN-KENTA-2;
GATÍ S.H., Shi Y.P., Goldman I., Nahlen B., Tibayrenc M., Lal A.A.;
Mol. Biochem. Parasitol. 0:0-0(1998).
EMBL. AF040568; AAC39098.1; -.
InterPro; IPR000561; EGF-11ke.
PF00008; EGF; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5833;
                                                                                                                                         Length 373;
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100.0%; Pred. No. 3.1e-05; ....matches 0; Indels
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373 373
373 AA; 42902 MW; 86CD4B721E605A5F CRC64;
                                                                                         42873 MW; 886CF169A7AF5194 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN-1 (FRAGMENT).
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100.0%; Pred. No. 3.1e-05;
iive 0; Mismatches 0;
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   Mol. Biochem. Parasitol. 0:0-0(1998).
EMBL; AF040567; AAC39097.1; -.
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Matches 17; Conservative
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Matches 17; Conservative
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STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20656; AAA65116.1; -.
InterPro; IPR000651; EGF-1ike.
                                                                                                                                                                                                                                                                Gaps
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                                         Oloo A.G., Lal A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-KENYA-1;
Qari S.H., Shi Y.P., Goldman I., Nahlen B., Tibayrenc M., Lal A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 88; DB 5; Length 372; 100.0%; Pred. No. 3.1e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                             100.0%; Score 88; DB 5; Length 372;
100.0%; Pred. No. 3.1e-05;
tive 0; Mismatches 0; Indels
SEQUENCE FROM N.A.
STRAIN-INECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
SALAY-INECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G.,
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: U20655; AAA62215.1;
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InterPro; IPR000561; EGF-11ke.
Pfam; PGF00008; EGF; 1.
                                                                                                                                           1 1
372 372
372 AA; 42686 MW; 583A33972DB05FB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AA; 42686 MW; 583A33972DB05FB4 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
MEROZOITE SURFACE PROTEIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                               118 GISYYEKVLAKYKDDLE 134
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                                                                                                                                                                                                                                                                                                  1 GISYYEKVLAKYKDDLE 17
                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
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SEQUENCE
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SEQUENCE
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                  1 GISYYEKVLAKYKDDLE 17
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                                           Conservative
                                                                                                                                                           PRELIMINARY;
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                Query Match
Best Local Similarity
Matches 17; Conserv
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Q25724;
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Q25727
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STRAIN-INECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20728; AAA62219.1; -.
InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL, U20727; AA62218.1; -.
InterPro: IPR000561; EGF-1ike.
Pfam: PF00008; EGF; 1.
                                                                                     Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA.C-TERMINAL REGION (FRAGMENT).
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=5833,
                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 88; DB 5; Length 373; 100.0%; Pred. No. 3.1e-05; tive 0; Mismatches 0; Indels
                                                          Length 373;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
                                                                                    Indels
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1 1
373 373
373 AA, 42848 MW; EE0700233D7F4D4E CRC64;
                                                          ; Score 88; DB 5; Lk; Pred. No. 3.1e-05; 0; Mismatches 0;
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                                                                                                                                                                                                     PRT; 373 AA.
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                                                           100.0%;
illarity 100.0%;
Conservative 0
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                                                                                                             1 GISYYEKVLAKYKDDLE 17
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Best Local Similarity 100.
Matches 17; Conservative
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373 AA;
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Best Local Similarity
Matches 17; Conserv
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Q25723
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STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM B.L., OLOO A.G., Lal A.A.;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 10207323, AAA62223.1;
InterPro; IPPRO00661; EGF-11ke.
PF000008; EGF; 1.
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                                                                                                                        Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1096 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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NCBL_TaxID=5833;
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NCBI_TaxID=5833;
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100.0%; Score 88; DB 5; Length 373; 100.0%; Pred. No. 3.1e-05;
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STRAIN-INFECTED HUMAN BLOOD SAMPLE FROM PAPUA NEW GUINEA;
Shi Y.P., Alpers M.P., Povoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20733; AAA62224.1; -.
InterPro; IPR000561; EGF-11ike.
Pfam; PF0008; EGF; 1.
Merozoite.
NON_TER 1 1
NON_TER 373 373
SEQUENCE 373 AA, 42815 MW; 9CF4DDAF38CC4054 CRC64;
                                                  Gaps
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 1, 42 KDA C-TERMINAL REGION (FRAGMENT).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Best Local Similarity 100.0%; Pred. No. 3.1e-05; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 AA.
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                                                                                                                                   PRELIMINARY;
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DT 01-N
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Search completed: January 29, 2002, 11:12:13 Job time: 769 sec

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Gaps

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Plasmodium falcipa
Sequence of Ag513
Merozite surface a
Plasmodium falcipa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merozite surface a
Recombinant vaccin
Antigenic peptide
Equine neraminidas
Equine influenza v
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Merozite surface a
                                                   January 29, 2002, 10:21:46 ; Search time 310.82 Seconds (without alignments) 1.907 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                              522463
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                         522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                      OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR05876
AAB18202
AAR05879
AAR05877
AAR05878
AAY70278
AAR03985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY 70290
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                   US-09-763-397A-14
                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                        A_Geneseq_1101:*
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Match Length DB
                                                                                                                      1 SNTFINNA 8
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300
350
17
469
470
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Perfect score:
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No.
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A P S S S S S S S S S S S S S S S S S S

AAP70712

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merozoite surface protein-7 (MSP-2) of the asexual blood stage of plasmodium falciparum. It is used in the construction of recombinant protein CDC/NITMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melitin signal peptide, conficuence of the recombinant protein comprises, melitin signal peptide. CF from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (CSP), sporozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-15 (EBA-15), rhoper associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="It contains two identical copies of a 32 AA unit
arranged in tandem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Hydrophobic sequence presumed to be an integral membrane protein anchor sequence"
        Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                     present sequence is the antigenic epitope P543, derived from
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 41; DB 21; Length 8; 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of Ag513 a putative merozoite surface antigen of Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Core of a signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anders RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smythe JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP80365 standard; protein; 264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SARA-) SARAMANE PTY LTD (EPPI/).
                                                                         Claim 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87WO-AU00227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNTFINNA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO8800595-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saul AJ;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP80365;
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Geysen HM;

Coppel RL,

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An antigen having the AA sequence in AAP80365 or an antigenic fragment thereof is claimed. Also claimed is a recombinant DNA molecule comprising all or a portion of a nuclectide sequence which is capable of being expressed as polypeptide having the antigenicity of the above antigen or an antigen fragment. Monoclonal antibodies produced using the antigens prevent release of merozoites into the Blood stream of an infected individual. The antigens can also be used for actively immunising a host against P. Talciparum. The antibodies can also be used for purificn. or detection of P. Falciparum.
                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                 Merozoite surface antigen of Plasmodium falciparum - used for active immunisation or for producing monoclonal antibodies for passive immunisation, purificn. or diagnosis
                                                                                                                                                                                                                                                                                      Query Match 100.08; Score 41; DB 9; Length 264; Best Local Similarity 100.08; Pred. No. 1.6; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merozite surface antigen-2 of the P.falciparum 3D7 isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207..214
/label= Antigenic sequence
/note= "Claim 12"
221..228
/label= Antigenic sequence
/note= "Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Thr repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27..34
/label= Antigenic Sequence
/note= "Claim 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSA2; Indochina 1 isolate; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR05876 standard; protein; 272 AA.
                                                                                         Claim 3; Fig 6; 59pp; English.
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Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
WPI; 1988-036431/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-115951/15
                                                                                                                                                                                                                                                      264 AA
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27 sntfinna 34
           N-PSDB; AAN80340
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12-SEP-1988;
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Irving DO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR05876;
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can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB1814 to AAB18352 represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be see also AAR05876-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allelic variants of P falciparum merozoite surface antigen - used in prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                             Score 41; DB 21; Length 272; Pred. No. 1.6; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merozite surface antigen-2 of the P.falciparum Kl isolate.
                                                                                                                                                                      specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109..108
/label- Repeat unit
/note- "Repeated four times"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05879 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSA2; Indochina 1 isolate; malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                 Conservative
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Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum.
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N-PSDB; AAQ03879.
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                      272 AA;
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12-SEP-1988;
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Irving DO,
                                                                                                                                                                                                       Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins)
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                         detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                  Allelic variants of P falciparum merozoite surface antigen - used in prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum chromosome 2 related protein SEQ ID NO:59
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                                                                                                                                                                                                                                                               100.0%; Score 41; DB 11; Length 272; 100.0%; Pred. No. 1.6;
                                                                                                           The merozite surface antigen-2 may be used to generate Abs
                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18202 standard; Protein; 272 AA.
                                                                              Disclosure; Fig 1; 53pp; English.
                                                                                                                                                                     recognised by specific probes.
See also AAR05876-9.
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                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365347/31
                                                                                                                                                                                                                  272 AA;
    N-PSDB; AAQ03876.
                                                                                                                                                                                                                                                                                                                                            1 SNTFINNA 8
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                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18202;
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Jones GL;

Sequence

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AAR05877;

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RESULT

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; arczoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be see also AAR05876-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allelic variants of P falciparum merozoite surface antigen - used in prodn. of antibodies and in vaccines against malaria.
                                                                                 Merozite surface antigen-2 of the P.falciparum MAD71 isolate
                                                                                                                                                                                                                                                                                                                                                                              Jones GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 11;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                Saul AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                   Location/Qualifiers
129..136
/label= Thr repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                              Coppel RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70278 standard; Protein; 350 AA.
AAR05878 standard; Protein; 300 AA.
                                                                                                               MSA2; Indochina 1 isolate; malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 53pp; English.
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88AU-0000382.
                                                       11-DEC-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                    (SARA-) SARAMANE PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                Anders RF,
                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                             Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-115951/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA;
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27 sntfinna 34
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ03876
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                                                                                                                                                                                                                                                                                   12-SEP-1989;
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12-SEP-1988;
                                                                                                                                                                                                                            WO9002752-A.
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ω
                                                                                                                                                                                                                                                                                                                                                                                 Smythe JA,
Irving DO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be see also AAR05876-9.
                                                                                                                                                                                                                                                                                      Merozite surface antigen-2 of the P.falciparum Indochina 1 isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allelic variants of P falciparum merozoite surface antigen - used in prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                        0;
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                                          Length 280;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones GL;
                                                                        ö
                                            Score 41; DB 11;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saul AJ,
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    127..134
/label= Thr repeat region
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Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                     AAR05877 standard; Protein; 287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 53pp; English.
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                                            100.0%;
100.0%;
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88AU-0000382
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                                                                                                                                                                                                                                                                                                                  MSA2; 3D7 isolate; malaria.
                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
                              Query Match
Best Local Similarity
8; Conserv?
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 AA;
    280 AA;
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                                                                                                                     1 SNTFINNA 8
                                                                                                     1 SNTFINNA 8
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12-SEP-1988;
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Irving DO,
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Gaps

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Sequence

RESULT AAR05878

ò pp

Length 300; Indels Jones GL;

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Pept 1de

Protein

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The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be
                                                                                                                                                                                                                                                                                                                                                                  Allelic variants of P falciparum merozoite surface antigen – used in prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vaccines; equine influenza virus; haemagglutinin; H7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 37; DB 11; Length 17; 100.0%; Pred. No. 0.54; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Saul AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86US-0888250, US-747020.
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 12; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR04944 standard; protein; 469 AA.
                                                                                                                                                                                                                                                                           Anders RF, Coppel RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N7 (EIV-A1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recognised by specific probes
See also AAR05876-9.
                                                                                                                                                                                89AU-0005962
88AU-0000382
                                                                                                                                                89WO-AU00388
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 MSA2; 3D7 isolate; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                     (SARA-) SARAMANE PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equine influenza virus.
                                     Plasmodium falciparum
                                                                                                                                                                                                                                                                                            Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine neraminidase
                                                                                                                                                                                                                                                                                                                              WPI; 1990-115951/15
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N-PSDB; AAQ04598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuraminidase; N7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
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                                                                                                                                              12-SEP-1989;
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                                                                                                                                                                                  24-AUG-1989;
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                                                                                                                                                                                                                                                                       Smythe JA,
Irving DO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US4920213-A.
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                                                                        WO9002752-A
                                                                                                        22-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag. T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falloparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic peptide fragment of MSA2 of P. falciparum Indochina 1 isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                           23.350
/label= Mature_CDC/NITMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
honey bee.
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                                                                                                                                              1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                      (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 43-44; 52pp; English
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                                                   Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                 99WO-US18869
                                                                                                                                                                                                                                                                                                                                                                                    98US-0097703
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                                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
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cal AA,

Sequence

AAR03985;

XEXEXEX

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AAR03985 RESULT

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Gaps

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Recombinant vaccines against equine influenza virus – produced using DNA sequences encoding haemagglutinin and neuraminidase glycoprotein(s).
                                                                                H7 and N7 are virally encoded glycoproteins which confer the immunological characteristics of influenza virions. There are nine neuraminidase (RA) subtypes and twelve haemagalutinin (HA) subtypes. The strain carrying H7N7 glycoproteins is designated equine influenza virus (EVI).A1. The cDNA sequences encoding these will be useful in the construction of diagnostic probes for the disease and of probes for obtaining new cDNAs of the mutated form of the virus. Recombinant See also AAQ04596.Q04599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides derived from the haemagglutinin H7 and H3 and neuraminidase N7 and N8 genes may be used to derive antigenic peptides useful in vaccination against equine influenza virus infection. Abs raised to the peptides may be used in diagnosis of the infection and construction of probes to mutated forms of the virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventing equine influenza virus infection - using recombinant vaccines produced using DNA sequences encoding haemagglutinin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equine influenza virus strain H7N7 (EIV-A1) neuraminidase N7 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70712 standard; protein; 470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuraminidase glyco:proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOT-) BIOTECHN RES PARTNE.
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                                                          Disclosure; ; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85US-0747020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equine influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HA; vaccine; Vaccina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordell B;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 AA;
                                                                                                                                                                                                                                          469 AA;
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61 ntyinna 67
                                                                                                                                                                                                                                                                                                                                                2 NTFINNA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product.
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (I) nuclectice sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal artibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in infection, or they can be used to identify drug resistance in P. falciparum control of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the cumplexity of the parasite biology, a process hampered by the complexity of the parasite biology, and provide new targets for resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB1814 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                         falciparum; chromosome 2; human malaria parasite; vaccine;
11; malaria; protozoacide; infection; insecticide.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                         Plasmodium falciparum chromosome 2 related protein SEQ ID NO:75.
                                     ;
0
 Length 470;
                                       Indels
                                       ö
core 34; DB 8;
red. No. 67;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 177-182; 577pp; English.
     Score 34;
Pred. No.
                                                                                                                                                                                                  AAB18218 standard; Protein; 2010 AA
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   82.9%;
85.7%;
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                                                                                                                                                                                                                                                                       (first entry)
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                               antimalarial; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VENTER J C.
                Best_Local Similarity
Matches 6; Conserv
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61 ntyinna 67
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                                                                         2 NTFINNA 8
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                                                                                                                                                                                                                                                                                                                                               Plasmodium
                                                                                                                                                                                                                                      AAB18218;
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF/)
(CARU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VENT/)
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                                                                                                                                                                                   AAB18218
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Gaps

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Indels

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Mismatches Score 34; Pred. No. (

82.9%;

DB 11; Length 469; 67;

Score 33; DB 21; Length 2010;

80.5%;

Query Match

2010 AA;

Sequence

7

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Rouquier S,
                                                                                                                                                                                                                                                                               Matches
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              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olfactory receptor; primate; mouse; human; food processing industry;
                                                                                                                                                                                                                                                                                    cDNA of human origin and proteins coded by it - which may be expressed by in vivo or in vitro translation using sense RNA or antisense DNA corresponding to the cDNA.
             ;
                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                             mRNA expressed in human fibrosarcoma cell line HT-1080 was isolated and used to construct a cDNA library using vector pKA1. Clone HP00038 encoding DEAD ATP helicase-like protein
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                   Sekine S;
      Pred. No. 4.8e+02; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 15;
Pred. No. 22;
1; Mismatches 1.
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                                                                                                                                  Human cDNA; library; enzyme; protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papio hamadryas olfactory receptor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG98434 standard; Protein; 216 AA
                                                                                                                                                                                                                                                  Iwahori A, Kato S, Kato T, Kim
                                                                                                                                                                                                                                                                                                               Claim 1; Page 37; 167pp; Japanese.
                                                                           AAR46082 standard; Protein; 68 AA.
100.08;
                                                                                                                   DEAD ATP helicase like protein.
                                                                                                                                                                                                                                    (SAGA ) SAGAMI CHEM RES CENTRE.
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75.0%;
                                                                                                                                                                                                       92JP-0208077.
92JP-0327619.
93JP-0061431.
                                                                                                                                                                                          93WO-JP01095
                                                                                                     19-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
             6; Conservative
                                                                                                                                                                                                                                                                WPI; 1994-065688/08.
     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 68 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAQ57421
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37 attfinna 44
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735 ntfinn 740
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                          2 NTFINN 7
                                                                                                                                                                                                       04-AUG-1992;
13-NOV-1992;
26-FEB-1993;
                                                                                                                                                Homo sapiens
                                                                                                                                                                                          04-AUG-1993;
                                                                                                                                                             WO9403599-A.
                                                                                                                                                                            17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG98434;
                                                                                        AAR46082;
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The invention relates to olfactory receptors (AAC98432-AAC98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection of toxic substances and/or trapping of odours).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding primate and murine olfactory receptors, useful for analysis odours e.g. in food processing and perfumery -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 42-43; 482pp; English.
aromas; perfumery; toxic substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG98448 standard; Protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                      22-DEC-1999; 99US-0171746.
21-DEC-2000; 2000US-0747155.
                                                                                                                                                                                                                             22-DEC-2000; 2000WO-IB02017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000; 2000WO-IB02017.
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21-DEC-2000; 2000US-0747155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Giorgi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-381911/40.
N-PSDB; AAH84126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gorilla olfactory
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123 sdtfinn 129
                                                        Papio hamadryas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200146262-A2.
                                                                                                              WO200146262-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Rouquier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2001
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The invention relates to olfactory receptors (AAG98432-AAG98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection of toxic substances and/or trapping of odours).
                                                                Nucleic acids encoding primate and murine olfactory receptors, useful for analysis odours e.g. in food processing and perfumery - \,
                                                                                                                                 Claim 3; Page 89-90; 482pp; English.
WPI; 2001-381911/40.
N-PSDB; AAH84131.
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Search completed: January 29, 2002, 10:21:47 Job time: 423 sec

1 SNTFINN 7 |:||||| 123 sdtfinn 129

οp Qγ

Gaps 0;

Query Match

78.0%; Score 32; DB 22; Length 216;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels

Sequence

e 1, Appli 10, A

Sequence Seq

Appli Appli Appli

Sequence Seguence 10, Appl 2, Appli

Sequence Sequence Sequence

Seguence :

Run on:

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Spendsen, Allan
APPLICANT: Sengi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%; Score 31; DB 2; Length 499; 75.0%; Pred. No. 1.5e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DEACHOR
SOFTWARE: FeatSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,315
FILING DATE: 27-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROZek, Carol
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 5200.200-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acid
           US-08 452-052-1

US-08-015-986A-14

US-08 446-363-14

US-08 446-164-1

US-08 448-164-1

US-08 448-164-1

US-08 456-830-1

US-09 456-830-17

US-08 925-035A-1

US-08 925-035A-1

US-08 423-441-2

US-08 462-949-2

US-08 48-196A-8

US-08 462-949-2

US-08 462-949-2

US-08 462-949-2

US-08 48-196A-8

US-08 48-196A-8
                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09032315 Patent No. 5985818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.6
Best Local Similarity 75.0
Matches 6; Conservative
260
270
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TNFFINNA 342
 STRANDEDNESS:
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 ZIP:
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1.352 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Al
Sequence 4, Al
Sequence 4, Al
Sequence 18,
                                                                                 ; Search time 133.18 Seconds
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Sequence 10
Sequence 10
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Sequence 2
Sequence 2
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Sequence 2
Sequence 3
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COWB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COWB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COWB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COWB.pep:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-687-289A-6
US-09-124-900-10
US-08-388-353-644
US-08-488-551B-644
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US-09-032-315-3
US-08-993-318A-3
US-09-396-260-3
US-09-576-281-3
US-08-441-147-4
US-08-441-147-4
US-08-445-909A-18
US-08-445-909A-18
US-08-445-909A-18
US-08-441-147-10
PCT-US95-07536-4
US-08-441-147-10
PCT-US95-07536-10
US-08-441-147-10
US-08-441-177-10
US-08-441-177-17
US-08-441-17
US-08-38-526-1
US-08-461-22
US-08-465-157-2
US-08-465-157-2
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                               January 29, 2002, 10:24:06
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                US-09-763-397A-14
                                                                                                                                                                                                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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                                                                                                                              Title:
Perfect score:
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                                                          OM protein
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Gaps

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75.6%;
75.0%;
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LENGTH: 499 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0°
"^a 6; Conservative
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-399-886-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| |||||
335 TNFFINNA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10174
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STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-396-260-3
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                                                                                                                                                                                                                                                No. 59983530 No. 5998353disk of No. 5998353th America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,318A

FILING DATE: December 18, 1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gregg, Valeta A.

REGISTRATION NUMBER: 33,728

REFRENCE/DOCKET NUMBER: 5032.200-US

TELECPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 2; Lenyc...
No. 1.5e+02;
1; Indels
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Svendsen, Anders
APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
APPLICANT: Cherry, Joel
APPLICANT: Cherry, LacCASE MUTANTS
NUMBER OF INVENTION: LacCASE MUTANTS
CORRESPONDENCE ADDRESS:
                                                                                                                            APPLICANT: Svendsen, Allan
APPLICANT: Schneider, Palle
APPLICANT: Rasmussen, Grethe
APPLICANT: Cherry, Joel
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09399886 Patent No. 6140092 GENERAL INFORMATION:
                                                       Sequence 3, Application US/08993318A Patent No. 5998353
                                                                                                                                                                                                                                                                  : 405 Lexington Avenue
New York
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 3:
                                                                                            GENERAL INFORMATION:
APPLICANT: Pedersen, Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| |||||
335 TNFFINNA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNTFINNA 8
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                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
ZIP: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-993-318A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-399-886-3
                           RESULT 2
US-08-993-318A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                     STREET:
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335 TNFFINNA 342
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355 TNFFINNA 362
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                                                                                                US-08-462-484-4
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APPLICANT: Pedersen, Anders
APPLICANT: Svendsen, Allan
APPLICANT: Schoelder, Palle
APPLICANT: Schoelder, Palle
APPLICANT: Cherry, Joel
TITLE OF INVENTION: LACCASE MUTANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 62776110 NO. 6277611th America
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                                                                                                                                                                                                                 Length 499;
                                                                                                                                                                                                           75.6%; Score 31; DB 4; Length 49975.0%; Pred. No. 1.5e+02;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10.74

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
APPLICATION DATA:
APPLICATION UNMBER: US/09/576,281
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:
33,728
RE: 5032.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/993,318
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09576281
Patent No. 6277611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 5032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
              INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 499 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 amino acids
                                                                                                                                                                                                             Query Match 75.6
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-576-281-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                              CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                         1 SNTFINNA 8
  TELEFAX:
                                                                                                                                                     US-09-396-260-3
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-576-281-3
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                                                               APPLICANT: Yaver, Debbie Sue
APPLICANT: Xu, Feng
APPLICANT: Xu, Feng
APPLICANT: Dalboge, Henrik
APPLICANT: Schneider, Palle
APPLICANT: Schneider, Palle
APPLICANT: Aslyng, Dorrit A.
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56675310 No. 5667531disk of No. 5667531th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.6%; Score 31; DB 1; Length 519; 75.0%; Pred. No. 1.6e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-64D FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Xaver, Debbie Sue
APPLICANT: Dalboge, Henrik
APPLICANT: Schneider, Palle
APPLICANT: Asalyog, Dorrit Propress APPLICANT: PUNENTION: PUNENTION: NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4185.010-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/462,484 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/441,147
Sequence 4, Application US/08462484 Patent No. 5667531 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08441147
Patent No. 5770418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lowney, Karen A.
REGISTRATION NUMBER: 31,274
REFRENCE/DOCKET NUMBER: 4185
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPHONE: 212 879 9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/44
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 519 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.6
Best Local Similarity 75.0
Matches 6; Conservative
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MOLECULE TYPE: protein
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Gaps

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Gaps

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Sequence 18, Application US/08445909A

Sequence 18, Application US/08445909A

Patent No. 577296

GENERAL INFORMATION:
APPLICANT: ATKINSON, Antony
TITLE OF INVENTION: Pharmaceutical Compositions
TITLE OF INVENTION: Stearothermophilus and Bacillus Stearothermophilus and Bacillus COMPUTER READABLE FORM:
MUMBER OF SEQUENCES: 29

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC c
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TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                   Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                      Score 31; DB 5; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%; Score 30; DB 1; 83.3%; Pred. No. 23; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,909A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,697
FILING DATE: 02-FEB-1993
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                         75.6%;
                              INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                         Query Match 75.6
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-445-909A-18
212 878 9655
                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein pcr-US95-07536-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 TNFFINNA 362
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34 SNTFVN 39
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US-08-445-909A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-988-876-5
   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                      ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc. ADDRESSEE: No. 57704180 No. 5770418disk of No. 5770418th America, Inc. STREDT: New York
CITY: New York
STAFE: New York
COUNTR: New York
COUNTR: New York
COUNTR: U.S.A.
ZIP: 10174-6401
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC with STAFE STAFE No. Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,147
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY, METER A. 17.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 1; Length 519
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, Suite 6400 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lowney, Karen A.
REGISPRATION NUBBER: 31,274
REFERENCE/DOCKET NUMBER: 4185.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELERAX: 212 878 9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4185.204-WO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
PCT-US95-07536-4
; Sequence 4, Application PC/TUS9507536
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LOWNEY, Karen A. REGISTRATION NUMBER: 31,274 REFERENCE/DOCKET NUMBER: 41E TELECOMMUNICATION INFORMATION: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.6
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-441-147-4
                                                   CORRESPONDENCE ADDRESS
                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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355 TNFFINNA 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Gaps

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ADDRESSEE: No. 57704180 NO. 5770418disk of No. 5770418th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
CITY: New York
COUNTRY: U.S. A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/41,147
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08441147
Patent No. 5770418
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Xu, Feng
APPLICANT: Scheider, Palle
APPLICANT: Scheider, Palle
APPLICANT: Palboge, Henrik
APPLICANT: Passlyng, Dorrit A
TITLE OF INVENTION: PURFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
                     APPLICATION NUMBER: US/08/462,484 FILING DATE: 05-JUN-1995 CLASSIFICATION: 435
                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,147
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           NAME: LOWNEY, KATEN A.
REGISTRATION NUMBER: 31,274
REPERDE/DOCKET NUMBER: 4185
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0123
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Polyporus pinsitus
US-08-462-484-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lowney, Karen A. REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 416
TELECOMMUNICATION INFORMATION: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 527 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.2
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212 878 9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 SNFFINN 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 309;
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08462484

Patent No. 5667531
GENERAL INFORMATION:
APPLICANT: Yaver, Debbie Sue
APPLICANT: Xu, Feng
APPLICANT: Schneider, Balle
APPLICANT: Dalboge, Henrik
APPLICANT: Schneider, Palle
APPLICANT: Daslyng, Dorrit A.
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 56675310 NO. 5667531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                  SEE: Incyte Pharmaceuticals, Inc.: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY: GenBank
; CLONE: 1314667
US-08-988-876-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||:||
190 SDTFLNN 196
                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNTFINN 7
                                                                                    STATE: CA
COUNTRY: US
ZIP: 94304
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US-08-486-270-2
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07536

FILING DATE: 15-June-1995

PRIOR APPLICATION NUMBER: 08/265,534

FILING DATE: 24-June-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 527;
                                                                                                                                                                          Length 527;
                                                                                                                                                                           Db 1,
. 2.5e+02;
. . . . 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
TITLE OF INVENTION: PURIFIED POLYPORUS LACCASES AND
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.2%; Score 30; DB 5; I
llarity 85.7%; Pred. No. 2.5e+02;
Conservative 0; Mismatches 1.
                                                                                                                                                                      Score 30; DB 1;
Pred. No. 2.5e+02
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application PC/TUS9507536 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION UNDERS: 31,274
REGISTRATION UNDERS: 31,274
REFERENCE/DOCKET UNDERS: 4185.
TELEFONENCE 12 867 0123
TELEFONE: 212 867 0123
TELEFONE: 212 867 0123
TELEFONE: 212 878 9555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Polyporus pinsitus
                                                                                                     Polyporus pinsitus
                                                                                                                                                                          73.2%;
85.7%;
 527 amino acids
                TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: POLYPOLUS pir
                                                                                                                                                                           Ouery Match 73.2
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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360 SNFFINN 366
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360 SNFFINN 366
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PCT-US95-07536-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
LENGTH:
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RESULT

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Sequence 2, Application US/08486270

Sequence 2, Application US/08486270

Sequence 2, Application US/08486270

Batent No. 5807689

GENERAL INFORMATION:
APPLICANT: Bilas, Steven B.
APPLICANT: Bilas, Chan
APPLICANT: Double Chan
APPLICANT: HOSON, Edwin C.
APPLICANT: HOSON, Edwin C.
APPLICANT: HOSON, HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TILLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TILLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TILLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TILLE OF LINCENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR GLUTAMATE RECEPTORS,
TILLE OF LINCENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR GLUTAMATE RECEPTOR GLUTAMATE RECEPTOR GLUTAMATE
Sequence 2, Application US/08072574

Patent No. 5521297

GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie
APPLICANT: Liaw, Chen
APPLICANT: Poncisler, Aaron
APPLICANT: PONCISLER, Aaron
TITLE OF INVENTION: HUMAN MATABOTROPIC GLUTAMATE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 6.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: US/08/072,574
FILING DATE: 19930604
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9383
TELECOMMUNICATION INFORMATION:
TELEFAN: 213-622-7700
TELEFAX: 213-489-4210
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.78;
83.38;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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; MOLECULE TYPE: protein
US-08-072-574-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Los Angeles
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868 SNTFLN 873
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COMPUTER READABLE FORM:

MEDIUM TYPES: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Flow PC Compatible
COMPUTER: Flow PC Compatible
COMPUTER: Flow PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,270
FILING DATE: 02-UN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/072,574
FILING DATE: 04-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 1192
REFERENCE/DOCKET NUMBER: FP41 9772
TELEPHONE: 619-546-4737
```

Search completed: January 29, 2002, 10:24:07 Job time: 513 sec

1 SNTFIN 6 ||||:| 869 SNTFLN 874

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0; Gaps

Query Match

70.7%; Score 29; DB 1; Length 906; Best Local Similarity 83.3%; Pred. No. 6.6e+02; Matches 5; Conservative 1; Mismatches 0; Indels

Orgen) NNA 18 39Å9 SIHT

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 10:26:42; Search time 144.96 Seconds (without alignments) 4.204 Million cell updates/sec Run on:

US-09-763-397A-14

1 SNTFINNA 8 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	merozoite surface	merozoite 45K surf	Merozoite surface	merozoite surface	merozoite surface	merozoite surface	merozoite 45K surf	merozoite surface	merozoite 45K surf	merozoite 45K surf	merozoite 45K surf	merozoite 45K surf	ribosomal protein	exo-alpha-sialidas	virion protein - h	hypothetical prote	virion protein [im	phosphatase (acid	hypothetical prote	probable olfactory	probable olfactory	hypothetical prote		coat protein VP2 -	coat protein VP2 -	membrane protein E	hypothetical prote	hypothetical coile	hypothetical prote
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		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1																													
		a .	539311	A31818	S55367	G71618	A45632	S39310	C39112	B45632	B39615	A39112	A39615	B39112	S78382	NMIVEA	F56653	S48399	T44010	B71616	T18995	S58004	S 57995	T19259	T26153	VVVP2B	WVVPAS	\$45053	T16136	T50085	H85554
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		Length	256	264	264	272	274	278	280	286	287	300	302	347	202	469	378	436	552	2010	3036	157	157	321	321	351	351	614	644	176	1645
æ		Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.5		80.5	80.5	80.5	80.5	80.5	78.0	8		ω.	٠				78.0	78.0
		Score	41	41	41	41	41	41	41	41	41	41	41	41	37	34	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32
	Result	S.	1	2	m	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

88 2 T30366 110 2 S61540 180 2 B45613 253 2 T40687 336 2 E96773 380 2 F18509 511 2 H86684 511 2 C86778 551 2 C86778 567 2 S58750 573 2 S5061 670 2 S57194	occlusion-derived	surface antigen FU	hypothetical prote	ribose-phosphate p	probable lipase/ac	hypothetical prote	hypothetical prote	prophage pil prote	prophage p13 prote	probable membrane	NADH dehydrogenase	hypothetical prote	PTS system, fructo	calpain (EC 3.4.22	hypothetical prote
88 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	T30366	B45613	T40687	T52589	E96773	T18509	F71055	H86684	C86798	S63148	S58750	S50661	D70178	S57194	T16588
	88 2	80 2	53 2	37 2	66 2	80 2	07 2	11 2	11 2	58 2	67 2	73 2	26 2	00	035 2
	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.	75.
8.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
31 75. 31 75. 31 75. 31 75. 31 75. 31 75. 31 75.	30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

merozoite surface antigen - malaria parasite (Plasmodium falciparum)
C; Species: Plasmodium falciparum
C; Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Nov-2000
C; Accession: S39311
R; Ramasamy, R.; Ranasinghe, C.
Submitted to the EMBL Data Library, November 1993
A; Description: Cycle ds DNA sequencing of a malaria parasite protein from infected bl. A; Reference number: S39310
A; Reference number: S39310
A; Reseasion: S39311
A; Actual: preliminary
A; Molecule type: DNA
A; Cross-references: EMBL:X76298; NID:q434997; PID:g836640
C; Superfamily: Epstein-Barr virus nuclear antigen

Gaps ; 0 Ouery Match . 100.0%; Score 41; DB 2; Length 256; Best Local Similarity 100.0%; Pred. No. 0.87; Matches 8; Conservative 0; Mismatches 0; Indels

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A31818

merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 17-Nov-2000
C.Accession: A31818
R.Smythe, J.A.; Coppel, R.L.; Brown, G.V.; Ramasamy, R.; Kemp, D.J.; Anders, R.F.
Proc. Natl. Acad. Sci. U.S.A. 85, 5195-5199, 1988
A; Title: Identification of two integral membrane proteins of Plasmodium falciparum. A; Reference number: A31818
A; Accession: A31818
A; Accession: A31818
A; Residues: 1-264 <SMY>
A; Cross-references: GB:J03828; NID:g160352; PID:g160353
C; Superfamily: Epstein Barr virus nuclear antigen
C; Keywords: surface antigen
C; Keywords: surface antigen #status predicted <AMT>
F; 21-204/Domain: signal sequence #status predicted *Status predicted <AMT>

Gaps ö Query Match
Best Local Similarity 100.0%; Score 41; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 8; Conservative 0; Mismatches 0; Indels

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R;Smythe, J.A.; Coppel, R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; An Proc. Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991
A;Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen A;Reference number: A39112; MUID:91156685
A;Accession: C39112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <8M>A;Residues: 1-280 <8M>A;Cross-references: GB:M59768
C;Superfamily: Epstein-Barr virus nuclear antigen
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C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C; Accession: S39310
R; Ramasamy, R; Ranasinghe, C.
submitted to the EMBL Data Library, November 1993
A; Description: Cycle ds DNA sequencing of a malaria parasite protein from infected bl
                                                                                                    C;Accession: A45652
R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Rwl. Blochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA A;Reference number: A45632; MUID:92178286
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C;Species: Plasmodium falciparum
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
C;Accession: C39112
                                                  C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary
A.Status: DNA
A.Molecule type: DNA
A.Residues: 1-274 <AMR>
A.Cross-references: GB:M73810; NID:g160484; PID:g160485
A.Cross-references: CB:M73810; NID:g160484; PID:g160485
C.Superfamily: Epstein-Barr virus nuclear antigen
C.Superfamily: Epstein-Barr virus nuclear antigen
C.Keywords: surface antigen
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
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A; Residues: 1-278 <RAM>
A; Cross-references: EMBL:X76087; NID:g434996; PID:g836639
C; Superfamily: Epstein-Barr virus nuclear antigen
C; Keywords: surface antigen
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A, Accession: S39310
A, Status: preliminary
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Best Local Similarity
Matches 8; Conserv
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C.Species: Plasmodium falciparum
C.Species: Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Nov-2000
C.Accession: S5367
R.Chauhan, V.S.
R.Shauhan, V.S.
R.Shauhan, V.S.
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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A;Molecule type: DNA
A;Residues: 1-54, Tr.56-272 <SMY>
A;Cross-references: GB:M28891; NID:9160458; PID:9160459
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0; Mismatches 0
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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Matches 8; Conservative
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A.Cross references: GB:M28892; NID:g160488; PID:g160489
R;Fandeur, T.; Bonnefoy, S.; Mercereau-Puijalon, O.
Mol. Bloochem. Parasitol. 47, 167-178, 1991
A.Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are ge A;Reference number: A45613; MUID:92049549
A.Accession: A45613
A.Accession: A45613
A.Accession: A5613
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: nucleic acid
A.Residues: 28, E', 30-186, R', 188-230, 'IH' <FAN>
A.Residues: 28, E', 30-186, R', 188-230, 'IH' <FAN>
C.Superfamily: Epstein-Barr virus nuclear antigen
C.Superfamily: Epstein-Barr virus nuclear antigen
C.Superfamily: Epstein-Barr virus nuclear antigen
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A; Fille: Structural diversity in the Plasmodium falciparum merozoite surface antigen A; Reference number: A39112; MuID: 91156685
A; Reference number: A39112; MuID: 9115688
A; Residues: 1-300 <SMY>
A; Residues: 1-300 <SMY>
A; Residues: 1-300 <SMY>
A; Residues: 1-300 <SMY>
C; Superfamily: Epstein-Barr virus nuclear antigen C; Keywords: surface antigen
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Pred. No.
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                                               A; Residues: 1-186, 'R', 188-287 <SMY>
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(;Species: Plasmodium falciparum
(;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
(;Accession: B45632
R:Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
R:Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
A:Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
R:Reference number: A45632; MUID:92178286
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N.Alternate names: membrane antigen pf7
C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Sacession: B39615; A36018; B44950; A45613
R.Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Scaif
A.Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite sur A; Reference number: A39615; MUID:91117264
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A;Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS ce A; Reference number: A36018; WUID:90349616
A;Status: preliminary
A;Molecule type: DNA
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A; Residues: 1-287 cELL>
A; Cross-references: GB:M28890; NID:9160405; PID:9160407
R; Smythe, J.A.; Peterson, M.G.; Coppell, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F.
Mol. Blochem. Parasitol. 39, 227-234, 1990
A; Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi
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A;Residues: 1-286 <MAR>
A;Residues: 1-286 <MAR>
A;Experimental source: isolate 311
A;Note: sequence extracted from NCBI backbone (NCBIN:85255, NCBIP:85259)
C;Superfamily: Epstein Barr virus nuclear antigen
C;Reywords: surface antinom
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100.0%; Pred. No. 0.97;
.ive 0; Mismatches 0; Indels
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Accession: B44950
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A;Residues: 1-287 <FEN>
A;Cross-references: EMBL:X53833
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C; Keywords: surface antigen
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Best Local Similarity
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C;Species: influenza A virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C;Accession: A25615
R;Dale, B.; Brown, R.; Miller, J.; White, R.T.; Air, G.M.; Cordell, B.
Virology 155, 460-468, 1986
A;Title: Nucleotide and deduced amino acid sequence of the influenza neuraminidase ge A;Reference number: A94349; MUID:87071664
A;Recession: A25615
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C; Superfamily: influenza virus exo-alpha-sialidase
C; Superfamily: influenza virus exo-alpha-sialidase
C; Superda yt propriotain; glycosidase; hydrolase; transmembrane protein
C; Reywords: glycoprotain: transmembrane #status predicted <TMM>
F; 25-80 /Region: hypervariable stalk
F; 89-469 /Region: head of exo-alpha-sialidase
F; 28, 32, 46, 55, 66, 85, 143, 198, 232, 399/Binding site: carbohydrate (Asn) (covalent) #stat
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-378 < GON
A; Residues: 1-378 < GON
A; Cross-references GB: X64320; GB: S50422; GB: S58505; GB: S58506; NID: 9296190; PIDN: CAA
A; Cross-references strain U1102
A; Note: sequence extracted from NCBI backbone (NCBIN: 120533, NCBIP: 120551)
C; Superfamily: varicella-zoster virus gene 34 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Westques: 1-409 <UAL)
A; Cross-references: GB:M14916; NID:g323979; PIDN:AAA43093.1; PID:g323980
A; Cross-references: GB:M14916; NID:g323979; PIDN:AAA43093.1; PID:g323980
A; Note: this enzyme exists as a tetramer in the viral membrane; the amino-terminal hy C; Comment: This enzyme catalyzes the cleavage of the terminal sialic acid (N-acetylne ing the carbohydrate residues from the viral envelope.
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Pred. No. 37;
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85.7%; Pred. No. 46;
iive 0; Mismatches
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That 6; Conserve
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A; Residues: 1-469 <DAL>
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|141 NTFFNNA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       merozolte 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (isol C; Species: Plasmodium falciparum alciparum alciparum falciparum falciparum) (isol C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000 C; Accession: B39112 R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; Ander Proc. Natl. Acad. Sci. U.S.A. 88, 1751-1755, 1991 A; Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2. A; Reference number: A39112; MUID:91156685 A; Status: preliminary
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C;Species: plastid Epifagus virginiana (beechdrops)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 13-Aug-1999
C;Accession: S78838
R;Wolfe, K.H.; Morden, C.W.; Ems, S.C.; Palmer, J.D.
J. Mol. Evol. 35, 304-317, 1992
R;Title: Rapid evolution of the plastid translational apparatus in a nonphotosynthetin A;Reference number: S78382
R;Accession: S78382
R;Access
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                                                Length 302;
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                                           Score 41; DB 2;
Pred. No. 1;
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4.1;
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C;Superfamily: Escherichia coli ribosomal protein S4
C;Keywords: plastid; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nuclear antigen
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100.0%;
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C,Superfamily: Epstein-Barr virus
C,Keywords: surface antigen
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (POTENTIAL).
-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIGEN 2.
DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-29118803;

Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;

"Sequence comparison of allelic forms of the Plasmodium falciparum merozolice surface antigen MSA2.";

MOI. Blochem. Parasitol. 43:211-220(1990).

-i. FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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             Q01056
P53957
P02211
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Q04699
Q95157
P21075
                                                                                                                           001221
P33878
P54487
                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING
(BY SIMILARITY).
POLYMORPHIC REGION.
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N-LINKED (GLCNAC. . . ) (POT
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YNE3_YEAST
GLB_APLKU
GLB_APLLI
YOGE_BACST
MALD_STRPN
OLF4_CANFA
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VB17_VACCV
VB17_VARV
YQGE_BACSU
 CAN2 CHICK
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                            Compugen Ltd.
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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MSA2_PLAF9
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01-0CT-1996 (Rel. 34, Created)
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01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
264 AA.
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GPI-anchor; Merozoite.
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Best Local Similarity
Matches 8; Conserv
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P50498;
MSA2_PLAFJ
P50499;
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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MEROXOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
POLYMORPHIC REGION.
2 X 32 AA PERFECTS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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0
                                                                                                                                                                                                                                                                                                   "Identification of two integral membrane proteins of Plasmodium
                                                                                                                                 01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (MEROZOITE 45 KDA
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-88276924; PubMed-3293051;
Smythe J.A., Coppel R.L., Brown G.V., Ramasamy R., Kemp D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 41; DB 1; Length 264; 100.0%; Pred. No. 0.22; iive 0; Mismatches 0; Indels
                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03828; AAA29627.1; ALT_SEQ.
EMBL; A12418; CAA01031.1; -
PIR, A1818; A31818.
InterPro; IPR001136; MSA_2.
Pfam; PF00989; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat; GPT-anchor; Merozolite.
SIGNAL.
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66DEF3B8357FEF3D CRC64;
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264 AA;
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Best Local Similarity
Matches 8; Conserv
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P19599;
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           Gaps
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-!- MISCELLANEOUS: SAME SEQUENCE IN INDIAN ISOLATES FIS1 AND FIJ4.
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HYDROPHOBIC, REMOVED DURING MATURATION
(BY SINILARITY).
2 X 32 AA PERFECTS REPEATS.
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-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (isolate fid3 / India).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70152;
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
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CARBOHYD CARBOHYD

DOMAIN REPEAT REPEAT

DOMAIN

CHAIN PROPEP

CARBOHYD CARBOHYD

RESULT

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us-09-763-397a-14.rsp

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antigen 2 (MSA-2) of Plasmodium falciparum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                            "Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodium falciparum.";
                                                                                                                                                                                        -! - DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
POLYMORPHIC REGION.
                                                                                                                                                                  -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                  . Biochem. Parasitol. 39:227-234(1990).
FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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(POTENTIAL).
(POTENTIAL).
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                                                                                       Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J.,
                 Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=57269;
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                                                                                                                                                                                                                                                                                                    EMBL; M28891; AAA29686.1; -.
InterPro; IPR001136; MSA_2.
Fam; PF00985; MSA_2: 1.
Malaria: Membrane: Glycoprotein; Antigen; Signal; Repeat; GPI-anchor; Merozoite.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
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SNTFINNA 34
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P50497;
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CARBOHYD
CARBOHYD
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CARBOHYD
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SEQUENCE
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MSA2_PLAF6
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                                                                                                                                           -!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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(BY SIMILARITY).
POLY-WORPHIC REGION.
POLY-THR.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
Sequence comparison of allelic forms of the Plasmodium falciparum merozoite surface antigen MSA2.";
Mol. Blochem. Parasitol. 43:211-220(1990).
--- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                       -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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Mol. Biochem. Parasitol. 50:181-184(1992).
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(GLCNAC...) (POTENTIAL).
(GLCNAC...) (POTENTIAL)
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=57266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 41; DB 1; Length 274; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
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MSA2_PLAF8
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MSA2_PLAFH
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       and for commercial
                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDIINE=91156685; PubMed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface antigen 2:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                       POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOEIC, REMOVED DURING MATURATION (BY SIMILARITY).
POLYMORPHIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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NCBL_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 1; Length 276; ilarity 100.0%; Pred. No. 0.23; Conservative 0; Mismatches 0; Indels
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MEROZOITE SURFACE ANTIGEN 2.
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                                                                                               InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
         Usage by
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N-LINKED (GLCNAC. . .) (POLY-THEED (GLCNAC. . .) (POLY THEED (GLCNAC. . .) (POLY THEED (GLCNAC. . .) (FOLY THEED (GLCNAC. .) (FOL
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01-0cr-1996 (Rel. 34, Last sequence update)
01-0cr-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate Kl / Thailand)
           modified and this statement is not removed.
                                             or send an email to license@isb-sib.ch).
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Pfam; PF00985; MSA_2; 1.
                                                                                 EMBL; M60190; AAA29690.1;
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SIGNAL 1 20
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Best Local Similarity
Matches 8; Conserv
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-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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HYDROPHOBIC, REMOVED DÜRING MATÜRATION (BY SIMILARITY).
POLYWORPHIC REGION.
POLY-THR.
HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-29118803;

MEDLINE-29118803;

Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;

"Sequence comparison of allelic forms of the Plasmodium falciparum morzozite surface antigen MSA2.";

Mol. Biochen. Parasitol. 43:211-220(1990).

-i. FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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(GLCNAC. .) (POTENTIAL)
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01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 3).
                                                                                             (POTENTIAL)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-70151;
                                                                                                                                                                                                                                                                    100.0%; Score 41; DB 1; Length 280; 100.0%; Pred. No. 0.23;
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pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprot
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29542 I
                                                                                                                                                                                                                                                                                                               Conservative
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280 AA;
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Best Local Similarity
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27 SNTFINNA 34
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 2)
(MEMBRANE PROTEIN PF7).
                                                                                                                     Plasmodium falciparum (isolate FCR-3 / Gambia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5838;
                                                                                                                                                                                         MEDLINE-90349616; PubMed-1696728;
Elliott J.F., Albrecht G.R., Gilladoga A., Handunnetti S.M.,
Neequaye J., Lallinger G., Minjas J.N., Howard R.J.;
"Genes for Plasmodium falciparum surface antigens cloned by
                                                                                                                                                                                                                                          expression in COS cells.";
Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990)
                                                                                                                                                                                SEQUENCE FROM N.A.
                                  MSA2_PLAFG
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PROPEP
           RESULT 10
MSA2_PLAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
-i- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                         Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.;
"Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2) of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 50:181-184(1992).
-1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate 311).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=57265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 41; DB 1; Length 286; llarity 100.0%; Pred. No. 0.24; Conservative 0; Mismatches 0; Indels
                                  h 100.0%; Score 41; .DB 1; Length 281; Similarity 100.0%; Pred. No. 0.23; 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfan, Pr00985; MSA_2; 1.
Malaria, Membrane, Glycoprotein, Antigen, Signal, Repeat,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D1F4947CE68D5805 CRC64;
 50598AA42D64CCBC CRC64;
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N-LINKED GLCNAC...) (
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                                                                                                                                                                                        01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                    286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                    PRT;
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28892 MW;
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28844 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001136; MSA_2.
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                                                                                                                                                                   STANDARD;
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SIGNAL 1 20
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Best Local Similarity
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115
22
36
163
235
259
260
286 AA;
 281 AA;
                                                Best Local Similarity
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27 SNTFINNA 34
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                                                                                1 SNTFINNA 8
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P50496;
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CARBOHYD
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CARBOHYD
SEQUENCE
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                                                   Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D., Ridley R., Scaife J.G., McBride J.S., "Scaife J.S., "Scaife J.S.," "Structural and antigence polymorphism of the 35- to 48-kilodalton merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
-1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROZOITE SURFACE ANTIGEN 2. HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
                                                                                                                                                                                                                                                          -i - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOLYMORPHIC REGION.
N.LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
GPI-anchor; Merozoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
SEQUENCE FROM N.A. MEDLINE-91117264; PubMed-1990294;
                                                                                                                                                                                    Mol. Cell. Biol. 11:963-971(1991)
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236 N-
260 N-
261 N-
28555 MW;
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EMBL; X53832; CAA37829.1; -.
EMBL; M60188; AAA29688.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A36018; A36018
PIR; B39615; B39615
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260
261
287 AA;
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                                                                                                                                                               falciparum.
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CARBOHYD
CARBOHYD
SEQUENCE
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300 AA.

PRT;

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Plasmodium falciparum (isolate mad71 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=70154;
                                         01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).
                                 01-OCT-1996 (Rel. 34, Created)
           MSA2_PLAF2
003645;
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                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROZOITE SURFACE ANTIGEN 2. HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                 -! - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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                                                                                                                                                                                                                                                                                                                     antigen 2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
; Score 41; DB 1; Length 287;
; Pred. No. 0.24;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.LINKED (GLCNAC...) (POT W. AOIEI7D36075D7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYMORPHIC REGION
                                                                                                                                                     01-0cr-1996 (Rel. 34, Created)
01-0cr-1996 (Rel. 34, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
115-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                             300 AA.
                                                                                                                                                                                                               Plasmodium falciparum (isolate imr143).
                                                                                                                                PRT;
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    100.0%;
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               Similarity 100.8; Conservative
                                                                                                                                STANDARD;
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300
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129
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177
249
273
300 AA;
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8; Conserv
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                                                                                                                                                                                                                                    NCBI_TaxID=57268;
                                               1 SNTFINNA 8
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27 SNTFINNA 34
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ID MSA2_PLAFI
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Best Local
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-91156685; PubMed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES
                                                                                                                                                                            -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
POLYMORPHIC REGION.
POLYTHR.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                       antigen 2.";
proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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GPI-anchor; Merozoite.
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E4116107747AA10D CRC64;
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01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).
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InterPro; IPR001136; MSA_2.
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300
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                  ERYTHROCYTE
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ID MSA2_PLAF9
AC Q03994;
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Gaps

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SNTFINNA 34

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SNTFINNA 8

Matches

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324
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P30056;
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CARBOHYD
CARBOHYD
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CARBOHYD
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RR4_EPIVI
                                                                                                                                                                                                                                                                                 CHAIN
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                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

MEROZOITE SURFACE ANTIGEN 2.

HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).

POLYMORPHIC REGION.

POLYTHE.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                   SEQUENCE FROM N.A.
MEDLINE=91117264; PubMed=1990294;
Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
Falley R., Scalfe J.G., WeBride J.S.,
"Structural and antigenic polymorphism of the 35- to 48-kilodalton
merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps

    -!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.

                                                                                                                                MOI. Cell. Biol. 11:963-971(1991).
-i- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.
-i- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-91156685; PubMed-2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
         Plasmodium falciparum (isolate tak 9).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota, Alveolata, Apicomplexa, Haemosporida; Plasmodium.
NCBI_TaxID=70150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 41; DB 1; Length 302; 100.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                              PIR; A39615; A39615.
InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria: Membrane: Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E0A7EB08227CF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AA
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                                                                                                                                                                                                                                                                                                     EMBL; X53833; CAA37830.1; -.
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                                                                                                                                                                                                                                                                                                                                                                       20
278
302
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138
                                                                                                                                                                                                                                                                                                                                                             GPI-anchor; Merozoite.
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131
22
36
179
251
275
302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                NCBI_TaxID=57276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNTFINNA 34
                                                                                                                                                                                                                                                                                                                                                                                   21
279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SNTFINNA 8
                                                                                                                         falciparum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSA2_PLAF2
Q03646;
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                (POTENTIAL).
-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Orobanchaceae; Epifagus.
                                                                                                                                                      SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-THR.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                       antigen 2.";

Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).

-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.
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MEDLINE=93066301; PubMed=1332054;
Wolfe K.H., Morden C.W., Palmer J.D.;
"Function and evolution of a minimal plastid genome from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABCF24BB560BF537 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
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01-APR-1993 (Rel. 25, Last sequence update)
01-MAY-2000 (Rel. 39, Last annotation update)
CHLOROPLAST 30S RIBOSOMAL PROTEIN S4.
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MEDLINE-93021155; PubMed-1404416;
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InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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320
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347 AA;
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Best Local Similarity
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Wolfe K.H., Morden C.W., Ems S.C., Palmer J.D.;
"Rapid evolution of the plastid translational apparatus in a nonphotosyythetic plant: loss or accelerated sequence evolution of tRNA and ribosomal protein genes.";
J. Mol. Evol. 35:304-317(1992).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA
                                                                                                                                  (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 S4 RNA-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 1; Length 202; 100.0%; Pred. No. 1.1; 0; Indels tive 0; Mismatches 0; Indels
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Mendel, 4196: EPIVI; rps4:1.
InterPro: IPR001912; Ribosomal_S4.
InterPro: IPR001942; S4.
InterPro: IPR001943; S4.
InterPro: IPR00179; S4: 1.
SMART; SM00363; S4: 1.
SMART; SM00363; S4: 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
RIBOSOMAL S4: 1.
PROSITE; PS00632; RIBOSOMAL_S4; 1.
RIBOSOMAL S9: 136
SMART S9: 136
SMART SP01786516BA691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M81884; AAA65853.1; -.
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Best Local Similarity 100.۰
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Search completed: January 29, 2002, 11:13:44 Job time: 820 sec

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094667
099qy3
                                                                                                                                                                                                                                                                                                    Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 41; DB 5; Length 108; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 10897 MW; C317035F0D1A46C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FBE-1997 (TrEMBLrel. 02, Created)
01-FBE-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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                                                                                                                                                                                                                        ALIGNMENTS
         098JP4
0960Z8
09BJR5
09BJP3
                                      Q9BJP1
Q9BJN2
                                                    09GQX7
09GQX8
09GQZ2
09GQX9
09BJR9
09BJP8
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09GQY6
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09BJQ6
09BJN5
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Q9BJS5
Q9BJS1
Q94667
Q9GQY3
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SNTFINNA 17
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                          473505 segs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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sp_human:*
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sp_phage:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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NCBI_TaxID=5833;
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                                                        Coppel R.L.;
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                                              SEQUENCE FROM N.A.
STRAIN-OKSIBLL SERIES 4, PATIENT 3;
MEDLINE-98084480; PubMed-9423864;
MEDLINE-38084480; PubMed-94.1864;
Eisen D. Billman-Jacobe H., Marshall V.F., Fryauff D., Coppel R.L.;
"Temporal variation of the merozoite surface protein-2 gene of
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Baddeley A., Eri R., Saul A.;

"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasamodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329575; AAK19394.1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 0; Indels
               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                           Query Match 100.0%; Score 41; DB 5; Length 111; Best Local Similarity 100.0%; Pred. No. 0.45; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                             111 AA; 11470 MW; 4501F8D2AF843585 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MERÇZOITE SURFACE PROTEIN (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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                                                                                                      Plasmodium falciparum.";
Infect. Immun. 66:239-246(1998).
EMBL; 072950; AAC02230.1; -.
Interpro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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       Plasmodium falciparum
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                                                        "Antibody responses to infections with strains of Plasmodium falciparum expressing diverse forms of Merozoite Surface Protein 2."; Infect. Immun. 0:0-0(2001).
EMBL; AF104692; ARG47600.1; -.
Interpro, IPRO01136; MSA_2.
Pfam; PF00985; MSA_2: 1
NNN_TER 11
NON_TER 116
NON_TER 116
SEQUENCE 116 AA; 11854.MM; 6BF44658DD9497BA CRC64;
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STRAIN=VN9;
Weisman S., Wang L., Billman-Jacobe H., Hanh Nhan D., Richie T.L.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
Plasmodium falciparum.
PLRARYOTE 3.1veolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Created)
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01-MAR-2001 (TrEMBLrel. 16, Last anno
MEROZOITE SURFACE PROTEIN (FRAGMENT).
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Best Local Similarity 100.
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117 AA;
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MEROZOITE SURFACE PROTEIN (FRAGMENT)
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Best Local Similarity 100.0%;
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         Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;
"Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface protein 1-19 and merozoite surface isolates of Plasmodium falciparum.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
MON_TER 117 117
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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Weisman S., Wang L., Billman-Jacobe H., Hanh Nhan D., Richle T.L., Coppel R.L.;

"Antibody responses to infections with strains of Plasmodlum falciparum expressing diverse forms of Merozoite Surface Protein 2."; Infect. Immun. 0:0-0(2001). - EMBL; AF104708; AAG47616.1; -.
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"Antigenic drift and immune selection acting on merozoite surface
protein 1-19 and merozoite surface protein 2 in independent field
isolates of Plasmodium falciparum.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF329566; AAK19385.1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                           100.0%; Score 41; DB 5; Length 119; llarity 100.0%; Pred. No. 0.48; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.48;
Mismatches 0; Indels
119 AA; 12070 MW; E379E605000E61E1 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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EMBL; AF104699; AAG47607.1; Interpro; IPR001136; MSA_2.

Pfam; PF00985; MSA_2.

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Coppel R.L.;
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BBL: AF329576; AAK19395.1; -...
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
Plasmodium falciparum.
Eukaṛyota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                  Query Match 100.0%; Score 41; DB 5; Length 120; Best Local Similarity 100.0%; Pred. No. 0.48; Matches 8; Conservative 0; Mismatches 0; Indels
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125 AA; 12605 MW; CFA34C33DEF8ABC6 CRC64;
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122 AA; 12497 MW; C3601DB85982D1CB CRC64;
120
11456 MW; D8420C7AC4AC3ED5 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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EMBL; AF104694, ARG47602.1; -.
InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2: 1.
NON_TER 128 128
NON_TER 128 A3; 13038 MW; 4FCIDFFD3402065D CRC64;
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Weisman S., Wang L., Billman-Jacobe H., Hanh Nhan D., Richie T.L.,
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 8; Conservative 0; Mismatches 0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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MEROZOLIFE SURFACE PROTEIN (FRAGMENT).
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    protein search, using sw model

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WO200011179-A1.
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merozotte surface protein-2 (MSP-2) of the assual blood stage of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (MSP-1), MSP-2, apical membrane antigen-1, merozoite surface protein-1 antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1), msp. 2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="It contains two identical copies of a 32 AA unit arranged in tandem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Hydrophobic sequence presumed to be an integral
            Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                    present sequence is the antigenic epitope P544, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 52; DB 21; Length 8; 100.0%; Pred. No. 4.3e+05;
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                                                                                  Claim 2; Page 17; 52pp; English.
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Geysen HM;

Coppel RL,

Anders RF,

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An antigen having the AA sequence in AAP80365 or an antigenic fragment thereof is claimed. Also claimed is a recombinant DNA molecule comprising all or a portion of a nuclectide sequence which is capable of being expressed as polypeptide having the antigenicity of the above antigen or an antigen fragment. Monoclonal antibodies produced using the antigens prevent release of merozoites into the blood stream of an infected individual. The antigens can also be used for actively immunising a host against P.falciparum. The antibodies can also be used for purificn. or detection of P.falciparum.
                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                     Merozoite surface antigen of Plasmodium falciparum - used for active immunisation or for producing monoclonal antibodies for passive immunisation, purificn. or diagnosis
                                                                                                                                                                                                                                                                                      100.0%; Score 52; DB 9; Length 264; 100.0%; Pred. No. 0.15; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merozite surface antigen-2 of the P.falciparum 3D7 isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saul AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27..34
/label- Antigenic Sequence
/note= "Claim 12"
207..214
/label- Antigenic sequence
/note= "Claim 12"
21..28
/label- Antigenic sequence
/note= "Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Thr repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR05876 standard; protein; 272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coppel RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSA2; Indochina 1 isolate; malaria
                                                                                          Claim 3; Fig 6; 59pp; English.
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                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
WPI; 1988-036431/05.
N-PSDB; AAN80340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-115951/15
                                                                                                                                                                                                                                                   264 AA;
                                                                                                                                                                                                                                                                                                                                                           198 gqhghmhg 205
                                                                                                                                                                                                                                                                                                                                            1 сонсимис в
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Active-site
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Irving DO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR05876;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                         Query Match
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Plasmodium falciparum.
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                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                 272 AA;
                                                                                                                                                                                                                                                 206 gqhghmhg 213
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                                                                                                                                                                                                                              1 GQHGHMHG
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12-SEP-1988;
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Irving DO,
                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins)
                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                   Gaps
                                                                            The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be recognised by specific probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                      Allelic variants of P falciparum merozoite surface antigen - used
                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 2 related protein SEQ ID NO:59
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                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum; chromosome 2; human malaria parasite; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                            Length 272;
                                                                                                                                                                                                                 0; Indels
                                 In prodn. of antibodies and in vaccines against malaria
                                                                                                                                                                                            Score 52; DB 11;
Pred. No. 0.15;
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                                                                                                                                                                                         Query Match
100.0%; Score 52; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 139; 577pp; English.
                                                                                                                                                                                                                                                                                                                    AAB18202 standard; Protein; 272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gardner M,
                                                     Disclosure; Fig 1; 53pp; English.
                                                                                                                         recognised by specific probes
See also AAR05876-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365347/31
                                                                                                                                                          272 AA;
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206 gqhghmhg 213
N-PSDB; AAQ03876.
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                                                                                                                                                                                                                                                                                                                                             AAB18202;
                                                                                                                                                           Sequence
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AAB18202
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can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be recognised by specific probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lelic variants of P falciparum merozoite surface antigen - used prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 52; DB 21; Length 272; 100.0%; Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saul AJ, Jones GL;
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/label- Repeat unit
/note= "Repeated four times"
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Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR05879 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSA2; Indochina 1 isolate; malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 4; 53pp; English.
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T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The merozite surface antigen-2 may be used to generate Abs for detection and treatment of malaria, and in vaccination against the Plasmodium parasite. The isolate has conserved N- and C-terminal regions, but differs in central regions, sufficient that it may be recognised by specific probes.
                                                                                     Merozite surface antigen-2 of the P.falciparum MAD71 isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allelic variants of P falciparum merozoite surface antigen in prodn. of antibodies and in vaccines against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                      Saul AJ, Jones GL;
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                                                                                                                                                                            Location/Qualifiers
129..136
/label= Thr repeat region
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                                                                                                                                                                                                                                                                                                                                                                                                      Coppel RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY70278 standard; Protein; 350 AA
AAR05878 standard; Protein; 300 AA.
                                                                                                                    MSA2; Indochina 1 isolate; malaria.
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Dyer SL;
                                                                                                                                                 Plasmodium falciparum.
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N-PSDB; AAQ03876.
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Matches 8; Conserv
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Irving DO,
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                     the P.falciparum Indochina 1 isolate
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                                           Score 52; DB 11; Length 280;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allelic variants of P falciparum merozoite surface antigen in prodn. of antibodies and in vaccines against malaria.
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                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saul AJ, Jones GL;
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                                                                            Mismatches
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/label= Thr repeat region
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                                                                                                                                                                                                              AAR05877 standard; Protein; 287 AA
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100.0%;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                             Conservative
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Dyer SL;
                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
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                                              Ouery Match
Best Local Similarity
Matches 8; Conserv
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214 gqhghmhg 221
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N-PSDB; AAQ03877
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12-SEP-1988;
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Irving DO,
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                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AAA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                    Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
                                                                                                     23..350
/label- Mature_CDC/NIIMALVAC-1
/note- "Recombinant multivalent malarial vaccine"
Rf927; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody; honey bee.
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                                                                             1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
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US DEPT HEALTH & HUMAN SERVICES.
                                                                   Location/Qualifiers
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                           Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
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Matches 8; Conservative
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N-PSDB; AAZ51336.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 100.
Matches 6; Conservative
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99US-0147038.
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99US-0151066.
99US-0151080.
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99US-0157117.
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99US-0153758.
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99US-0149929
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99US-0149930
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99US-0144352
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06-AUG-1999;
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15-SEP-1999;
16-SEP-1999;
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27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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13-AUG-1999;
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20-AUG-1999;
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23-AUG-1999;
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Gaps
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                                                                                                                                                                                                                                                                                                                  78.8%; Score 41; DB 21; Length 408; 100.0%; Pred. No. 17; 0; Indels ive 0; Mismatches 0; Indels
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/label= Signal_peptide
19..85
/label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAR26414 standard; Protein; 85 AA.
         990S - 0158029
990S - 0158232
990S - 0159233
990S - 0159294
990S - 0159329
990S - 0159329
990S - 0159330
990S - 0159331
990S - 0159637
990S - 0159634
990S - 0160741
990S - 0160767
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990S-0161405.
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990S-0161359.
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99US-0160989
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99US-0161920
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                                                                                                                                                                                                                                                                                                                   Query Match 78.8
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Food additive protein
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237 hghmhg 242
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06-0CT-1999;
07-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
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25-0CT-1999;
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AAR26414
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Scarselli M;
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                                                                                                     The sequence given is a protein which is useful as an antimycotic agent. The protein has a molecular weight of approx. 13000 and is thermostable for 5-10 minutes when heated to 100 degrees C. The protein may be incorporated into food additives for humans and animals. The protein can be obtained by collecting the body fluids of insect larvae of Diptera or Hymenoptera (eg. sarcophaga peregrina), centrifuging the solution and subjecting the supernatant to reverse
                                                                                                                                                                                                                                                                            Gaps
                                            Abtimycotic protein useful as food additive - found in insect larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis ORF 568 protein sequence SEQ ID NO:1694.
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Scalato E, S
                                                                                                                                                                                                                                                     DB 13; Length 85;
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Ratti G,
                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                     Score 40;
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                      AAY75110 standard; Protein; 256 AA.
                                                                                 Disclosure; Page 8; 9pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
                                                                                                                                                                                                                                                   76.9%;
ilarity 75.0%;
Conservative
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                                                       diptera or hymenoptera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-062150/05.
        WPI; 1992-363111/44.
N-PSDB; AAQ27738.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                  85 AA;
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gqhgyahg 63
                                                                                                                                                                                                                                                                                                    1 СОНСНМИС 8
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02-SEP-1998;
02-SEP-1998;
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09-OCT-1998;
09-OCT-1998;
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Tettelin H,
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                                                                                                                                                                                             ohase, HPLC
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                                                                                                                                                                                                                     Sequence
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, antibodies and composition. The polypeptides, and invention of the present invention of manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. menhalgitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypuctocolis.
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Scarselli M;
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                                  AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
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Scalato E, So
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16;
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Ratti G,
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                    Score 40; Pred. No. 10
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                             AAY75109 standard; Protein; 257 AA.
         Page 873; 1453pp; English.
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98US-0103749.
98US-0103794.
98US-0103796.
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98US-0094869.
98US-0098994.
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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I, Pizza M, R
I, Venter JC;
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
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Tettelin H,
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25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAY75109;
          5
                                                                                                                                                                                                                     Sequence
            Claim
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5437 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA of human origin and proteins coded by it - which may be expressed by in vivo or in vitro translation using sense RNA or antisense DNA corresponding to the cDNA.
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                                                                                                                                                                                                                                                                                        Score 40; DB 21; Length 257; Pred. No. 16; 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sekine S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA; library; enzyme; protein.
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Claim 2; Page 872; 1453pp; English.
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92JP-0327619.
93JP-0061431.
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Similarity 85.7%;
6; Conservative (
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N-PSDB; AAQ57426.
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Best Local Similarity
Matches 6; Conserv
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237 gqhghrh 243
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13-NOV-1992;
26-FEB-1993;
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                                                                                                                                                                                                                                               Sequence
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102 AA;

Sequence

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Score 39; DB 15; Length 102;
Pred. No. 8.6;
                         Indels
                         0; Mismatches
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Job time: 423 sec
 75.0%;
75.0%;
                         6; Conservative
 Query Match
Best Local Similarity
Matches 6; Conserv
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92 gghghshg 99
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Sequence 4 Sequence Sequence Sequence Sequence

Sequence

Sequence 2 Sequence 2 Sequence 6

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Searched:

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Seguence:

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GENERAL INCORMATION:
APPLICANT: MATSUSHIRO, Aizo
TITLE OF INVENTION: PEARL PROTEIN(NACREIN) AND PROCESS FOR
TITLE OF INVENTION: THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STARET: Illinois
CITY: United States of America
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 398;
                 US-09-461-474-10
US-08-155-171B-37
US-08-202-3899-29
US-08-155-171B-32
US-08-135-171B-32
US-08-135-171B-32
US-08-133-3438-5
US-08-123-3438-5
US-09-431-573-4
US-09-431-573-5
US-08-202-389-2
US-08-202-389-2
US-08-466-589-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Sakal, Hajiane
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT APPLICATION NUMBER: US/09/461,474
CURRENT APPLICATION NUMBER: 60/112,562
EARLIER FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                JS-08-496-855A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 4
Pred. No. 53;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                     US-08-202-389-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-461-474-17; Sequence 17, Application US/09461474; Patent No. 6278042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08945848
Patent No. 5968772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-461-474-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
:||| ||
217 EHGHSHG 223
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  8001883333333558
8444443333335556
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1.352 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, A Sequence 31, Sequence 12, Sequence 4, A
                                                                                                                                          ; Search time 133.18 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20
Sequence 1
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Sequence 2
Sequence 4
Sequence 7
Sequence 6
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-461-474-17
US-08-945-848-8
US-09-046-848-8
US-09-461-474-12
US-09-461-474-12
US-09-107-858-4
US-08-137-614A-26
US-08-137-614A-26
US-08-137-614A-26
US-08-107-064-4
US-08-107-064-4
US-08-107-064-8
US-08-107-064-8
US-08-107-1064-8
US-09-612-126-6
US-09-612-126-6
US-09-612-126-6
US-09-612-126-11
                                                                                                                                                                                                                                                                                                                                                                                                         Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        January 29, 2002, 10:24:07

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                         US-09-763-397A-15
52
1 GQHGHMHG 8
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Maximum DB seq length: 200000000
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Match Length
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Gaps

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Gaps ö

Indels

Length 211;

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RESULT 5
US-08-758-621-4
Sequence 4, Application US/08758621
Sequence 4, Application US/08758621
Sequence 5.846812
GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 349;
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                 core 35; DB 4;
red. No. 58;
Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Railaski, Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Plant Metal Transporters
FILE REFERENCE: BB1303 US NA
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: 60/112,562
EARLIER APFLICATION DATE: 1998-11-16
NUMBER OF SEG ID NOS: 17
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35;
Pred. No.
                                                                                                                                 Score 35;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/758,621 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/018,578
                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09461474; Patent No. 6278042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 0219-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ilarity 83.3%;
Conservative
LENGTH: 211 amino acids TYPE: amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Glycine max
US-09-461-474-12
                                                                                                                                                 Best Local Similarity
Matches 5; Conserv
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                    TYPE: amino
STRANDEDNESS
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3 HGHSHG 8
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                                                         ; TOPOLOGY:
US-09-046-894-31
                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-461-474-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 12
LENGTH: 349
                                                                                                                                     Query Match
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APPLICANT: Ralph, David
APPLICANT: An, Gang
APPLICANT: O'Hara, Mark S.
APPLICANT: O'Hara, Mark S.
APPLICANT: Veltri, Robert
TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING MRNA
TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,848
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr, Thomas A.
REGISTRATION NUMBER: 19036/34324
RECEROMONICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (312) 474-6300
TELEFAN: (312) 474-6448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,894
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 2;
Pred. No. 83;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIORA APPLICATION DATA:
PRIORA APPLICATION NUMBER: US 60/041,576
FILING DATE: 24 MAR-1997
ATTORNEY AGENT INFORMATION:
NAME: NAKASHIMA, RICHARD A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UNCC:014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09046894 Patent No. 6190857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                            not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%;
62.5%;
                                                                                                                                                                                                                                                                                                                       LENGTH: 430 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.2
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-945-848-8
                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 GENGHKHG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GQHGHMHG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Gaps

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1; Indels

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Score 35; DB 1; Length 617;
Pred. No. 1.7e+02;
1; Mismatches 1; Indels
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOUTHOR DATE: 15-0CT-193
FFILING DATE: 15-0CT-193
CLLASSIFICATION NUMBER: US/08/137,614A
FILING DATE: 110-0MBER: 34,103
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/120
TELECPOMINICATION INPORMATION:
TELEPHONE: (716)263-1600
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
CLASSIFICATION: 435
PRIOR APPLICATION WHEER: WS 770,881:
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Monttgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08072064 Patent No. 6008046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARROLL, PETER G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||| ||
436 EHGHGHG 442
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Patent No. 5487976
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Solderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-0999CDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT. FILING DATE: 1998-06-30
EARLIER APPLICATION NUMBER: 08/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PAtentin Ver. 2.0
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98;
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No. 9
                                                                                        DCI-099CP
             ATTORNEY AGENT INFORMATION:
NAME: S1lver1, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-O
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09107858 Patent No. 6162900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT.; ORGANISM: Arabidopsis thaliana US-09-107-858-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.38;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.3%;
Best Local Similarity 83.3%;
Matches 5; Conservative
  FILING DATE: 29-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-758-621-4
                                                                                                                                                                                                                                                                         linear
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185 HGHTHG 190
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US-09-107-858-4
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Gaps

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US-08-072-064-6
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                                                                                                                                                                                                                                                           1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPEY DISK
COMPUTER: TEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
CLASSIFICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00574
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
                  TOPOLOGY: unknown

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
ORGANISM: GENOME:
CHROMOSOME/SEGENT: III; polytene subregion 66F
MAP POSITION: approximately map unit 26
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-072-064-4

Sequence 4, Application US/08072064

Sequence 4, Application US/08072064

GENERAL INC. 6008046

GENERAL INCORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 3; 1
Pred. No. 1.8e+02;
1; Mismatches 1,
                                                                                                                                                                                                                    Score 35; DB 3; I
Pred. No. 1.8e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.38;
71.48;
                                                                                                                                                                                                                      67.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 637 amino acids
AMINO ACID
                                                                                                                                                                                                     Query Match
Best Local Similarity 71.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 637 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-072-064-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
AMINO ACID
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457 EHGHGHG 463
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                                                              APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
MEDIUM TYPE: Floppy disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08072064
Patent No. 6008046
GENERAL INFORMATION:
PAPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
ITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
NUMBER OF SEQUENCES: 20
NUMBER OF SEQUENCES: 20
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
CLASSIFFTANTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 35; DB 3; 71.4%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COMPUTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPHD-00574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19930602
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
Sequence 6, Application US/08072064; Patent No. 6008046; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OP!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 637 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-072-064-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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457 EHGHGHG 463
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US-08-072-064-8
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                                                                                                                                   Score 35; DB 5; Length 637;
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
COUNTRY: USA
ZUP: 02109-1024

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,980B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/177001
TELEPHONE: 617/723-4123
TELEFAX: 617/723-8962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
              POSITION IN GENOME:
CHROMOSOME/SEGMENT: III
MAP POSITION: approximately map unit 26
PCT-US92-08558-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.5;
Pred. No. 1(
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Horvitz, H. Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: TREATMENT AND PR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08023980B Patent No. 5843641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-486-953A-22
Sequence 22, Application US/08486953A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Clark & Elbing LLP
STREET: 585 Commercial Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-023-980B-27
                                                                                                                                   Query Match 67.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.3
Best Local Similarity 66.7
Matches 6; Conservative
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18 GEHGFHVHG 26
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US-08-023-980B-27
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PCT-US92-08558-1
Sequence 1, Application PC/TUS9208558
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: MOLECULAR CLONING AND TRANSFORMATION OF CYCLODIENE RESISTANCE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08558
FILING DATE: 19921002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/770,881
FILING DATE: October 4th 1991
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRF D-1052
                                                                                                                                                                                                                   OPHD-00574
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,064
FILING DATE: 19930602
                                               PILING DATE: 19930602
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 0PHD-005
TELECHOMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEPHONE: 415/797-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-072-064-8
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | | | | 457 EHGHGHG 463
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US-09-612-126-4
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Sequence 4, Application US/09612126
Sequence 4, Application US/09612126
Sequence 4, Application US/09612126
Sequence 4, Application
Sequence 4, Application OF Application OF Application OF Application OF Application OF Application OF Application NUMBER: US/09/612,126
CURRENT APPLICATION NUMBER: US/09/612,126
SPRIOR APPLICATION NUMBER: PCT/US99/26377
PRIOR APPLICATION NUMBER: PCT/US99/26377
SPRIOR APPLICATION NUMBER: PCT/US99/26377
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
Patent No. 5849290
GENERAL INFORMATION:
APPLICANT: Brown, Robert
APPLICANT: Rosen, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: SOMEONING AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                    CIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,953A
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/204,052
FILING DATE: 28-FEB-1994
ATTORNEY/ACENT INFORMATION:
NAME: Clark, Paul T:
RECIESTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 00786/223002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617/428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.5;
Pred. No. 10;
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE:
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.38;
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18 GEHGFHVHG 26
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US-09-612-126-4
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COTHER INFORMATION: Description of Artificial Sequence: Human high OTHER INFORMATION: Description of Artificial Sequence: Human high OTHER INFORMATION: molecular weight kininogen light chain amino acids; OTHER INFORMATION: Gly(456) through Lys(502)

OCHER INFORMATION: Gly(456) through Lys(502)

OLGENY MATCH

OLGENY MATCH

EST Local Similarity 71.4%; Score 34; DB 4; Length 47;

Best Local Similarity 71.4%; Pred. No. 18;

MATCHES 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHGHMHG 8

:||| || ||
Db 25 KHGHGHG 31

Search completed: January 29, 2002, 10:24:07
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us-09-763-397a-15.rpr

Page 1

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January 29, 2002, 10:26:42; Search time 144.96 Seconds (without alignments) 4.204 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                              219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       219241 seqs, 76174552 residues
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
1 GOHGHMHG 8
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pirl:*
2: pir2:*
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4: pir4:*

Database :

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Description	(((())) (() () () () () ()		Surrac	surface annigen to merozoite surface		surf	merozoite surface	merozoite surface	merozoite surface	merozoite 45K surf	merozoite surface			merozoite 45K surf	45K	ZIP4, probable zin	hypothetical prote	hemolymph antifung	transcription fact	transcription fact	transcription fact	hypothetical prote	$\overline{}$	hypothetical prote	_		hypothetical prote		řΩ
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stomatin-like prot	hypothetical prote	conserved hypothet	hypothetical prote	PRL2 protein - Ara	protein F6N18.13 [hypothetical prote	hypothetical prote	FKBP-type peptidyl	peptidyl-prolyl ci	probable peptidylp	19K membrane-bound	hypothetical prote	probable fkbP-type	chorion protein s3	cation efflux syst
S60260	T32404	D69986	T36240	S49821	D86452	B83515	E86669	A81075	E83541	D64087	C41892	D85999	A49987	S07193	A75437
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39	39	38	38	38	38	37	37	37	37	37	37	37	37	37	37
30	. 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B45637 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum) (fragments) C; Species: Plasmodium falciparum
<pre>C;Date: 22-Apr-1993 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000 C;Accession: B45637 R;Snewin, V.A.; Herrera, M.; Sanchez, G.; Scherf, A.; Langsley, G.; Herrera, S.</pre>
MOL. Blochem. Parasitol. 49, 255-275, 1991 A.Title: Polymorphism of the alleles of the merozoite surface antigens MSAl and MSA2 A.Reference number: A45637, MUID:92131063
A;Accession: B45637 A;Status: preliminary A;Molecule types: DNA A:Residues - 1-148 < SNE>
A.Experimental source: isolate COL8 A.Experimental source: isolate COL8 A.Note: sequence extracted from NCBI backbone (NCBIN:78806, NCBIP:78808) C.Superfamily: Epstein-Barr virus nuclear antigen C.Keywords: surface antiqen
Query Match 100.0%; Score 52; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 0.046; Matches R. Conservative O. Mismatches O. Indels O. Gans O.
Db 137 GQHGHMG 144
RESULT 2 A45637
merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum) (fragments) C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000 C;Accession: A45637
R;Snewin, V.A.; Herrera, M.; Sanchez, G.; Scherf, A.; Langsley, G.; Herrera, S. Mol. Biochem. Parasitol. 49, 265-275, 1991
A;Title: Polymorphism of the alleles of the merozoite surface antigens MSA1 and MSA2 A;Reference number: A45637; MUID:92131063
A;Status: preliminary
A; Residues: 1-17 < SNB
A:Experimental source: isolate COL5 A:Note: sequence inconsistent with the nucleotide translation A:Note: sequence extracted from NCBI backbone (NCBIN:78805, NCBIP:78809)
C;Superfamily: Epstein-Barr virus nuclear antigen C;Keywords: surface antigen

100.0%; Score 52; DB 2; Length 172; 100.0%; Pred. No. 0.054;

Query Match Best Local Similarity

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Gaps

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C; Species: Plasmodium falciparum
C; Species: Si Species: Sp
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C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Nov-2000
C;Accession: S55367
R;Chauhan, V.S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S55367
A;Accession: S55367
                                         A,Molecule type: mRNA
A;Residues: 1-264 <SWN-
A;Cross-references: GB:J03828; NID:g160352; PID:g160353
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-264/Product: merozoite 45K surface antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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A;Molecule type: DNA
A;Residues: 1-54, T',56-272 <SMY>
A;Cross-references: GB:M28891; NID:g160458; PID:g160459
C;Genetics:
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100.08; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 8; Conservative
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A; Molecule type: DNA
A; Residues: 1-264 <CHA>
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198 GQHGHMHG 205
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A; Accession: A31818
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A.Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are genet A.Reference number: A45613; MUID:92049549
A.Accession: B45613
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C; Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Nov-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Nov-2000
C; Accession: S39311
R; Ramasamy, R.; Ranasinghe, C.
submitted to the EMBL Data Library, November 1993
A; Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood A; Reference number: S39310
A; Accession: S39311
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C;Species: Plasmodium falciparum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Nov-2000
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C;Superfamily: Epstein-Barr virus nuclear antigen
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A; Residues: 1-256 <RAM>
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Cipacies: Plasmodium falciparum
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Mol. Biochem. Parasitol. 50, 181-184, 1992
A.Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA A.Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA A.Reference number: A45632; MUID:92178286
A; Reference number: A45632; MUID:92178286
A; Reference number: A45632
A; Molecule type: DAR
A; Residues: 1-286 cAMR>
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N;Alternate names: membrane antigen pf7
C;Specias: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 01-bec-2000
C;Accession: B39615; A36018; B44950; A45613
R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Sc Mol. Cell. Biol. 11, 993-971, 1991
A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite A;Reference number: A39615; MUID:91117264
A;Status: preliminary
A;Status: preliminary
A;Status: Dreliminary
A;Residues: 1-287 <FRN:
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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A; Note: clone T9-94
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Best Local Similarity 100.0
Local 8; Conservative
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Matches 8; Conservative
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214 GQHGHMHG 221
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R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Rol. Blochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2) A;Reference number: A45632; MUID:92178286
A;Contents: KF1916
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A;Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
A;Reference number: S39310
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C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
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C;Species: Plasmodium falciparum
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S;3310
R;Ramasamy, R.; Ranasinghe, C.
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A;Note: sequence extracted from NCBI backbone (NCBIN:85252, NCBIP:85257)
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 8; Conservative 0; Mismatches 0; Indels
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
                                C;Superfamily: Epstein-Barr virus nuclear antigen C;Keywords: surface antigen
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A:Molecule type: DNA
A;Residues: 1-274 <MAR>
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A;Molecule type: DNA
A;Residues: 1-278 <RAM>
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206 GQHGHMHG 213
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208 GOHGHMHG 215
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212 GQHGHMHG 219
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A; Gene: PFB0300c
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281 GQHGHMHG 288
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236 GQHGHMHG 243
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C;Species: Plasmodium falciparum
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C;Species: Plasmodium falciparum
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
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R;Fandeur, T.; Bonnefoy, S.; Mercereau-Puljalon, O.
Mol. Biochem. Parasitol. 47, 167-178, 1991
A;Title: In vivo and in vitro derived Palo Alto lines of Plasmodium falciparum are genet A;Reference number: A45613; MUID:92049549
A;Accession: A45613
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A;Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen 2. A;Reference number: A39112; MUID:91156685
A;Accession: A39112
R;Elliott, J.F.; Albrecht, G.R.; Gilladoga, A.; Handunnetti, S.M.; Neequaye, J.; Lalling Proc. Natl. Acad. Sci. U.S.A. 87, 6363-6367, 1990
A;Title: Genes for Plasmodium falciparum surface antigens cloned by expression in COS of A;Reference number: A36018; MUID:90349616
                                                                                                                                                                                                                                              R;Smythe, J.A.; Peterson, M.G.; Coppel, R.L.; Saul, A.J.; Kemp, D.J.; Anders, R.F. Mol. Biochem. Parasitol. 39, 227-234, 1990
A;Title: Structural diversity in the 45-kilodalton merozoite surface antigen of Plasmodi A;Reference number: A44950; MUID:90205972
A;Accession: B44950
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A; Residues: 28, E', 30-186, R', 188-230, TH' <FAN>
A; Experimental source: Uganda Palo Alto strain, merozoite
A; Note: sequence extracted from NCBI backbone (NCBIP:65035)
C; Superfamily: Epstein-Barr virus nuclear antigen
C; Keywords: membrane protein; surface antigen
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A;Residues: 1-300 <SMY>
A;Cross-references: GB:M59765
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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Residues: 1-186,'R',188-287 <SMY>
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234 GQHGHMHG 241
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A;Molecule type: DNA
A;Residues: 1-287 <ELL>
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merozoite 45K surface antigen precursor - malaria parasite (Plasmodium falciparum) (i
C;Species: Plasmodium falciparum
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 17-Nov-2000 C;Accession: A39615; S13802 R;Fenton, B.; Clark, J.T.; Khan, C.M.A.; Robinson, J.V.; Walliker, D.; Ridley, R.; Sc Mol. L. Bold. 11, 963-971, 1991 A;Title: Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite A;Reference number: A39615; MuID:91117264 A;Accession: A39615 MuID:91117264 A;Accession: A39615 A;Accession: A39615 A;Accession: A39615 A;Accession: A39615 C;Separal A;Accession: 
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R; Smythe, J.A.; Coppel, R.L.; Day, K.P.; Martin, R.K.; Oduola, A.M.J.; Kemp, D.J.; An Proc. Natl. Acad. Scil U.S.A. 88, 1751-1755, 1991
A; Title: Structural diversity in the Plasmodium falciparum merozoite surface antigen A; Reference number: A39112; MUID: 91156685
A; Reference number: A39112
A; Reference number: A39112
A; Reference procession: B3912
A; Reference procession: B39
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C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 17-Nov-2000
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100.0%; Pred. No. 0.11;
:ive 0; Mismatches 0;
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C;Superfamily: Epstein-Barr virus nuclear antigen
C;Keywords: surface antigen
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January 29, 2002, 11:13:44; Search time 80.65 Seconds (without alignments) 3.637 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-763-397A-15 52 1 GQHGHMHG 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_39:*

		d			SUMMARIES	
Result		Query				
Ño.	Score	Match	Length	BB	ΩI	Description
П	52	100.0		-	MSA2_PLAFC	17
7	52	100.0		-	MSA2_PLAFF	
m	52	100.0		Ή,	MSA2_PLAFJ	
4	52	100.0		-	MSA2_PLAF7	
S	52	100.0		Н	MSA2_PLAF6	
9	52	100.0		Н	MSA2_PLAF8	
7	52	100.0		-	MSA2_PLAFK	
80	52	100.0		-	MSA2_PLAFH	
σ	52	100.0		-	MSA2_PLAF1	
10	52			-	MSA2_PLAFG	
11	52			Н	MSA2_PLAFI	
12	52	100.0		Н	MSA2_PLAFZ	
13	52	100.0		~	MSA2_PLAF9	
14	52	<u>.</u>		Н	MSA2_PLAF2	
15	41	78.8		Н	CSUP_DROME	Q9v3a4 drosophila
16	40	76.9		Н	ANTF_SARPE	-
17	40	76.9		П	OCT6_HUMAN	
18	40	76.9		-	OCT6_MOUSE	P21952 mus musculu
19	40	76.9		-	OCT6_RAT	P20267 rattus norv
20	39	75.0		Н	KE4_PIG	Q29175 sus scrofa
21	39	75.0		П	SLYD_AERHY	O07046 aeromonas h
22	39	75.0		Н	KE4_HUMAN	Q92504 homo sapien
23	39	75.0		Н	KE4_MOUSE	Q31125 mus musculu
24	39	75.0		Н	MEC2_CAEEL	_
25	38	73.1	171	Н	YSNB_BACSU	P94559 bacillus su
56	38	73.1	352	Н	KE4_BRARE	Q9pub8 brachydanio
27	38			Н	PRL2_ARATH	Q39190 arabidopsis
28	37	71.2		Н	SLYD_HAEIN	P44830 haemophilus
29	37	71.2		Н	HUPE_RHILV	P27650 rhizobium l
30	37	Н		-	SLYD_ECOLI	P30856 escherichia
31	37	\leftarrow	286	Н	CH36_DROME	P07182 drosophila
32	36	69.2		٦	NB2M_HUMAN	043676 homo sapien
33	36	69.5	242	٦	PR38_YEAST	Q00723 saccharomyc

Q62655 rattus norv	P15881 canis famil	P15884 homo sapien	Q60722 mus musculu	. P31725 mus musculu	P50117 oryctolagus	O54422 actinobacil	Q09463_caenorhabdi	P26410 rhodobacter	P11088 mus musculu	Q62941 rattus norv
ITF2_RAT	ITF2_CANFA	ITF2_HUMAN	ITF2_MOUSE	S109_MOUSE	S109_RABIT	UREE_ACTPL	YQ57_CAEEL	HYPB_RHOCA	FILA_MOUSE	ZNT2_RAT
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428	642	299	670	112	118	187	235	332	336	359
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34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AFC ST. 1996 (Rel. 1996 (Rel. 1996 (Rel. TE SURFACE	ta; Alveolata; xID=5835; E FROM N.A. =91218803; Pubh A.W., Carr D.A. ce comparison te surface anti	FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE. SUBSCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (POTENTIAL). DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGE	ISS-PROT entry is copyright. It is produced throug the Swiss Institute of Bioinformatics and the opean Bioinformatics Institute. There are no res	opean Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no d and this statement is not removed. Usage by and for commers requires a license agreement (See http://www.isb-sib.ch/annon an email to license@lsb-sib.ch).	an equal to a constant to a co
MSA2_PLAFC ID MSA2_PLAFC AC 099317; DT 01-0CT-1996 DT 01-0CT-1996 DT MSA2.	Plasmodium falciparum (isolate Camp / Malaysia). Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBL_TaxID=5835; [1] SEQUENCE FROM N.A. MEDLINE-91218803; Pubmed-2090943; Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.; "Sequence comparison of allelic forms of the Plasmodium falcipar merozoite surface antigen MSA2."; MODIUM Plasmodium falcipar MODIUM Plasmodium falcipar merozoite surface antigen MSA2.";	-!- FUNCTION ERYTHR -!- SUBCEL (POTEN -!- DEVELO	s SWIS ween Europ	Europ by fled ties tend a	or send an email to licensedish-sib.ch). Interpro; 1PR001136; MSA_2. Pfam; PF00186; AAA29687.1; Pfam; PF00186; MSA_2; 1. Pfam; PF00186; MSA_2; 1. Malaria; Membrane; Glycoprotein; Antigen GPI-anchor; Merozoite. SIGNAL 1 20 POTENTIAL. CHAIN 21 238 MEROZOITE SPROPEP 239 262 HYDROPHOBIC 248BOHYD 23 22 N-LINKED (GCARBOHYD 23 36 N-LINKED (GCARBOHYD 23 235 N-LINKED (GCARBOHYD 235 235 N-L

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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96360470; PubMed=8719253;
Bhattacharya P., Malhotra P., Sharma P., Okenu D.M.N., Chauhan V.S.;
Bhattacharya P., Malhotra P., Sharma P., Okenu D.M.N., Chauhan V.S.;
"Merozoite surface antigen 2", "Merozoite surface 3", "Merozoite surface antigen 2", "Merozoite surface 3", "Merozoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
-i- MISCELLANEOUS: SAME SEQUENCE IN INDIAN ISOLATES FISI AND FIJ4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
POLYMORPHIC REGION.
2 X 32 AA PERFECTS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                 MOI. Biochem. Parasitol. 74:125-128(1995).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=70152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
GPI-anchor; Merozoite
                                                01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last Sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                           Plasmodium falciparum (isolate fid3 / India)
264 AA.
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InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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Best Local Similarity
Matches 8; Conserv
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MSA2_PLAFJ
P50499;
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SEQUENCE
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MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION (BX SIMILARITY).
POLYMORPHIC REGION.
2 X 32 AA PERFECTS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
-i- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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66DEF3B8357FEF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 85:5195-5199(1988).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.
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                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (MEROZOITE 45 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of two integral membrane proteins of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-88276924; PubMed-3293051; Smythe J.A., Coppel R.L., Brown G.V., Ramasamy R., Kemp D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 52; DB 1; Length 264; 100.0%; Pred. No. 0.027; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
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                                                                                                                                                                                              264 AA.
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EMBL; A12418; CAA01031.1; -.
PIR, A31818; A31818.
Interpro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
                                                                                                                                                                                                PRT;
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Best Local Similarity
Matches 8; Conserv
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198 GQHGHMHG 205
                                                1 GQHGHMHG 8
                     1 СОНСИМИС 8
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P19599;
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01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
01-007-1996 (Rel. 34, Last annotation update)
MEROZOTTE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KDA MEROZOITE
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100.0%; Score 52; DB 1; Length 264; 100.0%; Pred. No. 0.027; ive 0; Mismatches 0; Indels
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antigen 2 (MSA-2) of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 50:181-184(1992).
-i- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                            GPI-anchor; Merozoite.
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223
248
274 AA;
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208 GQHGHMHG 215
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ID MSA2_PLAF8
AC 099320;
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROZOTTE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
POLYMORPHIC REGION.
POLY-THR.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                          Anders R.F.; Structural diversity in the 45-kilodalton merozoite surface antigen
                                                                                                                                                                                                                                            (POTENTIAL).
-1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            ERYTHROCYTE.
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                 of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 39:227-234(1990).
-1- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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                                                                                        SEQUENCE FROM N.A.
MEDLINE-90205972; Pubmed-2181307;
Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J.,
Anders R.F.;
                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haémosporida; Plasmodium.
NCBL_TaxID=57269;
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01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
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                              Plasmodium falciparum (isolate 3D7).
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(Rel. 34, Last seq!
(Rel. 34, Last anno
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InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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245
246
272 AA;
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Best Local Similarity
Matches 8; Conser
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206 GQHGHMHG 213
 SURFACE ANTIGEN).
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P50497;
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SEQUENCE
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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                           (POTENTIAL).
-1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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POLYMORPHIC REGION.
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Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;
Sequence comparison of allelic forms of the Plasmodium falciparum merozoite surface antigen MSA2.";
Mol. Biochem. Parasitol. 43:211-220(1990).
-i- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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01-007-1996 (Rel. 34, Last sequence update)
01-007-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 1; Length 274; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
MEROZOITE SURFACE ANTIGEN 2.
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N-LINKED (GLCNAC. . .)
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100.0%;
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Pfam; PF00985; MSA_2; 1.
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Best Local Similarity 100.0
Energy B; Conservative
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MSA2_PLAFH
Q99319;
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SEQUENCE
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PROPEP
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MSA2_PLAFH
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                                                                                                                                                                                                                                                                                      MEROZOTTE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).
POLYMORPHIC REGION.
POLY "THR.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-91156685; Pubmed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen 2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
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NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 52; DB 1; Length 276; Best Local Similarity 100.0%; Pred. No. 0.028; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M59766; AAA29693.1; -.
InterPro: IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                           Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKED (GLCNAC. . .) (PA 85FA62A70400DEB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (isolate K1 / Thailand)
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                                                                                                                       EMBL; M60190; AAA29690.1; -
                                                                                                                                                   InterPro; IPR001136; MSA_2.
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                                                                                                                                                                                                                                  GPI-anchor; Merozoite.
SIGNAL 1 20
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105
22
36
153
225
250
276 AA;
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ID MSA2_PLAFK
AC Q03643;
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-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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    REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI - ANCHOR
HYDROPHOBIC, REMOVED DURING MATURATIO
(BY SIMILARITY).
POLYMORPHIC REGION.
POLY-SER.
N.LINKED (GLCNAC. .) (POTENTIAL).
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(POTENTIAL).
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(POTENTIAL).
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 3).
                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate thtn / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=70151;
                                                                                                                                                                                                                                                                      Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                              9395D8AFB6B473EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
POLYMORPHIC REGION.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                      100.0%; Score 52; DB 1; ilarity 100.0%; Pred. No. 0.029; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 AA
                                                                                                                                                                                                                                                                                                             0;
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Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycopro
                                                                                                                                                                                                                  29542
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281
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1118
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SIGNAL 1 20
                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conserv
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160
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287 AA

PRT;

STANDARD;

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MSA2_PLAFG
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PROPEP
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                        RESULT 10
MSA2_PLAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                    Gaps
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-i- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
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DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1 - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92178286; PubMed-1542312; MEDLINE-92178286; PubMed-1542312; Marshall V.M., Coppel R.L., Anders R.F., Kemp D.J.; Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2) of Plasmodium falciparum."; Mol. Biochem. Parasitol. 50:181-184(1992).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=57265;
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                                                                          Ouery Match 100.0%; Score 52; DB 1; Length 281; Best Local Similarity 100.0%; Pred. No. 0.029; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat; GPI-anchor; Merozoite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROZOITE SURFACE ANTIGEN
50598AA42D64CCBC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                                                                                                                                                                                                                            286 AA
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28892 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 N 28844 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00985; MSA_2; 1.
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115
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286 AA;
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Best Local Similarity
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215 GOHGHMHG 222
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263
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P50496;
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DOMAIN
CARBOHYD
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SEQUENCE
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MEROZOITE SURFACE ANTIGEN 2.

HYDROPHOBIC, REMOVED DURING MATURATION
(BY SIMILARITY).

POLYMORPHIC REGION.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91117264; PubMed-1990294; Featon B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D., Ridley R., Scaife J.G., McBride J.S., Ritley R., Scaife J.G., McBride J.S., Structural and antigenic polymorphism of the 35- to 48-kilodalton merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
-1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91218803; PubMed=2090943; Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.; Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.; Sequence comparison of allellor forms of the Plasmodium falciparum merozoite surface antigen MSA2."; Mol. Biochem. Parasitol. 43:211-220(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MERCZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 2)
(MEMBRANE PROTEIN PF7).
                                                                                                                                                                                                             MEDLINE-90349616; PubMed-1696728;
Elliott J.F., Albrecht G.R., Gilladoga A., Handunnetti S.M.,
Neequay J., Lallinger G., Minjas J.N., Howard R.J.;
"Genes for Plasmodium falciparum surface antigens cloned by
                                                                                                  Plasmodium falciparum (isolate FCR-3 / Gambia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodlum.
NCBI_TaxID=5838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001136; MSA_2.
Pfam; PR00085; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
GPI-anchor; Merozoite.
                                                                                                                                                                                                                                                                                      expression in COS cells.";
Proc. Natl. Acad. Sci. U.S.A. 87:6363-6367(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 11:963-971(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M28890; AAA29650.1; -.
EMBL; X53832; CAA37829.1; -.
EMBL; M60188; AAA29688.1; -.
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PIR; B39615; B39615.
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164
236
260
261
287 AA;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERYTHROCYTE.
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SEQUENCE
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MSA2_PLAFZ
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SEQUENCE
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MSA2_PLAF9
RESULT 12
MSA2_PLAFZ
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-91156685; PubMed-2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROZOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
POLYMORPHIC REGION.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERYTHROCYTE.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen 2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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NCBL_TaxID=57268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 52; DB 1; Length 300; 100.0%; Pred. No. 0.031; ve. 0; Mismatches 0; Indels
                 100.0%; Score 52; DB 1; Length 287; 100.0%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; MS9767; AAA29695.1; -.
InterPro; IPRO01136; MSA_2.
Pfam; PF00985; MSA_2.
Malaria: Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (P. A01E17D36075D7D6 CRC64;
                                                                                                                                                                                                                                                                                                 01-0cr-1996 (Rel. 34, Created)
01-0cr-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum (isolate imr143).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30131 MW;
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                                                                  Conservative
                                                                                                                                                                                                                                                              STANDARD;
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300
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SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AA;
                        Query Match
Best Local Similarity
                                                                                                                                                   221 GQHGHMHG 228
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDIINE=91156685; PubMed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface antigen 2.";
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-!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES
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HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
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0
                                                                                                                                      Plasmodium falciparum (isolate mad71 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 52; DB 1; Length 300; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Antigen; Signal; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E4116107747AA10D CRC64;
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                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
300 AA.
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InterPro; IPR001136; MSA_2.
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Malaria; Membrane; Glycoj
GPI-anchor; Merozoite.
SIGNAL
1 20
CHAIN
  STANDARD;
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Best Local Similarity
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234 GQHGHMHG 241
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SEQUENCE FROM N.A.
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281 GQHGHMHG 288
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NCBI_TaxID=7227;
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324
                                                                              (POTENTIAL)
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                        antigen 2.
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CARBOHYD
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CSUP_DROME
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0
                                                   SEQUENCE FROM N.A.
MEDLINE=91117264; Pubmed=1990294;
Fenton B., Clark J.T., Khan C.M.A., Robinson J.V., Walliker D.,
RIdley R., Scalfe J.G., WeBride J.S.;
"Structural and antigenic polymorphism of the 35- to 48-kilodalton
merozoite surface antigen (MSA-2) of the malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                            (POTENTIAL).
-1- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                  MIGEN 2. DURING MATURATION
                                                                                                                                                                  -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                               MOI. Cell. Biol. 11:963-971(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-91156685; PubMed-2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
  Plasmodium falciparum (isolate tak 9).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=57276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 52; DB 1; Length 302; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                         Interpro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
MEROŻOITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING
(BY SIMILARITY).
POLYMORPHIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4E0A7EB08227CF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA
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                                                                                                                                                                                                                                                                                                                                                                                 278
302
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138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
275
276
302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GOHGHMHG 243
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NCBI_TaxID=70150;
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131
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                                                                                                                        falciparum."
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01-OCT-1996
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Q03646;
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CARBOHYD
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The catecholmaines up (Catsup) protein of Drosophila melanogaster functions as a negative regulator of tyrosine hydroxylase activity."; Genetics 153:361-382(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                                 -!- DEVELOPMENTAL STAGE: DURING THE TROPHOZOITE AND SCHIZONT STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROPHOBIC, REMOVED DURING MATURATION
                                                                                                                                                           SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                      Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: MAY PLAY A ROLE IN THE MEROZOITE ATTACHMENT TO THE ERYTHROCYTE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 52; DB 1; Length 347; 100.0%; Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
MEROZOITE SURFACE.ANTIGEN 2.
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POLYMORPHIC REGION.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CATECHOLAMINES UP PROTEIN.
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347 AA;
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.E.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutron G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Bradon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Bardon R.C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G.,
RA Barla J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis R.D., Devery S., Dallike C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Burtis R.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischman R.,
RA Bocken K., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
Allock A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser R.,
Allock A., Gong F., Morland T.J., Wei M.-H., Ibeywan C.,
Jalali M., Kalush F., Kalren G.H., Ke Z., Kulp D., Lai Z.,
Lux, Mattei B., McIntosh T.C., McIeod M.P., Ibraris M.,
Lux, Mattei B., McIntosh T.C., McIeod M.P., Parly V., In X.,
Lux, Mattei B., McIntosh T.C., McIeod M.P., Parly W., Rese M.G.,
Rhamel B.E., Solder Klamos I., Simpson M., Stupski M.P., Sanith T.,
Shue B.C., Siden Klamos I., Simpson M., Stupski M.P., Sanith T.,
Rhamer B.C., Sperdling A.C., Shapleton M., Stupski M.P., Sanith H.O.,
Rhamis S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Wang Z.-Y., Woolse F.W., Rollson M., Strong R., Walsenberd J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
Rhyers R., Shore E.W., Rollson M., Strong R., Sanith H.O.,
Rhyers R., Hosen D.R., Worley E.W., Wollon W., Shore R., Sanith H.O.,
Rhyers R., Shore S.W., Rollson W., Shore R., Shore S., Sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i - FUNCTION: NEGATIVELY REGULATES TYROSINE HYDROXYLASE ACTIVITY .
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MEDLINE=20196006; PubMed=10731132;
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75.0%;
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449 AA;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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2 (FRAGMENT).
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EBML, AF010460; ASC38840.1; -.
InterPro: IPR001136; MSA_2.
Pfam: PF00985; MSA_2: 1.
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                                                                               Search time 285.36 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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MEDLINE-98156776; PubMed-9497062; Irion A., Beck H.-P., Felger I.; Indon A., Beck H.-P., Felger I.; "New repeat unit and hot spot of recombination in FC27-type alleles of the gene coding for Plasmodium falciparum merozoite surface protein
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                  plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 52; DB 5; Length 152; 100.0%; Pred. No. 0.11; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hosse R.J. Melsinger K., Engelbrecht F.;.
"Plasmodium falciparum msp2 allelic variants.";
"Plasmodium falciparum msp2 allelic variants.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR13219; AR206418.1;
InterPro; IRR001136; MSA_2.
PF00985; MSA_2: 1.
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157 157
157 AA; 15839 MW; 528D977160C2B00D CRC64;
                                                                                                                                                                                                                                                                                                       152 AA; 15268 MW; 0FE3718127D038A6 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOLIE SURFACE PROTEIN 2 (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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EMBL, AF010455; AAC38835.1;
InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Merozoite.
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Matches 8; Conserv
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Best Local Similarity
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                                                                                NCBI_TaxID=5833;
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MEDLINE-98156776; Pubmed-9497062;
Irion A., Beck H.-P., Felger I.;
"New repeat unit and hot spot of recombination in FC27-type alleles of the gene coding for Plasmodium falciparum merozoite surface protein
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                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF033859; AAB87520.1; -.
InterPro; IFR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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NON_TER 137 137 AA: 14053 MW; ED878BA4ECAABB5D CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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015683; 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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Mol. Biochem. Parasitol. 90:367-370(1997).
EMBL; AF010461; AAC38841.1;
InterPro; IPR001136; MSA_2.
Plen; PF00985; MSA_2; 1.
Merozoite.
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Best Local Similarity
Matches 8; Conserv
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MEDLINE-98156776; PubMed-9497062;
Irion A., Beck H.-P., Felger I.;
"New repeat unit and hot spot of recombination in FC27-type alleles of the gene coding for Plasmodium falciparum merozoite surface protein
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Irion A., Beck H.-P., Felger I.;
"New repeat unit and hot spot of recombination in FC27-type alleles
the gene coding for Plasmodium falciparum merozoite surface protein
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                 Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                     Length 164;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2091 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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100.0%; Score 52; DB 5;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.12;
iive 0; Mismatches 0,
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EMBL; AF010462; AAC38842.1; -
InterPro; IPR001136; MSA_2.
Figha; PF00985; MSA_2; 1.
Merozolte.
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Mol. Biochem. Parasitol. 90:367-370(1997).
EMBL. AF010458. AAC38838.1;
InterPro, IPR001136; MSA_2.
Pfam; PF00985; MSA_2: 1.
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Matches 8; Conservative
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                                                                                                               SEQUENCE FROM N.A.
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                                                                             NCBI_TaxID=5833;
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                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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                                                                                                                                         STRAIN-RHO210;
Hosse R.J., Metsinger K., Engelbrecht F.;
Plasmodium falciparum msp2 allelic variants.",
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF148222; AAD37405.1;
InterPro; IPR001136; MSA_2.
Merozoite.
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163 163
163 AA; 15612 MW; 1108FB27FAEB9677 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-1901 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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Matches 8; Conservative
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                                                                Plasmodium falciparum.
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DT 01
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Q9XZM4
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Dobano C., Taylor R.R., McBride J.S.;
Dobano C., Taylor R.R., McBride J.S.;
"Analysis of the structural diversity of Plasmodium falciparum merozoite surface protein 2 (MSP-2) in Gambia.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U91666; AAF21489.1;
InterPro: IPR001136; MSA_2.
Pfam: PF00985; MSA_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doback C., Taylor R.R., McBride J.S.;
Doback C., Taylor R.R., McBride J.S.;
"Analysis of the structural diversity of Plasmodium falciparum merozoite surface protein 2 (MSP-2) in Gambia.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U91669; AAR21492.1; -
InterPro; IPR001185, MSA_2.
Pfam; PF00985; MSA_2; 1.
                                                                                                 Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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176 176
176 AA; 18142 MW; A13140FCE312A0D2 CRC64;
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176 176
176 AA; 18083 MW; DE89779E85B03DEB CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 (FRAGMENT).
                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 (FRAGMENT).
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176 AA
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Irlon A., Beck H.-P., Felger I.;
"New repeat unit and hot spot of recombination in FC27-type alleles of
the gene coding for Plasmodium falciparum merozoite surface protein
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"Analysis of the structural diversity of Plasmodium falciparum merozoite surface protein 2 (MSP-2) in Gambia.";
Submitted (MRR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 091652; AAR21475.1;
InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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174 174
174 AA: 17582 MW; 7FA69C70996F8BFD CRC64;
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01-JAN-1998 (TrEMBirel. 05, Last sequence update)
01-JUN-2001 (TrEMBirel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE ANTIGEN 2 (FRACMENT).
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100.0%; Pred. No. 0.1
tive 0; Mismatches
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EMBL; AF010457; AF028837.1; -.
Interpro: IPR001136; MSA_2.
Pfam; PF00998; MSA_2: 1.
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Best Local Similarity 100.
Matches 8; Conservative
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Elsen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;
Elsen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;
Elsen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;
Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falloiparum.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF329539; AAK19358.1;
NON_TER
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Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Eisen D.P., Cloonan N., Baddeley A., Eri R., Saul A.;

Antiquaic drift and immune selection acting on merozoite surface protein 1.9 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329540; AAK19359.1; -.

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SEQUENCE 176 AA, 18256 MW; 3FCIA48233972B63 CRC64;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEROZOITE SURFACE PROTEIN 2 (FRAGMENT).
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159 GQHGHMHG 166
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Zea mays protein f
Arabidopsis thalia

Title: Perfect score:

Seguence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
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AAG34425
AAG36584
AAG26587
AAM15106
AAW15100
AAG44660
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AAG44659
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AAG22810
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WO200011179-A1.
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4.290 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                                     January 29, 2002, 10:21:47
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AAR68840
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    protein search, using sw model

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AAP91632
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                    100
1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                        US-09-763-397A-16
                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
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100.0
100.0
95.0
95.0
66.0
67.5
47.5
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47.5 47.5 47.5

Score

Result Š 100 100 100 95 95 66

Zea mays protein f Zea mays protein f CFE 41 protein seq Pneumocystis carin

Zea mays protein Zea mays protein Zea mays protein Sequence of the Ri

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The present sequence is the antigenic epitope P600, derived from apical membrane antigen-1 (AMA-1) of the asexual blood stage of plasmodium falciparum. It is used in the construction of recombinant protein comprises, malitivalent, multistage malarial vaccine. The recombinant protein comprises, malitim signal peptide, vaccine. The recombinant protein comprises, malitim signal peptide, cancine. The recombinant protein comprises, malitim signal peptide, vaccine. The recombinant protein comprises, malitim signal peptide, cancine protein-2 from circumsporozoite protein (SSP-1), merozoite surface protein-1 (SSP-2), liver stage antigen-1 (SA-1), merozoite surface protein-1 (SSP-1), merozoite surface protein-1 cancine. Thopity associated protein-1 (RAP-1) and gamete specific antigen-175 (EBA-175), rhopity associated protein-1 (RAP-1) and gamete specific antigen of P. falciparum. CDC/NIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of antiparal infections. Anti-CDC/NIMALVAC-1 antibodies can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; csp: circumsporozoite protein; CSP; sporozoite surface protein:2; SSP-2; apical stage antigen:1, ESA-1; merozoite surface protein:1, MSP-1; MSP-2; apical membrane antigen:1, AMA-1; erythrocyte binding antigen:175; EBA-175; rhoptry associated protein:1; RAP-1; gamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
    Novel recombinant protein as vaccine for treating malarial infection comprises antiquence peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 100; DB 21;
100.0%; Pred. No. 3.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                             detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                       Claim 2; Page 16; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0097703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 dqncediphynefsaidl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200011179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical antigen-1 (LSA-1), revitable binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Ffg27. These epitopes were obtained at different stages of the life cycle of presmodium falloparum (CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silva A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhoptry membrane antigen of Plasmodium falciparum - used for producing antibodies and in immunisation, diagnostic and treatment methods for malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marshall VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 100; DB 21;
100.0%; Pred. No. 1.1e-08;
21ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria; rhoptry membrane antigen-1; antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smythe JA,
                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP91632 standard; protein; 622 AA.
                                                                                                                                                                                     Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                         plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88AU-0006743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89WO-AU00056.
                                                     Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crewther PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAIM-) NAT INST IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhoptry membrane antigen-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SARA ) SARAMANE PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-263714/36.
                                                                                   2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                             350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN90703
                                                                                                 N-PSDB; AAZ51336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peterson MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP91632;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                        Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AAP91632
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AAR68840 standard; Protein; 622 AA.

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RESULT

AAR68840

AAR68840;

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Gaps

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immune response to malaria, and antibodies which the parasite. RMA-1 initially has mol. wt. 80 kD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                      Recombinant poxvirus; antimalarial vaccine; malaria; immunise;
                                                                                                        Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 13; Length 622;
Pred. No. 1.4e-07;
); Mismatches 1; Indels
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant pox:virus - contg. Plasmodium DNA, useful as antimalarial vaccine
                                                                                                       Score 100; DB 10;
Pred. No. 2.1e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tine JA;
                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                               Plasmodium falciparum AMA1 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 5; 74pp; English.
                                                                                                                                                                                                                                     AAR27532 standard; Protein; 622
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           Claim 1; Fig 3; 46pp; English.
                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-US02207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-0672183.
92US-0852305.
                                                                                                                                                                  317 dgncediphynefsaidl 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.48;
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                                                                                                                                                     1 DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoletti E,
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VIRO-) VIROGENETICS CORP
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                 RMA-1 can generate an
can inhibit growth of
                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-349203/42.
                                                                                                       Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 17; Conserv
                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ29189
                                                                     622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De TAISNE C,
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1991;
18-MAR-1992;
                                                                                                                                                                                                                                                                                      08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                 W09216616-A
                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1992
                                                                                                                                                                                                                                                                                                                                                   immunogen
                                                                                                                                                                                                                                                              AAR27532;
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                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                          Recombinant poxvirus contg. Plasmodium DNA in non-essential region – useful in vaccines against malaria and for prodn. oplasmodium immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95; DB 16; Length oz. Pred. No. 1.4e-07;
                                                                          Plasmodium falciparum AMA-1 gene; recombinant poxvirus; multicomponent multistage malarial vaccines; immunogens; malaria diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium knowlesi 66kD merozoite antigen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium merozoite antigens; malaria vaccine.
                                                   Plasmodium falciparum AMA-1 gene protein.
                                                                                                                                                                                                                                                                                                          Tine JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR10551 standard; Protein; 563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 5; 183pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%;
94.4%;
                                                                                                                                 Plasmodium falciparum (3D7)
                                                                                                                                                                                                             94WO-US06652
                                                                                                                                                                                                                                      93US-0075783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DGNCEDIPHVNEFSAIDL 18
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                        (first entry)
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                                                                                                                                                                                                                                                                                                        Paoletti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                 WPI; 1995-036113/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      622 AA;
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ80910
                                                                                                                                                                                                                                                                                                          De Taisne C,
                                                                                                                                                                                   22-DEC-1994.
                                                                                                                                                                                                             10-JUN-1994;
                                                                                                                                                                                                                                      11-JUN-1993;
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                                                                                                                                                        WO9428930-A.
                        24-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium vivax 66kD merozoite antigen protein partial sequence.
                                                                                                                                                                                 This protein is encoded by a recombinant DNA molecule comprising the complete P.Knowlesi merosoite antigen gene and e.g. a pUCL9 or vacchia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. It is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells. See also AAO10869.
                                                                                                                                            Plasmodium merozoite antigen proteins and DNA sequences – useful
in vaccine prodn., anti-malarial drug design, and in diagnostics
                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                              66.0%; Score 66; DB 12; Length 563; 66.7%; Pred. No. 0.0091; 1. Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium merozoite antigens; malaria vaccine.
                                                                                                                                                                                                                                                                                                                                                                    AAR10935 standard; Protein; 489 AA.
                                                                                                                                                                     Disclosure; fig 1; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0483516
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                                                                                                                                                                                                                                                                                                                        262 dgnceeipyvnevearsl 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) NAT INST OF HEALTH
                                                         90US-0483516
                                                                        90US-0483516
                                                                                                                                                                                                                                                                                                              1 DGNCEDIPHVNEFSAIDL 18
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                                                                                        (USSH ) NAT INST OF HEALTH.
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                                                                                                                                                                                                                                                                                                Conservative
                                                                                                        McCutchan TF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-044381/06.
N-PSDB; AAQ10869.
                                                                                                                       WPI; 1991-044381/06.
N-PSDB; AAQ10418.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
             Plasmodium knowlesi
                                                                                                                                                                                                                                                           563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium vivax.
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                                                         22-FEB-1990;
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                                                                         22-FEB-1990;
                           JS7483516-A
                                           15-JAN-1991
                                                                                                        Waters AP,
                                                                                                                                                                                                                                                                                                                                                                                     AAR10935;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                 This protein is encoded by a recombinant DNA molecule comprising the complete P.vivax merozoite antigen gene and e.g. a pUC19 or vaccinia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. It is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells.
plasmodium merozoite antigen proteins and DNA sequences – useful
in vaccine prodn., anti-malarial drug design, and in diagnostics
                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                               DB 12; Length 489; 0.011;
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                     Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG33060 standard; Protein; 135 AA.
                                                            Disclosure; fig 1; 31pp; English
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990S-0132484.
990S-0132486.
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188 dgnceeipyvkeveagdl 205
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                                                                                    Length 135;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                   Gaps
                                                   'n
                                Length 137;
                                                   Indels
                              47.5%; Score 47.5; DB 21;
61.1%; Pred. No. 2.3;
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P R R P P R R P P R R P P R R P P P R R P	7	P P P P P P P P P P P P P P P P P P P

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7

Gaps

3,

Score 47.5; DB 21; Length 146; pred. No. 2.4; 2; Mismatches 2; Indels 3

Ouery Match 47.5%; Best Local Similarity 61.1%; Matches 11; Conservative 2

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9905-0139463
9905-0139463
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990S-0144085
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990S-0144333
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99US-0141287
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29 - JUN - 1999;

30 - JUN - 1999;
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02-JUL-1999

06-JUL-1999

09-JUL-1999

13-JUL-1999

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15-JUL-1999

15-JUL-1999
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04-AUG-1999;
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                                                                                                                                                                                                                                                                                                                          6-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-1999
                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                       Zea mays protein fragment SEQ ID NO: 43950.
                                                                       AAG35922 standard; Protein; 160 AA
                                                                                                                                                                                                                                                                                        990S-0121825.
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990S-0125788.
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99US-0132484.
99US-0132485.
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990S-0134219.
990S-0134221.
990S-0134370.
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99US-0127462.
99US-0128234.
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99US-0130077.
99US-0130449.
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99US-0131449.
99US-0132048.
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99US-0134256.
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99US-0136392.
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99US-0139492.
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25-MAR-1999;
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06-MAR-1999;
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06 - MAY - 1999

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20 - JUN - 1999

03 - JUN - 1999
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                                                                                                                                                                                                                           EP1033405-A2
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                                                                                             AAG35922;
                                                   RESULT 11
AAG35922
e
                     81
                                                                                              õ
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                  Zea mays protein fragment SEQ ID NO: 50450.
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990S-0130449.
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99US-0132887.
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990S-0123548.
990S-0125788.
990S-0126685.
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99US-0131449
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99US-0132484
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                                                                                                                                      06-SEP-2000
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47.5; DB 21;
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990S-0161359
990S-0161360
990S-0161920
990S-0161992
990S-0161993
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Best Local Similarity 61.1%;
Matches 11; Conservative
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99US-0160770.
99US-0160814.
99US-0160981.
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|nc-diphynrteyglidi 97
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29-SEP-1999;
04-0CT-1999;
05-0CT-1999;
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08-0CT-1999;
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18-JUN-1999; 18-JUN-1999; 18-JUN-1999;

RESULT 1 . :.

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PR 01-UUL-1999; 99US-01400554.

PR 02-UNN-1999; 99US-0141287.

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PR 23-UNL-1999; 99US-0144334.

PR 23-UNL-1999; 99US-0144334.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5%; Score 47.5; DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays protein fragment SEQ ID NO: 39998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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21-JUN-1999;
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990S-0140823 99US-0141087 99US-01411842 99US-01411842 99US-0142055 99US-0142390 99US-0142390 99US-0142390 99US-0142920 99US-0143624. 99US-0144005. 99US-0144085. 99US-0144325. 99US-0144331. 990S-0144332 990S-0144334 990S-0144334 990S-0144335 990S-01448632 990S-0144814 990S-0144814 990S-0145086 990S-0145089 990S-0145089 990S-0145192 990S-0145192 990S-0145192 990S-0145951 990S-0146386. 990S-0146388. 990S-0146389. 990S-0147038. 990S-0147935. 990S-0148171. 990S-0148319. 990S-0148341. 990S-0148565. 990S-0148684. 990S-0149175. 990S-0149723. 99US-0149929. 99US-0149900. 99US-0149900. 99US-0150884. 99US-0150884. 99US-0151066. 99US-0151080. 99US-0145913. 99US-0145918. 99US-0145919. 99US-0147260. 99US-0147303. 99US-0147416. 99US-0147493. 99US-0140353. 99US-0140354. 99US-0140695. 99US-0143542 99US-0147302 99US-0147192 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; .9-JUL-1999 .9-JUL-1999; 20-JUL-1999, 09-AUG-1999; 10-AUG-1999; 11-AUG-1999 20-AUG-1999 20-AUG-1999 27-AUG-1999,

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Pred. No. 2.8;
2; Mismatches
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               99US-0151930.
99US-0153183.
99US-0153758.
99US-0153758.
99US-0154018.
99US-0154779.
99US-0155139.
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99US-0160770.
99US-0160814.
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990S-0161405
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990S-0161932
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99US-0156596.
99US-0157117.
99US-0157753.
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99US-0158029.
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61.1%;
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31-AUG-1999

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PR 01-JUL-1999; 99Us-0142154.

PR 02-JUL-1999; 99Us-0142055.

PR 06-JUL-1999; 99Us-0142050.

PR 12-JUL-1999; 99Us-0142070.

PR 11-JUL-1999; 99Us-014297.

PR 11-JUL-1999; 99Us-014327.

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PR 11-JUL-1999; 99Us-014432.

PR 11-JUL-1999; 99Us-0144312.

PR 11-JUL-1999; 99Us-0144313.

PR 11-JUL-1999; 99Us-0144313.

PR 11-JUL-1999; 99Us-0144313.

PR 21-JUL-1999; 99Us-0144313.

PR 22-JUL-1999; 99Us-0144314.

PR 22-JUL-1999; 99Us-0144314.

PR 22-JUL-1999; 99Us-0144318.

PR 22-JUL-1999; 99Us-0144319.

PR 23-JUL-1999; 99Us-014319.

PR 23-JUL-19
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; córn.
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Pred. No. 2.9;
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99US-0154779.
99US-0155139.
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99US-0156458.
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99US-01576575.
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99US-0159029.
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Ouery Match
47.5%; Score 47.5; DB 21; Length 192;
Best Local Similarity 61.1%; Pred. No. 3.3;
Matches 11; Conservative 2; Mismatches 2; Indels 3
9908-0157753.
9908-0157865.
9908-0158029.
9908-0158029.
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Search completed: January 29, 2002, 10:21:48 Job time: 424 sec

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TELEPHONE: (212) 840-0333
TELEFAX: (212) 840-0712
TELEX: 42506 CURTMS
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Sequence 2, Appli
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3.041 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Sequence 91, Sequence 2, A Sequence 2, A
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Sequence 9, A
Sequence 10,
                                                                                                          Search time 133.18 Seconds
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Sequence 12,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-068-655-11

US-09-068-655-4

US-09-058-489-18

US-09-058-489-91

US-09-058-489-91

US-09-080-044-3

US-08-91-714-9

US-08-09-714-9

US-08-09-714-9

US-08-177-4

US-08-171-158A-2

US-08-177-4

US-09-037-188-2

US-09-037-188-2

US-09-037-188-2

US-09-285-310-2

US-09-285-310-4

US-09-285-310-4

US-09-285-310-4

US-09-370-253-2

US-08-350-720A-2

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Maximum Match 100%
Listing first 45 summaries
                                                                                                        January 29, 2002, 10:24:07

    protein search, using sw model

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                                                                                                                                                                      US-09-763-397A-16
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Maximum DB seq length: 2000000000
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34.55
37.55
37.55
37.55
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APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: ElbM PC compatible
COMPUTER: ElbM PC compatible
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COMPUTER: TEM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTONINY/AGENT INFORMATION:
ANAME: ALCOMMANDING NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTONINY/AGENT INFORMATION:
ANAME: ACCOUNTY OF THE OFFICE OF THE OFFICE OFFIC
US-08-991-531-1

US-09-032-315-10

US-09-023-318-10

US-09-028-885-10

US-09-394-885-10

US-09-518-901-1

US-09-518-901-1

US-09-518-901-1

US-09-518-2

US-09-005-318-2

US-09-005-318-2

US-09-005-318-2

US-09-339-218A-2

US-09-339-218A-2

US-09-339-218A-2

US-09-336-651B-2

US-08-336-651B-2

US-08-336-651B-2

US-08-470-350B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08257073 Patent No. 5766597
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CORRESPONDENCE ADDRESS:
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single

STRANDEDNESS: TOPOLOGY: lin

Sequence 4, Ap Sequence 2, Ap Sequence 15, A

amino acid linear

MOLECULE TYPE: peptide

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GENERAL INFORMATION:
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; ORGANISM: Human
US-09-058-489-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                 APPLICANT: JACKSON, Ronald James
TITLE OF INVENTION: METHOD OF PRODUCING ALPHA 2,3-SIALYLTRANSFERASE
FILE REFERENCE: 026579-186
CURRENT APPLICATION NUMBER: US/09/068,655A
CURRENT APPLICATION NUMBER: US/09/068,655A
CURRENT APPLICATION NUMBER: AU PN 6587
EARLIER FILING DATE: 1995-011-15
EARLIER FILING DATE: 1995-11-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PALENTIN VET. 2.0
SSEQ ID NO 11
LENGTH: 145
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Pred. No. 7.5;
2; Mismatches 5; Indels
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                                                                        Score 95; DB 1; 1
Pred. No. 8.9e-08;
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                                                                                                           0; Mismatches
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; Sequence 11, Application US/09068655A
Pattent No. 6136579
; GENERAL INFORMATION:
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                                                                      Query Match 95.0%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                 317 DGNCEDIPHVNEFPAIDL 334
                                                                                                                                              1 DGNCEDIPHVNEFSAIDL 18
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Best Local Similarity 53.3
Matches 8; Conservative
   ; FRAGMENT TYPE: internal US-08-257-073-9
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US-09-068-655-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
CURRENT APPLICATION NUMBER: 0S/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
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50.0%; Pred. No. 69;
live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 3;
Pred. No. 69;
2; Mismatches
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; Sequence 91, Application US/09058489
; Patent No. 6103886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/07698926A
US-09-058-489-18; Sequence 18, Application US/09058489; Patent No. 6103886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.0%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 NCP--PHIENFSDIDM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NCEDIPHVNEFSAIDL 18
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Matches 8; Conserv
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us-09-763-397a-16.rai

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GENERAL INFORMATION:
APPLICANT: AUDONNET, Jean-Christophe F.
APPLICANT: AUDONNET, Jean-Christophe F.
APPLICANT: BAUDU, Philippe G.
APPLICANT: BAUDU, Philippe G.
TITLE OF INVENTION: I, PARTICULARLY FOR TREATING FELINE HERPES VIRUS TYPE
TITLE OF INVENTION: I, PARTICULARLY FOR TREATING FELINE INFECTIOUS
TITLE OF INVENTION: PERTYONITS
TITLE OF INVENTION: PERTYONITS
TITLE OF INVENTION: PERTYONITS
CURRENT APPLICATION NUMBER: US/09/080,044
CURRENT PAPLICATION NUMBER: PCT/FR96/01830
EARLIER APPLICATION NUMBER: PCT/FR96/01830
EARLIER APPLICATION NUMBER: 95/14450
EARLIER PILING DATE: 1995-11-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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63;
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Pred. No. 1.5e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                   TITLE DATE: 24 TOV 11933
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: ARCD:112/HYL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB Pred. No. 63; 3; Mismatches
UMBER: US/08/159,340A
24-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-943-714-9
Sequence 9, Application US/08943714
Patent No. 6187578
GENERAL INFORMATION:
APPLICANT: Blinkovsky, Alexander
APPLICANT: Brika, Randy
APPLICANT: Rey, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09080044 Patent No. 6074649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Feline herpesvirus 1
US-09-080-044-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.0%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.0
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.0
Best Local Similarity 46.7
Matches 7; Conservative
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99 CIEVVHSREYSAIQL 113
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CEDIPHVNEFSAIDL 18
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107 NIPHLSEFAKIKL 119
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 DIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                     US-08-159-340A-2
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US-09-080-044-3
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Sequence 2, Application US/08159340A
; Sequence 2, Application US/08159340A
; Sequence 2, Application US/08159340A
; Patent No. 556532
; GENERAL INFORMATION:
    APPLICANT: Papa, Feroz
    TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS
; TITLE OF INVENTION: DEUBIQUITINATING ENZYME: COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 44
; CORRESPONDENCES: AAA 4433
; CORRESPONDENCE ALOUGH, White & Durkee
STREET: P.O. Box 4433
; CITY: HOUSTON
; TATU
; TATU
; TATU
; TATU
; TATE: Texas
; COUNTRY: USA
; COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC COMPATION
; COMPUTER: IBM PC COMPATION
; SOFTWARE: PATENTIN Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: BEADOWN SETTION TO BE SOFTAME: PACHOLIN Release #1.0, Version #1.25
SOFTAME: Pacentin Release #1.0, Version #1.25
SOFTAME: APPLICATION DATE: 19910510
CLASSIFICATION NUMBER: US/07/698,926A
FILING DATE: 19910510
CLASSIFICATION NUMBER: US/07/698,926A
ATTORNEY/AGENT INFORMATION:
NAME: WOSSSNE, WARTEN D
REGISTMATION NUMBER: 600.217-US-01
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: A3100 AGID
TYPE: AMINO AGID
                GENERAL INFORMATION:
APPLICANT: Flickinger, Michael C.
APPLICANT: Flickinger, Michael C.
APPLICANT: Mills, David A.
TITLE OF INVENTION: Bacillus MGA3 Diaminopimelate
TITLE OF INVENTION: Decarboxylase Gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchant & Gould
STREET: 3100 No. 5426052west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
62;
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.0%;
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Best Local Similarity 37.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                         USA
Patent No. 5426052
                                                                                                                                                                                                                                             STATE: MN
COUNTRY: U
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Gaps

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APPLICANT: MACILLYRAY, Ross T.A.
APPLICANT: MACCILLYRAY, Ross T.A.
APPLICANT: MACSON, Anne B.
APPLICANT: MASON, Anne B.
APPLICANT: MASON, Anne B.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
TITLE OF INVENTION: MOLECULES AND MOTANTS THEREOF
CORRESPONDENCE ADDRESS:
                     19;
                                                                                                                                                                                                                                       APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; D.; HELLSTROM, KARL E.; ROSE, TIMOTHY M.; HELLSTROM, INGEGERD;
PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
OUMBER OF SEPULCATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 07-FEB-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 696;
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                     Indels
Pred. No. 1.1e+02;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.5; DB 6;
Pred. No. 1.9e+02;
                                                                                             38.5%; Scor.
43.5%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,158A
FILING DATE: Z8-DEC-1993
CLASSIFICATION NUMBER: US OF PRIOR APPLICATION NUMBER: US APPLICATION NUMBER: US OF FEB-1993
CLASSIFICATION NUMBER: US OF FEB-1993
ATTURE DATE: 06-FEB-1993
ATTURE DATE: US-PEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08175158A
Patent No. 5986067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 NCEDTPEAGYFAVAVVKKSASDL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NCEDIPHVNEF----SAIDL 18
                                                                 1 DGNCEDI-----
Best Local Similarity 24.3
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                             RESULT 11
5262177-4
;Patent No. 5262177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO:4:
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                                                                                                                                                 ADDRESSEE: No. 61875780 No. 6187578disk of No. 6187578th America, Inc. STREET: 405 Lexington Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 4; Length 423; Pred. No. 89;
    APPLICANT: Klotz, Alan
APPLICANT: Mathisen, Thomas Erik
APPLICANT: Dambmann, Claus
TITLE OF INVENTION: Carboxypeptidases And Nucleic Acids
TITLE OF INVENTION: Encoding Same
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,714
FILING DATE: 03-0CT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09370253
Patent No. 6165792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFRENCE/DOCKET NUMBER: 4990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.08;
53.88;
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 423 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Triticum aestivum
US-09-370-253-10
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GNCEDIPHVNEFS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GICETTPGVNQYS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-943-714-9
                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                            STATE: NY
COUNTRY: USI
ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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δ a

Gaps

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Boston
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    US-09-037-188-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.5%; Score 38.5; DB 2; Length 1074; 43.5%; Pred. No. 3.1e+02; tive 0; Mismatches 6; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08470058
Patent No. 5817789
CENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport TITLE OF INVENTION: of a Selected Substance Into Cells NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                            Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                        Query Match 38.5%; Score 38.5; DB 2; Best Local Similarity 43.5%; Pred. No. 1.9e+02; Matches 10; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE, DOCKET NUMBER: TKT93-01
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                  436 NCEDTPEAGYFAVAVVKKSASDL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NCEDIPHVNEF-----SAIDL 18
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-175-158A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-470-058-2
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STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-470-058-2
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RESULT 14

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Sequence 2, Application US/09037188
Sequence 2, Application US/09037188
Sequence 2, Application US/09037188
Setent No. 6027921
GENERAL INFORMATION:
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
UNMER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concinn, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 3.1e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FESTEED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION UNBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fraser, Ph.D., J.D., Janis K. REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/0090C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-285-310-2
; Sequence 2, Application US/09285310
; Patent No. 6262026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812 NCEDTPEAGYFAVAVVKKSASDL 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NCEDIPHVNEF----SAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/544 C.
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
CONTACT 1074 amino acids
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43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.5
Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-037-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PROOR APPLICATION NUMBER: 09/037,188
FILING DATE: Ph.D., J.D., Janis K.
ATTORNEY-AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 07/36/009002
FELEX: 200154
INFORMATION: 617/542-8906
FELEX: 200154
INFORMATION POR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acid
TYPE: amino acid
TOPOLOGY: unknown

WOLECULE TYPE: protein
US-09-285-310-2
MACCHAR SIMIlarity 43.5%; Pred. No. 3.18+02;
Matches 10; Conservative 0; Mismatches 6; Indels 7; Gaps 1;
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Search completed: January 29, 2002, 10:24:08 Job time: 514 sec

3 NCEDIPHVNEF----SAIDL 18

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4.5
Compugen Ltd
GenCore version
Copyright (c) 1993 - 2000
                                                                                                      January 29, 2002, 10:26:43
                                                                   OM protein - protein search, using sw model
                                                                                                      Run on:
```

Search time 144.96 Seconds (without alignments) 9.459 Million cell updates/sec ٠. US-09-763-397A-16 100 1 DGNCEDIPHVNEFSAIDL 18 Title: Perfect score: Sequence:

219241 seqs, 76174552 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table: Searched:

219241 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

pirl:* pir2:* pir3:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetícal prote probable adi - Myc multidrug resistan probable chromosom dihydrolipoamide S resistance protein resistance protein translation initia initiation factor translation initia translation initia apical membrane an apical membrane an 66k merozoite surf apical membrane an probable membrane translation initia multidrug resistan apical membrane an apical membrane an apical membrane an translation initia probable transport suppressor protein ring-infected eryt hypothetical prote hypothetical prote translation initia Description SUMMARIES T30563 T30562 S21058 F86272 S21060 S21059 FIAAA C84546 S69563 A32499 D44986 B44986 A44986 C44986 A44944 S67159 T01355 A41351 T27122 G70657 DVZQF T40171 A25526 T25955 S74669 T37256 A39238 C84954 Query Match Length DB 563 562 347 160 183 285 947 1419 967 396 1804 Score 100 93 93 66 63 47.5 44.5 Result Š.

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Gaps

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Length 622;

Score 93; DB 2; Length 622 Pred. No. 2.1e-07; 0; Mismatches 1; Indels

93.0%; 94.4%;

Query Match 93.0 Best Local Similarity 94.4 Matches 17; Conservative

g δ

metalloproteinase

major surface glyc	protein kinase SSK	 probable ubiquitin 	probable membrane	conserved hypothet	hypothetical prote	probable flavoprot	glycoprotein B - h	ring-infected eryt	DNA (cytosine-5-)-	probable retroelem	hypothetical prote	hypothetical prote	purine nucleotide	hypothetical prote	hypothetical prote
T30544	S59801	F84903	859389	T37674	S73049	E70843	T41941	A48440	G71402	G84493	B84683	T38787	T43541	T06637	T22520
7	~	~	7	7	7	7	7	7	7	7	7	7	7	7	7
1008	1579	266	272	315	401	290	822	838	1519	1611	2218	246	276	282	386
42.0	42.0	41.5	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	40.0	40.0	40.0	40.0
42	42	41.5	41	41	41	41	41	41	41	41	41	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 A3249 aptical membrane antigen 1 - malaria parasite (Plasmodium falciparum) C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jun-2000 C; Accession: A32499 R; Peterson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; A Wol. Cell. Biol. 9, 3151-3154, 1989 A; Title: Integral membrane protein located in the apical complex of Plasmodium falcip A; Reference number: A32499; MUID: 89384584 A; Scatus: preliminary A; Status: preliminary A; Status: preliminary A; Status: Preliminary A; Status: C; Peterson A; Cross-references: GB: A27133; NID: 9160072; PID: 9160073 C; Keywords: membrane protein; surface antigen
	Ouery Match 100.0%; Score 100; DB 2; Length 622; Best Local Similarity 100.0%; Pred. No. 1.4e-08; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 DGNCEDIPHVNEFSAIDL 18 Db 317 DGNCEDIPHVNEFSAIDL 334
•	RESULT 2 D44986 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain 7G8) C, Species: Plasmodium falciparum C, Species: Plasmodium falciparum C, Species: Plasmodium falciparum C, Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000 C, Accession: D44986 R, Thomas A. W.; Waters, A. P.; Carr, J. Mol. Blochem. Parasitol. 42, 285-288, 1990 A, Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate a A, Reference number: A44986; MUID:91101665 A, Accession: D44986 A, Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A, Molecule type: DNA A, Residues: 1-622 < THO> A, Residues: 1-622 < THO> A, Residues: 1-622 < THO> C; Keywords: membrane protein; surface antigen

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Gaps

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C;Species: Plasmodium fragile
C;Species: Plasmodium fragile
C;Species: Plasmodium fragile
C;Species: Plasmodium fragile
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: A44944
B;Peterson, M.G.; Mguyen-Dinh, P.; Marshall, V.M.; Elliott, J.F.; Collins, W.E.; Ande Mol. Biochem. Parasitol. 39, 279-284, 1990
A;Title: Apical membrane antigen of Plasmodium fragile.
A;Reference number: A44944; MUID:90205978
                                                                                                                                                                                                                  German Knowlesi
German Knowlesi
C.Species: Plasmodium knowlesi
C.Species: Plasmodium knowlesi
C.Species: Plasmodium knowlesi
C.Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C.Accession: A39238
C.Accession: A39238
A.Title: A merozoite receptor protein from plasmodium knowlesi is highly conserved an A:Reference number: A39238
A.Accession: A39238
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-563 < WART>
A.Cross references: GB:J05631
C.Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
867159
s67159
probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 05365
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
C;Accession: 867159
R;Jauniaux, J.C.: Poirey, R.
submitted to the Protein Sequence Database, July 1996
A;Reference number: 867143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 562;
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Length
DB 2; L
2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2;
Pred. No. 0.0055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 2;
Pred. No. 0.017;
Score 93; DB;
Pred. No. 2.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                        0;
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ilarity 61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%;
66.7%;
  93.0%;
94.4%;
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                                                                                                             317 DGNCEDIPHVNEFSANDL 334
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                                                                                     1 DGNCEDIPHVNEFSAIDL 18
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A, Molecule type: DNA
A; Residues: 1-562 < PET>
A; Cross-references: GB:M29898
    Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Matches 11; Conserv
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es 12; Conserv
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Matches
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R;Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti A;Reference number: A4986; MUID:91101665
A;Accession: B44986
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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A; Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Blochem. Parasitol. 42, 285-288, 1990
A; Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate a A; Reference number: A44986; WUID: 91101665
A; Accession: A44986
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                   apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain Thai In)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (strain CAMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strair
C;Species: Plasmodium falciparum
C;Date: 28-Apr.1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
                                                                                                C:Species: Plasmodium falciparum
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: B44986
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e-07;
0; Mismatches 1; Indels
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Pred. No. 2.1e-07;
0; Mismatches 1;
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A, Residues: 1-622 < TNO
A, Cross-references: GB:MA4552
C, Keywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-622 <THO>
A;Cross-references: GB:M34553
C;Keywords: membrane protein; surface antigen
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Local Similarity 94.4%;
les 17; Conservative
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.0°
Best Local Similarity 94.4°
Matches 17; Conservative
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Best Local Si
Matches 17;
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Gracession: G70657
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Conton, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Accession: G70657
A; Accession: G70657
A; Molecule type: DNA
A; Residues: 1-947 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27122
R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1999 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-285 <WIL>
A;Cross-references: EMBL:AL033536; PIDN:CAA22143.1; CESP:Y53C10A.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable adi - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                       T27122
hypothetical protein Y53C10A.7 - Caenorhabditis elegans
                                                                                     DB 2;
4.7;
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Pred. No. 29;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.0%; Score 45; DB 3 Best Local Similarity 45.0%; Pred. No. 7.7; Matches 9; Conservative 5; Mismatches
                                                                                                                                             Mismatches
                                                                                     Score 45;
Pred. No.
        F;172-176/Region: nucleotide-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone Y53C10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 DGNCDFTDVPIKHLSHFSRV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 12/2; 36/2; 61/3; 207/3
                                                                                45.0%;
illarity 47.1%;
Conservative
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                                                                                                                                                                                                                           115 DATLEDVKRVSKFAAID 131
                                                                                                                                                                                            1 DGNCEDIPHVNEFSAID 17
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Matches 7; Conservative
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789 QDLPHLPDFSEFDL 802
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A;Accession: T27122
                                                       Ouery Match
Best Local Similarity
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                        A;Molecule type: DNA
A;Residues: 1.347 <JAU>
A;Residues: 1.347 <JAU>
A;Cross-references: EMBL:275170; NID:g1420590; PID:e252113; PID:g1420591; GSPDB:GN00015;
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YOR262w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multidrug resistance protein mdr1 - malaria parasite (Plasmodium falciparum) (fragment) (Species: Plasmodium falciparum (C.Species: Plasmodium falciparum (C.Species: Plasmodium falciparum (C.Species: Plasmodium falciparum (C.Species: O.S.Accession: A41351  
R:Wilson, C.M.; Serrano, A.E.; Wasley, A.; Bogenschutz, M.P.; Shankar, A.H.; Wirth, D.F. Science 244, 1184-1186, 1989  
A:Title: Applification of a gene related to mammalian mdr genes in drug-resistant Plasmod A:Reference number: A41351; MUID:89266942
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C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
C;Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-loop
F;1-183/Domain: ATP-binding cassette homology (fragment) <ABC2>
F;1-9/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Description: precise role in initiation of protein synthesis is not yet known; seems C:Superfamily: translation initiation factor eIF-5A C:Keywords: hypusine; protein biosynthesis F:53/Modified site: N6-(4-amino-2-hydroxybutyl)lysine (Lys) #status predicted
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A:Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Zea mays (maize)
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Aug-2000
C; Accession: T01359
S; Korn, A. M.: Baysdorfer, C.
submitted to the EMBL Data Library, November 1997
A; Reference number: Z14300
A; Sccession: T01355
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-160 < KOR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation initiation factor eIF-5A [similarity] - maize
                                                                                                                                                                                 A;Map position: 15R
C;Keywords: transmembrane protein
F;152-168/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                      Score 51; DB 2;
Pred. No. 0.97;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                 h 51.0%;
Similarity 61.5%;
8; Conservative
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Best Local Similarity 61.15
Matches 11; Conservative
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167 DLPHINVFSKIDM 179
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A; Residues: 1-183 <WIL>
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867159
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Best Local S
Matches 8
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A;Gene: TIF5A
  A; Accession:
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Length 947; Indels

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dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) [imported] - Buchnera sp. (strain c)species: Buchnera sp. (strain c)species: Buchnera sp. (species: Buchnera sp. c;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: C84954 H. Rightenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Rightenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000 A;Fifterence number: A84930; MUID:20448173
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Pred. No. 16;
4; Mismatches
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A;Residues: 1-396 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
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A;Gene: aceF; BU206
C;Keywords: acyltransferase; coenzyme A
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Best Local Similarity 43.8%;
Matches 7; Conservative
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A; Residues: 1-1419 <TRI>A; Corsas-references: EMBL:X56851; NID:99935; PIDN:CAA40180.1; PID:99936
A; Cross-references: EMBL:X56851; NID:99935; PIDN:CAA40180.1; PID:99936
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1990
B; Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.
Cell 57, 921-930, 1989
A; Fitle: Applification of the multidrug resistance gene in some chloroquine-resistant is A; Reference number: A32547; MuID:89288297
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                                                                              C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001 C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001 C; Accession: S18204; A32347 B; Triglia, T.; Foote, S.J.; Kemp, D.J.; Cowman, A.F. Mol. Cell. Biol. 11, S244-5250, 1991 A; Title: Amplification of the multidrug resistance gene pfmdrl in Plasmodium falciparum A; Reference number: S18204; MUID:92017800 A; Accession: S18204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: mRNA
A; Residues: 1-1419 < CRO>
C; Superfamily: multidrug resistance protein; ATP-binding cassette homology
C; Superfamily: multidrug resistance protein; ATP-binding cassette homology
C; Reywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane F; 1-62, 655-1276, Region: duplication
F; 136-638 / Domain: ATP-binding motif A (P-loop)
F; 583-587 / Region: nucleotide-binding motif B
F; 1161-1168 / Region: nucleotide-binding motif A (P-loop)
F; 1161-1168 / Region: nucleotide-binding motif A (P-loop)
F; 1332-1336 / Region: nucleotide-binding motif A (P-loop)
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A;Rosdidues: 1-967 -CLYN>
A;Cross-references: EMBL:AL031262; PIDN:CAA20318.1; GSPDB:GN00067; SPDB:SPBC30B4.05
A;Experimental source: strain 972h-; cosmid c30B4
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multidrug resistance protein - malaria parasite (Plasmodium falciparum)
N.Alternate names: P-glycoprotein
C.Species: Plasmodium falciparum
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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OM protein - protein search, using sw model

January 29, 2002, 11:13:45; Search time 80.65 Seconds (without alignments) 8.183 Million cell updates/sec Run on:

US-09-763-397A-16 100 1 DGNCEDIPHVNEFSAIDL 18 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	escriptio	P22621 plasmodium						~	6	P13568 plasmodium		P24921 nicotiana p	nicotiana	solanum tu	P56337 solanum tub	_	Z,	P26564 medicago sa		P13830 plasmodium		Q50000 mycobacteri		P52352 human herpe		Q9hjm1 thermoplasm	P41023 bacillus me	Q06639 saccharomyc	P32571 saccharomyc	P34278 caenorhabdi	P28897 strawberry			P31069 escherichia
SUMMARIES	ID	AMA1_PLAFF	AMA1_PLAF8	AMA1_PLAFC	AMA1_PLAFG	AMA1_PLAFH	PK66_PLAKU	AMA1_PLAFR	IF5A_MAIZE	MDR_PLAFF	ODP2_BUCAI	IF51_NICPL	IF52_NICPL	IF54_SOLTU	IF55_SOLTU	IF51_SOLTU	IF53_SOLTU	IF5A_MEDSA	PSP1_YEAST	RESA_PLAFF	SSK2_YEAST	DXS_MYCLE	DDXY_HUMAN	VGLB_HSV7J	YDX1_SCHPO	SYD_THEAC	DCDA_BACMT	YD03_YEAST	UBP4_YEAST	YKK1_CAEEL	RRPO_SMYEA	RRPO_NMV	HIS7_PICPA	KCH_ECOLI
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6523 6637 1135 1147 1135 115 115 115 115 115 115 115 115 11		STANDARD: 1. 19, Created) 1. 19, Last seq 1. 40, Last ann ANTIGEN 1 PREC 1 parum (isolate clata; Apicompli 4; PubMed=27019 Marshall V.M., ann Protein loc 1 parum, 1; ANOUNED 11 PARA LOCATION: TYPE 2 protein loc 1 parum, 2 protein loc 1 parum, 3 protei
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		PLAFF AMALPLAFF STANDARD; PRT; 65 P22621 D1-AUG-1991 (Rel. 19, Created) O1-AUG-1991 (Rel. 19, Last sequence upo 20-AUG-2001 (Rel. 19, Last sequence upo APLCAL MEMBRANE ANTIGEN 1 PRECURSOR (MAA-1 OR PF83. Plasmoddium falciparum (isolate FC27 / Plasmoddium falciparum (isolate for Integral membrane protein located in Plasmoddium falciparum "; Integral membrane protein located in Plasmoddium and Integral interformatics interformatics interformatics locatement in out remembri, A08267; CAA00764.1; - Print A32499; A32499. Interpro; Improd3298; Apmem_A91. Pransmembrane; Analy A
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		# \$40 \$ 9 9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

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AMA-1 OR PF83
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P50490;
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        AMA1_PLAFC
P50489;
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EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                          01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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                                                                                                                                                                                                            Plasmodium falciparum (isolate 768).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=57266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 622;
N -> R (IN REF. 1; AAA29476).
; 7D41335E249FA18F CRC64;
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Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
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                                     Score 100; DB 1;
Pred. No. 4.8e-09;
Mismatches 0;
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Pred. No. 7.1e-08;
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MEDLINE=91101665; Pubmed=2270110;
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Best Local Similarity 94.4
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622 AA;
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Matches 18; Conserv
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P50492;
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                                                                                                                                                                                                                                                                                                                                   Thomas A.W., Waters A.P., Carr D.;
Thomas A.W., Waters A.P., Carr D.;
"Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 42:285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SIMILARITY: STRONG TO AWA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK66 FROM P.KNOWLESI.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
MM; 26CEBCF76D07C637 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
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Jasmodium falciparum (isolate FCR-3 / Gambia).

Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID-5838;
                                                                                                                                                                        Plasmodium falciparum (isolate Camp / Malaysia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5835;
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Pred. No. 7.1e-08;
0; Mismatches 1; Indels
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Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
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MEDLINE=91101665; PubMed=2270110;
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SEQUENCE FROM N.A.
MEDLINE-91101665; Pubmed-2270110;
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us-09-763-397a-16.rsp

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P. FRAGILE.
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                          -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND PK66 FROM P.KNOWLESI.
Thomas A.W., Waters A.P., Carr D.; "Analysis of variation in PF83, an erythrocytic merozoite vaccine antigen of Plasmodium falciparum."; mol. Blochem. Parasitcl. 42:285-287(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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01-ocr-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40 annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; Glycoprotein.
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N-LIKED (GLCNAC. .) (
N-LINKED (GLCNAC. .) (
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0; Mismatches 1
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Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane;
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94.4%;
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Matches 17; Conservative
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622 AA;
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P50491;
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CARBOHYD
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SEQUENCE
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AMA1_PLAFH
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANDOUS: PRÉ6 EXPRESSED IN MATURE SCHIZONTS IS RAPIDLY PROCESSED AS THE SCHIZONT RUPTURES, YIELDING A 42/44 KDA DOUBLET ASSOCIATED WITH THE SURFACE MEROZOITE.
-!- SIMILARITY: STRONG TO AMA-1/PF83 OF P.FALCIPARUM, P.CHABAUDI, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MEROZOITE RECEPTOR PK66 PRECURSOR (66 KDA PROTECTIVE MINOR SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91009268; PubMed=2211675; Maters A.P., Thomas A.W., Deans J.A., Mitchell G.H., Hudson D.E., Walter L.H., McGutchan T.F., Cohen S.; A merozoite receptor protein from Plasmodium knowlesi is highly conserved and distributed throughout Plasmodium."; J. Blol. Chem. 265:17974-17979(1990).
                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 622;
                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                APICAL MEMBRANE ANTIGEN 1.
                                                                                                                                                                                                                                                                                                                                                                                        1FDFA53593C94CC5 CRC64;
                                                                                                                                     Antigen; Glycoprotein.
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Pred. No. 7.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                     or send an email to license@isb-sib.ch)
                                                                                                                                                        POTENTIÁL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium knowlesi (strain nuri).
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0
                                                                                                                                     Malaria; Signal; Transmembrane;
                                                                                     InterPro; IPR003298; Apmem_Ag1.
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                                                                EMBL; M58547; AAA29720.1;
                                                                                                                                                                                                                                                                                                                                                                                             71989
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Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                           Pfam; PF02430; AMA-1;
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622 AA;
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POTENTIAL.

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-KINKED (GLCNAC...) (POTENTIAL).
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20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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NCBI_TaxID=5857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 563;
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InterPro; IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                    Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
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Pfam; PF02430; AMA-1; 1.
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(Rel. 40, Last anno
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                                                                                                                                                                                                                       EMBL; M61097; AAA29728.1; -
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563
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P22622;
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DOMAIN
CARBOHYD
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CARBOHYD
VARIANT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome analysis program.";
Theor. Appl. Genet. 93:997-1105(1996).
-!- FUNCTION: THE PERCISE ROLE OF EIE-5A IN PROTEIN BIOSYNTHESIS IS
-NOT KNOWN BUT IT FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Coleoptile;
Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                           Gaps
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                                                                    (POTENTIAL)
                                                                                             (GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
(GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                           ö
                                                                                                                                                                                Score 63; DB 1; Length 562;
Pred. No. 0.0063;
3; Mismatches 4; Indels
                       Korn A.M., Baysdorfer C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. A188;
Cordts S., Loerz H., Dresselhaus T.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
           APICAL MEMBRANE ANTIGEN 1.
                                                                                                                                                                                                                                                                                                                              MAALLE STANDAKU;
P80639; P56332;
01-OCT-1996 (Rel. 34, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y07920; CAA69225.1; -.
Maize-2DPAGE; P80639; COLEOPTILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF034943; AAB88614.1; -. EMBL; Y07920; CAA69225.1; -.
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                                                                                                                                           X
X
                                                                                                                                                                                 63.0%;
61.1%;
                                                                                                                                                                                                                                                        262 DGNCEEIPYVODVOAKDL 279
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                                                                                                                                          64488
                                                                                                                                                                                                              11; Conservative
21
562
484
507
562
562
84
1176
226
226
405
1
22
22
4885
508
84
176
405
4405
562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. B73;
                                           TRANSMEM
DOMAIN
                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                   Query Match
                                                                       CARBOHYD
                                                                                    CARBOHYD
                                                                                                  CARBOHYD
                                                                                                                                          SEQUENCE
                           DOMAIN
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE-9201800; PubMed-1922044;
MEDILINE-9201800; PubMed-1922044;
Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
"Amplification of the multidrug resistance gene pfmdrl in Plasmodium falciparum has arisen as multiple independent events.";
Mol. Cell. Biol. 11:5244-5250(1991).
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                     Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
"Amplification of the multidrug resistance gene in some chloroquine-
resistant isolates of P. falciparum.";
Cell 57:921-930(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93149200; Pubmed-8426608;
Wilson C.M., Volkman S.K., Thaithong S., Martin R.K., Kyle D.E.,
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Э,
                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN (CHLOROQUINE RESISTANCE PROTEIN).
                                                                                             DB 1; Length 160;
                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5837;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                        Plasmodium falciparum (isolate FC27 / Papua New Guinea)
              THOUSELF PROJECT TO THE PERSON OF THE PROSTRE, PROBLES TEST THE PROSTRE, PSO0302; IFSA_HYPUSINE, 1.

PROSTRE, PSO0302; IFSA_HYPUSINE, 1.

PROPERS 53 FAMILY PROSINE (BY SIMILARITY).

SEQUENCE 160 AA; 17497 MW; 7CCFADFBZEC09CAD CRC64;
                                                                                           Score 47.5; DB Pred. No. 0.66; 2; Mismatches
                                                                                                                                                                                                               PRT; 1419 AA
        InterPro; IPR001884; EIF5A_hypusine.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89288297; Pubmed-2701941;
                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M29154; AAA29646.1; -.
EMBL; X56851; CAA40180.1; -.
EMBL; S53996; AAD13870.1; -.
                                                                                            47.58; 61.18;
                                                                                                                                     3 NCEDIPHVN--EFSAIDL 18
                                                                                                                                                 Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A32547; DVZOF.
PIR; S18204; S18204
                                                                                            Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                             MDR_PLAFF
P13568;
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20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONTRESSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPTES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1). DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W, 0F96C7C1850B33D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                    ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat. DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 1; Length 1419;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                              POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
              InterPro; IPR001140; ABC_trnsportr_tmem.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                            POTENTIAL.
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ABC_transportr.
                                                                  Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
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20-AUG-2001 (Rel. 40, Last sequ
20-AUG-2001 (Rel. 40, Last anno
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Best Local Similarity 47.1.
Conservative
8: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                    1048
1083
1419
661
420
1168
721
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1188
212
212
2298
338
788
807
846
928
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                                                                                                                                                                                                                                                                                                                                                                                                          413
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P57302;
                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                         FRANSMEM
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                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                             PRANSMEM
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NP_BIND
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NCBI_TaxID=4092;
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                                                                                                                                                                                                                                                                                                                                           IF52_NICPL
P24922;
                                                                                                                                                                                                                                                                                                                    RESULT 12
IF52_NICPL
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                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: BIF-5A SEEMS TO BE THE ONLY EUKARYOTIC PROTEIN TO HAVE AN HYPUSINE RESIDUE WHICH IS A POST-TRANSLATIONAL MODIFICATION OF A LYSINE BY THE ADDITION OF A BUTYLAMINO GROUP (FROM SPERMIDINE).
-!- MISCELLANEOUS: THERE ARE AT LEAST TWO GENES FOR FIF-5A IN TOBACCO: 5A1 MAY REQUIATE THE LIGHT-DEPENDENT TRANSLATION OF SPECIFIC TRANSCRIPTS WHILE 5A2 MAY BE A HOUSEKEEPING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                           EMBL; AP001118; BAB12923.1; -.
InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR001019; Biotin_lipoyl.
InterPro; IPR001915; Lipoyl.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00198; 2-oxoacid_dh; 1.
Propom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 1.
Glycolysis; Transferase; Acyltransferase; Lipoyl; Complete proteome.
          FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                        .;
0
                                SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                 DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana plumbaginifolia (Leadwort-leaved tobacco), and Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                            1D5B49322AE963BC CRC64;
                                                                                                                                                                                                                                                                     LIPOYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
12-UL-1998 (Rel. 36, Last annotation update)
INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D).
                                                                                                                                                                                                                                                                                                                             44.0%; Score 44; DB 43.8%; Pred. No. 6.4; Live 4; Mismatches
                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92178957; PubMed=1542563;
                                                                                                                                                                                                                                                                                            45277 MW;
                       SYMMETRY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                   184 NWMNIPHVTQFDEVDI 199
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                             3 NCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4092, 4097;
                                                                                                                                                                                                                                                                                                                  396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IF51_NICPL
P24921;
                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                     BINDING
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Nucleic Acids Res. 20.665-669(1992).
-!- FUNCTION: THE PRECISE BOLE OF EIF-5A IN PROPEIN BIOSYNTHESIS IS
NOT KNOWN BUT IT FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIM: EIF-5A SEEMS TO BE THE ONLY EUKARYOTIC PROTEIN TO HAVE AN HYPUSINE RESIDUE WHICH IS A POST-TRANSLATIONAL MODIFICATION OF A LISTINE BY THE ADDITION OF A BUTYLAMINO GROUP (FROM SPERMIOINE). MISCELLANBOUS: THERE ARE AT LEAST TWO GENES FOR EIF-5A IN TOBACCO: 5A1 MAY REGULATE THE LIGHT-DEPENDENT TRANSLATION OF SPECIFIC TRANSCRIPTS WHILE 5A2 MAY BE A HOUSEKEEPING PROTEIN. SIMILARITY: BELONGS TO THE EIF-5A FAMILY.
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001884; EIF5A_hypusine.
Pfam; PF01287; eIF-5a; 1.
PROSITE, PS00302; IF5A_HYPUSINE; 1.
Protein biosynthesis; Initiation factor; Hypusine; Multigene family.
MOD_RES 52 HYPUSINE (BY SIMILARITY).
SEQUENCE 159 AA; 17370 MW; 5174BC5809E8B275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Rekaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chamot D., Kuhlemeter C.; "Differential expression of genes encoding the hypusine-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.5; DB 1;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last annotation update)
INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001884; EIF5A_hypusine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leaf;
MEDLINE=92178957; PubMed=1542563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01287; eIF-5a; 1.
PROSITE; PS00302; IF5A_HYPUSINE;
                                                                                                                                                                                                      EMBL; X63543; CAA45105.1; -. EMBL; X63541; CAA45103.1; -. PIR; S21060; S21060. PIR; S21058.
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Best Local Similarity 50.0.
Best Son 9; Conservative
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                                                                                                                                                                                                                                                                  STRAIN=CV. IRISH COBBLER;
In J.G., Fulino K., Mikuta Y.;
In J.G., Fulino K., Mikuta Y.;
"Nucleotide sequence of five cDNAs encoding eukaryotic translation initiation factor 5A (eIF-5A) from potato.";
(In) Plant Gene Register PGR97-147.
-!- FUNCTION: THE PRECISE ROLE OF EIF-5A IN PROPEIN BIOSYNTHESIS IS NOT KNOWN BUT IT FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST
                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: EIF-5A SEEMS TO BE THE ONLY EUKARYOTIC PROTEIN TO HAVE AN HYPUSINE RESIDUE WHICH IS A POST-TRANSLATIONAL MODIFICATION OF A LYSINE BY THE ADDITION OF A BUTYLAMINO GROUP (FROM SPERMIDINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Initiation factor; Hypusine; Multigene family.
HYPUSINE (BY SIMILARITY).
345 MW, 59D7B0C599FC5D2F CRC64;
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STRAIN=CV. IRISH COBBLER;
In J.G., Fujino K., Kikuta Y.;
In Jid., Fujino K., Kikuta Y.;
Initiation factor 5A (eIF-5A) from potato.";
(In) Plant Gene Register PGR97-147.
-I- FUNCTION: THE PRECISE ROLE OF EIF-5A IN PROTEIN BIOSYNTHESIS IS
                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4113;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
1NITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D).
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InterPro; IPR01884; EIF5A_hypusine.
Pfam; PF01287; eIF-5a; 1.
PROSITE; PS00302; IF5A_HYPUSINE; 1.
Protein biosynthesis; Initiation fact
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SEQUENCE 159 AA; 17345 MW;
                                                                                                              Solanum tuberosum (Potato).
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NC-DVPHVNRTDYQLIDI 96
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IF51_SOLTU
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In J.G., Fujino K., Kikuta Y.;
"Nucleotide sequence of five cDNAs encoding eukaryotic translation
initiation factor 5A (eIF-5A) from potato.";
(In) Plant Gene Register PGR97-147.

-I- FUNCTION: THE PRECISE ROLE OF EIF-5A IN PROTEIN BIOSYNTHESIS IS
NOT KNOWN BUT IT FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST
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InterPro; IPR001884; EIF5A_hypusine.
Pfam; PF01287; eIF-5a; 1.
PR051TE; PS00302; IFSA_HYPUSINE; 1.
Protein blosynthesis; Initiation factor; Hypusine; Multigene family.
MOD_RRS 52 52 HYPUSINE (BY SIMILARITY).
SEQUENCE 159 AA; 17318 MW; D3DFD223969E18E9 CRC64;
Protein biosynthesis; Initiation factor; Hypusine; Multigene family. MOD_RES 52 HYPUSINE (BY SIMILARITY). SEQUENCE 159 AA; 17363 MW; 69B7BF6322429D91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: EIF-5A SEEMS TO BE THE ONLY EUKARYOTIC PROTEIN TO HAVE AN HYPUSINE RESIDUE WHICH IS A POST-TRANSLATIONAL MODIFICATION OF LYSINE BY THE ADDITION OF A BUTYLAMINO GROUP (FROM SPERMIDINE). SIMILARITY: BELONGS TO THE EIF-5A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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15-JUL-1998 (Rel. 36, Last Sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D)
                                                                                                                                                                                                                                                                                                                                                     159 AA.
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Pred. No. 3;
4; Mismatches
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Mismatches
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80 NC-DVPHVNRTDYQLIDI 96
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AC P56336;
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NOT KNOWN BUT IT FUNCTIONS BY PROMOTING THE FORMATION OF THE FIRST
                                             -!- PTM: EIF-5A SEEMS TO BE THE ONLY EUKARYOTIC PROTEIN TO HAVE AN HYPUSINE RESIDUE WHICH IS A POST-TRANSLATIONAL MODIFICATION OF A LYSINE BY THE ADDITION OF A BUTYLAMINO GROUP (FROM SPERMIDINE).
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EMBL; AB004823; BAA20876.1; -.
InterPro; IPR001884; EIF5A_hypusine.
Pfam; PF01287; eIF-5a; 1.
PROSITE; PS00302; IF5A_HYPUSINE; 1.
Protein blosynthesis; Initiation factor; Hypusine; Multigene family.
MOD_RES 52 HYPUSINE (BY SIMILARITY).
SEQUENCE 160 AA; 17431 MW; E35BDF67185B9551 CRC64;
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43.5%; Score 43.5; DB 1; Length 160;
Best Local Similarity 50.0%; Pred. No. 3;
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STRAIN-NIGERIAN 036;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408311; CAC34752.1; -.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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                                                                                                                  Search time 285.36 Seconds
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09bh26
09bh26
09n9f2
09n9e1
09bhs1
09bhr1
09bhr1
09bhp9
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 473505 seqs, 146272329 residues
                                                                                                                January 29, 2002, 11:12:13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                  GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 summaries
                                                                                   sw model
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                               DGNCEDIPHVNEFSAIDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BHP6
Q9BHP2
Q9BH26
Q9N9E2
Q9N9E4
Q9N9E1
Q9N9E0
Q9BHS1
Q9BHS1
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Q9BHQ8
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sp_human:*
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sp_virus:*
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1: sp_archea:*
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Gaps

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STRAIN=C9-6.1;
MEDLINE=20416492; PubMed=10960173;
Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TATALN=NIGERIAN 100;
POLLBY S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 437;
                                                                                                                                                                                                                                                                                                             Length 437;
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                                                                                                  Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AJ408340; CAC34781.1; -.
NON_TER 437 437
SEQUENCE 437 AA; 50311 MW; 57D2DFEB99235EFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F35E75801A46F3BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09BH26;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                             100.0%; Score 100; DB 5;
100.0%; Pred. No. 9e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 AA.
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STRAIN-NIGERIAN 016, AND NIGERIAN 096;
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50240 MW;
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical
"Diversifying selection in domains of Plasmodium falciparum Apical
Bembrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408334; CAC34775.1;
NON_TER 1
NON_TER 437 A3, 50288 WW; F0756EE4695FFFAC CRC64;
                                                                                                                                                                                                  "Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1)."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ408312; CAC34753.1; -NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100; DB 5; Length 437;
Pred. No. 9e-09;
Mismatches 0; Indels (
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                     Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                             50356 MW; 734A74080D1BAC7F CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last snoc
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                          Plasmodium falciparum.
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STRAIN-NIGERIAN 088;
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FIRAIN=27-2.1;
MEDLINE=20416492; PubMed=10960173;
Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A.,
van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
"Molecular characterisation of Plasmodium reichenowi apical membrane
antigen-1 (AMM-1), comparison with P, falciparum AMA-1, and antibody-
mediated inhibition of red cell invasion.";
MOL Biochem. Parasitol. 109:147-156(2000).
EMBL; AJ271188; CAB97200.1; --
InterPro: IPRO03298; Apmem_Ag1.
                                                                                       MEDLINE-20416492; PubMed=10960173;

Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.;

"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P, falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";

Mol. Biochem. Parasitol. 109:147-156(2000).

EMBL; A.27.1189; CAB97197.1; -.

InterPro: IPR003298; Apmem_Ag1.
     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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PRINTS; PR01361; MEROZOITESA.
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Matches 18; Conservative
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526 AA;
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Best Local Similarity
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                                                         SEQUENCE FROM N.A.
                      NCBI_TaxID=5833;
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van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
"Molecular characterisation of Plasmodium reichenowi apical membrane
antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
mediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL. AJZ1169; CAB97181.1;
DinterPro; IPR003299; Apmem_A91.
Pfam; PF02430; AMA-1: 1.
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"Molecular characterisation of Plasmodium reichenowi apical membrane antiqen-I (AMA-I), comparison with P. falciparum AMA-I, and antibodymediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL, AJ71177; CAB97189.1;
DinterPro: IPR001298; Apmem_Agi.
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NCBI_TaxID=5833;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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Pred. No. 1.1e-08;
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MEDLINE=20416492; PubMed=10960173;
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Matches 18; Conservative
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STRAIN-WIGERLAN 034B;
POLID4S S.D., Conway D.J.;
Polleys S.D., Conway D.J.;
Polleys S.D., Conway D.J.;
Polleys S.D., Conway D.J.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; A1408309; CAC34750.1;
NON_TER 437 437
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-NIGERIAN 044;
POLISY S.D., CONWAY D.J.;
Polisy S.D., Conway D.J.;
Polisy S.D., Conway D.J.;
Polisy S.D., Antigen in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; _AJ408314; CAC34755.1; -.
                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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NCBI_TaxID=5833;
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Pred. No. 6.3e-08;
0; Mismatches 1; Indels
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437 AA; 50232 MW; BA3061373049C9CE CRC64;
                                                   17, Last sequence update)
17, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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APICAL MEMBRANE ANTIGEN I (FRAGMENT).
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 PRELIMINARY;
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01-JUN-2001 (
01-JUN-2001 (
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                                                                                                                                                                   STRAIN=25-6.1;

MEDLINE=20416492; PubMed=10960173;

Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A.,

Van der Wel A., Corum D.L., Sanni A., Thomas A.W.;

Wolecular characterisation of Plasmodium reichenowi apical membrane
antigen 1 (AMA-1), comparison with P, falciparum AMA-1, and antibody-
mediated inhibition of red cell invasion.";

EMBL, AJZ71189; CABSTZ01.1;

EMBL, AJZ71189; CABSTZ01.1;

FRIE, PRO2430; AMA-1;

PERM: PF02430; AMA-1;

PRO2430; PRO25017ESA.
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STRAIN-NIGERIAN 002;
PD11ey S.D. Conway D.J.;
Diversifying selection in domains of Plasmodium falciparum Apical
Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408300; CAC34741.1;
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 526;
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NCBI_TaxID=5833;
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                             Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN I (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 100; DB 5;
Pred. No. 1.1e-08;
; Mismatches 0;
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Pred. No. 6.3e-08;
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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100.0%; Pr
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Best Local Similarity 94.4
Matches 17; Conservative
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Best Local Similarity
Matches 18; Conserv
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Last sequence update) Last annotation update)

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RESULT Q9BHR5

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                                                                 SEQUENCE FROM N.A.
STRAIN=NIGERIAN 050;
POLICY S.D., Conway D.J.;
Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408317; CAC34758.1; -.
NON_TER 437 437
SEQUENCE 437 A43 50144 MW; 991DB6652BD8134F CRC64;
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                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                 Length 437;
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Best Local Similarity 94.4%; Pred. No. 6.3e-08;
Matches 17; Conservative 0; Mismatches 1; Indels
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O9BHQB;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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Search completed: January 29, 2002, 11:12:13 Job time: 769 sec (Orazu) NNALB ZOAG ZIHT

Pinus radiata cell Chlamydia pneumoni Rhoptry membrane a T cell antigen rec

epidermidis ope 6-Transmembrane T cell antigen rec Acetobacter xylinu Murine IL-2R gamma

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S. epidermidis ope
Human colon cancer
Plant SDF encoded
Plant SDF encoded
Arabidopsis thalia
Plant SDF encoded

Proteinase K varia Proteinase K varia S.thermophilus exo Chicken GalNAC-alp

Human adenosine nu S.thermophilus exo

Corynebacterium gl C glutamicum prote Natural resistance

Cenarchaeum symbio TCR beta V-N-J reg TCR beta V-N-J reg

Enterococcus

ALIGNMENTS

Enzyme EPS1 which Amino acid sequenc Proteinase K varia

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein: CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen, Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum AMA-1 antigenic epitope, P601.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                           AAB25391
AAY3566
AAY66908
AAY66908
AAY66908
AAR63034
AAR3234
AAR3234
AAR32470
AAR2477
AAR2477
AAR24715
AAR2495
AAR2495
AAR2495
AAR3621
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AAY90913
AAB15472
AAB15474
AAY00065
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 Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2000.
AAY70293;
 RESULT
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Recombinant vaccin
Rhoptry membrane a
Plasmodium falcipa
Plasmodium falcipa
Plasmodium vivax 6
Plasmodium knowles
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Novel human G-prot
Novel human G-prot
Plasmodium falcipa
                                                                                                                 (without alignments)
4.290 Million cell updates/sec
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                                                                                             January 29, 2002, 10:21:48; Search time 310.82 Seconds
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**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1981_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA1991_DAT:**

**Sinssy_gedata_geneseq_geneseqp_AA19
             4.5
Compugen Ltd.
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             GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAR27532
AAR68840
AAR10935
AAR10551
AAY966884
AAY93140
AAY93141

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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4597

Result õ Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of

plasmodium falciparum life cycle

US DEPT HEALTH & HUMAN SERVICES.

NAT INST IMMUNOLOGY

(NAIM-) (USSH)

Hasnain SE;

Shi YP,

Lal AA,

WPI; 2000-237654/20.

N-PSDB; AAZ51336.

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apical membrane antigen-1 (AMR-1) of the assual blood stage of plasmodium falciparum. It is used in the construction of recombinant protein Coc/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes (SSP-2). Hiver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete of the life cycle of P. falciparum. CDC/MIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/MIIMALVAC-1 vaccine has malarial infections. Anti-CDC/MIIMALVAC-1 unibodies can be used for hard-ning in it, in it, in it.
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                           Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                               present sequence is the antigenic epitope P601, derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                   plasmodium falciparum life cycle
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                                                                                              Claim 2; Page 16; 52pp; English.
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Best Local Similarity
Matches 18; Conserv
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-156 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treamment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhoptry membrane antigen of Plasmodium falciparum - used for producing antibodies and in immunisation, diagnostic and treatment methods for malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 102; DB 21;
100.0%; Pred. No. 5.3e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria; rhoptry membrane antigen-1; antibodies.
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                                                                                                                                                                                     Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP91632 standard; protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 gnaekydkmdepqhygks 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum D10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SARA ) SARAMANE PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                          350 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Recombinant poxvirus contg. Plasmodium DNA in non-essential region - useful in vaccines against malaria and for prodn. of Plasmodium immunogens
                                                                                                                                                                                                                              Plasmodium falciparum AMA-1 gene; recombinant poxvirus; multicomponent multistage malarial vaccines; immunogens; malaria diagnosis.
                                                                                                                                                                                     Plasmodium falciparum AMA-1 gene protein.
                                                           AAR68840 standard; Protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 5; 183pp; English.
                                                                                                                                                                                                                                                                                                               Plasmodium falciparum (3D7).
                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US06652.
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94US-0257073.
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Taisne C, Paoletti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-036113/05.
N-PSDB; AAQ80910.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1993;
09-JUN-1994;
                                                                                                                                             24-AUG-1995
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                                                                                                      AAR68840;
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                                                         RMA-1 can generate an immune response to malaria, and antibodies which can inhibit growth of the parasite. RMA-1 initially has mol. wt. 80 kD.
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the Plasmodium falciparum AMA1 antigen. cDNA encoding it was cloned into vaccinia donor plasmids a before being inserted into the vaccinia virus to be used in vaccine to stimulate an antimalarial immunological response, or for in virco prodn. of gene prods. for use as immunogens. As plasmodium genes are conserved among P. falciparum strains, they are widely
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                                                                                                                                                                                     622;
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Pred. No. 3.1e-07;
0; Mismatches 1; Indels
                                                                                                                                                                                     Length
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                                                                                                                                                                                   100.0%; Score 102; DB 10; 100.0%; Pred. No. 9.9e-09;
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                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             AAR27532 standard; Protein; 622 AA.
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                 Claim 1; Fig 3; 46pp; English.
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92US-0852305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Rest Local Similarity 94.4
17: Conservative
                                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                         622 AA;
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18-MAR-1992;
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                                                                                                                         Sequence
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Tine JA;

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Gaps
AAQ80910 encodes AAR68840 the P. falciparum AMA-1 gene product. New recombinant poxviruses containing either the SERA, ABRA, Pfhsp70, AMA-1, Pfs25, Fish, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1, MSA-1 (N-terminal p83 or C-terminal p942) genes, or a combination of these in non-essential regions of their genomes are claimed. These poxviruses (pref. with a virulence reducing genomic deletion or disruption) can be used as vaccines against malaria and for the produ. Of Plasmodium immunogens. These viruses provide multicomponent, multistage vaccines due to their expression of sporozite, liver stage, blood stage and sexual stage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium vivax 66kD merozoite antigen protein partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                         Score 93; DB 16; Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.1e-07;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                         91.28;
94.48;
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                                                                                                                                                                         Plasmodium merozoite antigen proteins and DNA sequences - useful in vaccine prodn., anti-malarial drug design, and in diagnostics
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                                                                                                                                                                                                                                                                                                                                             DB 12; Length 489;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium knowlesi 66kD merozoite antigen protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium merozoite antigens; malaria vaccine
                                                                                                                                                                                                                                                                                                                                                     ed. No. 0.11;
Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 59;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10551 standard; Protein; 563 AA.
                                                                                                                                                                                                     Disclosure; fig 1; 31pp; English
                                                                                                                                                                                                                                                                                                                                           57.8%;
62.5%;
                                                                 90US-0483516.
                                                                                   90US-0483516.
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                                                                                                       (USSH ) NAT INST OF HEALTH.
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                               NAEKYDKMDEPQHYGK 17
                                                                                                                                           WPI; 1991-044381/06.
N-PSDB; AAQ10869.
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                               489 AA;
                                                                                                                                                                                                                                                                                            See also AAQ10418
         Plasmodium vivax.
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                                                                22-FEB-1990;
                                                                                   22-FEB-1990;
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                           US7483516-A
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                                               15-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US7483516-A.
                                                                                                                         Waters AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waters AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10551;
                                                                                                                                                                                                                                                                                                               Sequence
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The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in synovial membranes of rheumatoid arthritis patients
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor; Vbeta chain; autoantigen; immunological tolerance.
                                                                                       This protein is encoded by a recombinant DNA molecule comprising the complete P.knowlesi merozoite antigen gene and e.g. a pUC19 or vaccinia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. It is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells.
Plasmodium merozoite antigen proteins and DNA sequences – useful in vaccine prodn., anti-malarial drug design, and in diagnostics
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                                                                                                                                                                                                                                                                                                                            Length 563;
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                                                                                                                                                                                                                                                                                                                      Score 56; DB 12;
Pred. No. 0.42;
4; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY66884 standard; peptide; 16 AA
                                                       Disclosure; fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                      54.9%;
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98JP-0328761.
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514 dkydkmdqaeaygkt 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-086978/07
N-PSDB; AAZ96614.
                                                                                                                                                                                                                                                                                                                                           Similarity 9; Conserv
                                                                                                                                                                                                                                                                  563 AA;
                                                                                                                                                                                                                            See also AAQ10869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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14-OCT-1998;
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Best Local 9
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RESULT AAY9314

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receptor (GPCR) genes and their encoded proteins. This sequence represents the protein sequence of a human GPCR. The DNAs and proteins are used for the treatment, prevention and diagnosis of disorders of the nervous system. The proteins and its fragments are also promoters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                                                                                                                                                                 G-protein coupled receptor; human; bovine; nervous system disorder;
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19;
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                                                                                                                                                                Novel human G-protein coupled receptor #2.
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                        AAY93141 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB18187 standard; Protein; 508 AA.
                                                                                                                                                                                                                                       rat; mouse; somatostatin excretion
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soya M, Kitada C;
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57.18;
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99JP-0060030.
99JP-0106812.
99JP-0166672.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 196 AA;
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                                                                                                                                                                                                                                                                                                                            WO200029441-A1
                                                                                                                                                                                                                                                                                   Homo sapiens.
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08-MAR-1999;
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04-AUG-1999;
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                                                                                                                    06-DEC-2000
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                                                                    AAY93141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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AAY93141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the isolation of novel G-protein coupled receptor (GPCR) genes and their encoded proteins. This sequence represents the protein sequence of a human GPCR. The DNAs and proteins are used for the treatment, prevention and diagnosis of disorders of the nervous system. The proteins and its fragments are also promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukusumi S;
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                                                                                                                       Gaps
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18;
                                                                 Score 45; DB 21; Length 16;
Pred. No. 0.58;
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                                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human G-protein coupled receptor #1.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rat; mouse; somatostatin excretion.
                                                                                                                                                                                                                                                                                                                            AAY93140 standard; Protein; 180 AA
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osoya M, Kitada C;
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                                                                    44.18;
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99JP-0221640
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
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4 assydslngpghf 16
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Best Local Similarity
Matches 8; Conserv
                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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16
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04-AUG-1999;
14-SEP-1999;
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08-MAR-1999;
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Fukusumi S;

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Length 196;

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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).

(I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyvolonal antisera or a monoclonal artibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many drugs. AAA70078 to AAA70287 and AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                               Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection
                                                                                                                                                                                                                                                                                        Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 108-110; 577pp; English.
                                                                                                                                                                                                                                                                                      Gardner M,
                                                                                                                                        98US-0107131
                                                                                                    99WO-US26796
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                            VENTER J C.
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                  WO200025728-A2
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Gaps
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2
                Pred. No. 55;
    Score 43;
    42.28;
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                                             2 NAEKYDKMDEPQHYGKS 18
Query Match
Best Local Similarity 47.1
Matches 8; Conservative
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AAG82140 standard; Protein; 134 AA. (first entry) 03-SEP-2001 AAG82140;

S. epidermidis open reading frame protein sequence SEQ ID NO:1374. Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.

Staphylococcus epidermidis

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CI) and (II) can have antibacterial activity and therefore can be used to reaction in the nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the containing them which are used to produce hosts cells which express the containing them which are used to produce sacis) may then be containing them which are used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53091 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polyputcleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to sequence listing of the present specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing of the present correction, however the sequence listing of the present specification, however the sequence are given in the disclosure for SEO ID NO:4454 so even to sequences are present for SEO ID NO:4455 to 4472, Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -Claim 18; Page 389; 2188pp; English. 09-NOV-2000; 2000WO-US30782. 99US-0164258 (GLAX) GLAXO GROUP LTD. WPI; 2001-316495/33. N-PSDB; AAH52990. 134 AA; WO200134809-A2 09-NOV-1999; Kimmerly WJ; Sednence NA X G X X B X X B X X B B X X B X

Gaps . 0 DB 22; Length 134; 19; 2; Indels Score 42; DB 2 Pred. No. 19; 2; Mismatches 5 41.28; 60.08; 6; Conservative Local Similarity 6 YDKMDEPQHY 15 Query Match . Matches δŏ

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AAW97359 standard; Protein; 592 AA. 12-MAY-1999 (first entry) |||:: | || 64 ydkinhpshy 73 AAW97359; AAW97359

alleyy astuminaturing the cerebilar degeneration; Alzeiner disease; Parkinson's disease; multiple sclerosis; amylotrophic lateral sclerosis; head injury damage; meurological abnormality; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischaemia repertusion injury; cardiovascular disease; kidney disease; liver disease; ischaemic injury; myocardial infarction; hypotension; hypotension; AIDS; myelodysplastic syndrome; hematological abnormality; aplastic anaemia; male pattern baldness; 6-Transmembrane protein; SDR2; cancer; inflammation; autoimmunity; allergy; asthma; rheumatoid arthritis; CNS inflammation; A 6-Transmembrane protein designated SDR2.

infection

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12-JAN-1999;
01-NOV-1999;
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20-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designated SDR2. SDR2 polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the SDR2 gene, and can diseases associated with SDR2 protein imbalance by determining SDR2 polypeptide expression levels. SDR2 polypeptides can be used to screen for agonists and antaqonists and to produce antibodies. Diseases diagnosed, prevented and treated include: cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, multiple sclenosis, amylotrophic lateral sclenosis, head injury damage, and other neurological abnormalities, septic shock, sepsis, stroke, cardiovascular disease, kidney disease, liver disease, ischaemic injury, cardiovascular disease, kidney disease, liver disease, ischaemic injury, myocardial infarction, hypotension, hypertension, AllSS, myelodysplastic syndromes and other hematological abnormalities, apastic anaemia, male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pattern baldness, and bacterial, fungal, protozoan and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signaling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a 6-Transmembrane protein polypeptide
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Pred. No. 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 6; 19pp; English.
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53.3%;
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97US-0055375.
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                                                                                                                                                                                                                                                                                                                 Albone EF, Kikly KK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-134642/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592 AA;
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                    Homo sapiens
                                                                                                                                                                                                   16-DEC-1997;
                                                                                                                                                                                                                        12-AUG-1997;
                                                                                                                                                     06-AUG-1998;
                                                              EP897979-A2
                                                                                                           24-FEB-1999
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and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monteery pine). The protein sequences are involved in cell signaling. The polynucleotide and protein sequences are involved in cell signaling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers or enhance altered fruit ripening and senescence of leaves and flowers or enhance conficuations can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life organs providing fruit and vegetables which have a longer shelf life constitutes plants. Other wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoldosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 40;
5; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 326-327; 527pp; English.
                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                             Strabala TJ, Nieuwenhuizen NJ;
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46.28;
                                                                          99US-0228986.
99US-0162866.
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97FR-0014673.
11-JAN-2000; 2000WO-US00724
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Best Local Similarity 46.2
Matches 6; Conservative
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| 124 kydqladpkfhgk 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to external signals -
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C ARY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae.

C ARY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX31990) of Chlamydia pneumoniae.

C ARY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX34590) of Chlamydia pneumoniae.

C C ARY34584-Y35879 represent the proteins encoded by all the open reading frames of the C. pneumoniae genome (see AAX34584-Y35879) can be used in munogenic compositions as vaccines. Vectors containing C. pneumoniae compositions as vaccines. Vectors containing C. pneumoniae compositions as vaccines as immunogenic compositions, epitope of C. pneumoniae.

C epitope of C. pneumoniae.
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Search completed: January 29, 2002, 10:21:49 Job time: 425 sec

4 EKYDKMDEPQHYG 16 :||| : | ||| 91 kkydalaapfhyg 103

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Ouery Match

40.2%; Score 41; DB 20; Length 294;
Best Local Similarity 53.8%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 4; Indels

Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

Sequence Sequence Sequence

Sequence

Appl Appl Appl Appli

Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence

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GENERAL INCORMATION:
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN 1994
PLOR APPLICATION: 424
PROR APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PROR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRICK APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRICK APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                       US-08-895-590-2
US-08-649-991-41
US-08-649-991-45
US-08-140-466-5
US-08-13-288B-18
US-08-313-288B-18
US-08-313-255-6
US-08-272-255-9
US-08-94-268-5
PCT-US95-08565-6
                                                                                                                                                                                                                                                                                                           US-08-836-567-8
US-08-202-389-27
PCT-US92-00282-6
US-08-202-389-12
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMUNICATION INFORMATION:
TELEPAN: (212) 840-333
FELERA: (212) 840-312
TELEX: (212) 840-312
TELEX: (212) 840-312
TELEX: (212) 840-312
TELEX: (212) 840-312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 amino acids
  2439
2516
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5933
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
    COUNTRY: UN
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US-08-257-073-9
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5, Appli
96, Appli
4, Appli
3, Appli
18, Appli
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9, Appl
9, Appl
9, Appli
                                                                                                                                                                                (without alignments)
3.041 Million cell updates/sec
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                                                                                                                                                      Search time 133.18 Seconds
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Sequence 69,
Sequence 19,
Sequence 19,
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Sequence
Sequence
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Sequence
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-257-073-9
US-08-991-813-2
US-08-991-813-2
US-08-91-813-2
US-08-31-219-19
US-08-912-314A-19
US-08-912-314A-19
US-08-183-438-7
US-08-183-81-28
US-08-183-91-56
US-08-837-828-56
US-08-837-828-56
US-08-935-268-56
US-08-935-268-56
US-08-935-268-56
US-08-935-268-56
US-08-935-268-56
US-08-935-268-56
US-08-935-160-96
US-08-938-34-10151A-56
US-08-938-34-18
US-08-938-54-18
US-08-938-54-18
US-08-938-54-18
US-08-938-534-18
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US-08-938-534-18
US-08-467-822-33
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US-08-467-822-33
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                                                                                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      January 29, 2002, 10:24:08

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                 102
1 GNAEKYDKMDEPQHYGKS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                               US-09-763-397A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Score

Result Ş TOPOLOGY: linear MOLECULE TYPE: peptide

Sequence

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Sequence 69, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OFT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                           CDNA AND
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Pred. No.
                                                                                                                                                                                                                                                                                                      APPLICALL..

FILING DATE:
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-193
ATORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800

"FIEFPAX: 212-751-6849
                                                                                                                                                                                                                                                                         SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
     LEONARD, WARREN J.
VENTION: MURINE IL-2R
VENTION: USES THEREOF
                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVE.
CITY: NEW YORK
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: MURINE INDIVIDUAL ISOLATE: IL-2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.2%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 42792
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FI
STREET: 345 PARK AVE.
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GNAEKYDKMDEPQHYG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: UNKNOWN MOLECULE TYPE: DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEW YORK
                                                                                                                                                                   USA
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                                                                                                                                                                                   10154
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PCT-US94-02891-69
                                                                                                                                                STATE: NE
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                                                                      Score 93; DB 1; Length 628;
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 592, 39;
                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ALBONE EARL
APPLICANT: KIKLY, KRISTINE
APPLICANT: KIKLY, KRISTINE
TITLE OF INVENTION: HUMAN SDR2 CDNA CLONE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FASTEEC FOR WINGOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,813
FILING DATE: 16-DEC-1997
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.2%; Score 42; DB
53.3%; Pred. No. 39;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/055,375
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTITA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70281
TELECHONE: 610-407-0701
                                                                                                                                                                                                                                                                 Sequence 2, Application US/08991813
Patent No. 6090579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-424-224-2
; Sequence 2, Application US/08424224
; Patent No. 5912173
; GENERA®, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH : 592 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                  91.2%;
ilarity 94.4%;
Conservative
                                                                                                                                                               576 GNAEKYDKMDEPQDYGKS 593
                                                                                                                                         1 GNAEKYDKMDEPQHYGKS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.3
Matches 8; Conservative
; FRAGMENT TYPE: internal
US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 EKYDVTDSPKNIGGS 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 EKYDKMDEPQHYGKS 18
                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
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CLASSIFICATION:
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US-08-991-813-2
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Gaps

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APPLICANT: Zohar, Y.
APPLICANT: Rivier, J.
APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Sherwood, N.
APPLICANT: Gothilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 1; Length 90;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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COUNTEY.

2 IP: 10036-2711

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC COMPALIDLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/912,314A

FILING DATE: 30-JUN-1997

CLASSIFICATION : 514

PRIOR APPLICATION NUMBER: 08/341,219

FILING DATE: 05-DEC-1994

ATTOMEX/AGENT INFORMATION:

WANTE COUNTEY AFFORMATION:
                                          NAME: Coruzzi,, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE TOOKET NUMBER: 839-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPA: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8399-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-912-314A-19
; Sequence 19, Application US/08912314A
; Patent No. 6210927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                              38.2%;
50.0%;
                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity bureases 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 EKYDKMDEPQHY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: |:| ||||:
48 KEVDQMAEPQHF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  2
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US-08-341-219-19
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APPLICANT: Rivier, J.
APPLICANT: Powell, J.
APPLICANT: Powell, J.
APPLICANT: Schilf, Y.
APPLICANT: Gothilf, Y.
TITLE OF INVENTION: Compounds and Methods For Controlling
TITLE OF INVENTION: Reproduction in Fish
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 5; Length 369;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                     2026-4061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/341,219
05-DEC-1994
                                                                                                                                                         CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 2026-406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08341219
Patent No. 5643877
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.2%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: MURINE
INDIVIDUAL ISOLATE: IL-2R
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                   TELERA: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4200BNCE CHARACTERISTICS: LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GSSQQWSKWSQPVHWG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-02891-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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Gaps

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ADDRESSEE:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR TITLE OF INVENTION: PRODUCING THE SAME NUMBER OF SEQUENCES: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                        Score 39; DB 4; Length 90;
Pred. No. 16;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM COMPATIble OPERATING SYSTEM: MS-DOS SOFTWARE: WORDERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2
Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/666,367B
FILING DATE: August 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08666367B Patent No. 5854042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: G. gallus (chicken)
US-08-666-367B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                        38.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                    Query Match 38.2
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.2
Best Local Similarity 66.7
Matches 8; Conservative
; TOPOLOGY: unknown

) MOLECULE TYPE: peptide

); HYPOTHETICAL: NO

US-08-912-314A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 EKYDKMDEPQHY 15
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48 KEVDQMAEPQHF 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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RESULT

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Sequence 7, Application US/09143438
Patent No. 6218161
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR TITLE OF INVENTION: PRODUCING THE SAME NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Sequence 2, Application US/08597236

Patent No. 5733770:
GENERAL INFORMATION:
APPLICANT: MOLLET, Beat
ITILE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                       ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4
Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,438
FILING DATE: August 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/666,367
FILING DATE: August 19, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: G. gallus (chicken)
US-09-143-438-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
اتامه 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 EKYDKMDEPQHY 15
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PRY: U.S.A.
20006
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U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: AN CLASSIFICATION:
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US-08-637-823B-28
Sequence 28, Application US/08637823B
Sequence 28, Application US/08637823B
Patent No. 6184031
Sequence 28, Application US/08637823B
Sequence 28, Application US/08637823B
THEORIES OF INVENTION:
TITLE OF INVENTION: DNA SEQUENCES THAT ENCODE A NATURAL
TITLE OF INVENTION: BEISTANCE TO INFECTION WITH INTRACELLULAR PARASITES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Ave
CITY: Hackensack Ave
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Pred. No. 1.2e+02;
1; Mismatches 5; Indels
                                              Score 39; DB 1; Length 484;
Pred. No. 97;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/637,823B
FILING DATE: 05/08/96
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: Blood
CELL TYPE: B-cell precursor
CELL LINE: 70/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%;
53.8%;
                                              38.2%;
ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.8-
F. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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| GGAESYSKSTDPQ 13
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U.S.A.
                                                 Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CLONE: MNramp-2
US-08-637-823B-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE PETENTIN SISTEM: E-LUCYMS-LUCS
SOFTWARE PETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: W108 #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION A.435
PRIOR APPLICATION DATE: 04.57,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FAILURY DATE: 30256
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
FILING DATE:
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08746682A
Patent No. 5786184
GENERAL INFORMATION:
APPLICANT: MOLLET, Franscesca
APPLICANT: MOLLET, Bat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.2%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 484 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                    : 484 amino acids
amino acid
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GNAEKYDKMDEPQHYG 16
                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-597-236-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New YC STATE: New 1 COUNTRY: U.S ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-08-746-682A-2

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42.1%; Pred. No. 1.3e+02;
Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Matthes, David
APPLICANT: Matthes, David
APPLICANT: O'Connor Timothy
ITILE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: SCIENCE & TECHNOLOGY LAW GROUP 268 Bush Street, Suite 3200
                                                                                                                       US/08/121,713D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Sequence 56, Application US/08835268
: Patent No. 5807826
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: B94-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : | | |:|:| |:
122 GNPKCWKIDGSDDPKHRGR 140
                                                                                                                     APPLICATION NUMBER: US/08
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GNAE--KYDKMDEPQHYGK 17
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 441 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 37.3
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 268 buc...
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                                  APPLICANT: Kridi, J.
APPLICANT: Kridi, J.
APPLICANT: Dehesh, K.
APPLICANT: Dehesh, K.
TITLE OF INVENTION: Engineering Plant Thioesterases For TITLE OF INVENTION: Altered Substrate Specificity.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Matthes, David
APPLICANT: Horley, David
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
WINBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 2;
Pred. No. 1e+02;
3; Mismatches
                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SCIENCE & TECHNOLOGY LAW GROUP 268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,845D
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa = Lys or Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 56, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INPERMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.3%;
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Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 355 residues
amino acid
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CITY: San Francisco
STATE: CA
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GENERAL' INFORMATION:
                                                                                                                                                                                                                                    Davis
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                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                         Query Match 37.3%; Score 38; DB 1; Length 441; Best Local Similarity 42.1%; Pred. No. 1.3e+02; Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 441;
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Pred. No. 1.3e+02;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/060,692

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.

REFERENCE/DOCKET NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/09060692
Sequence 56, Application US/09060692
Patent No. 5938065
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Matches, David
APPLICANT: Matches, David
APPLICANT: Matches, David
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
CITY: San Francisco
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-268-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
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|| : | | | :| | :
|12 GNPKCWKIDGSDDPKHRGR 140
                                                                                                                                                                                                                                                                                                  1 GNAE--KYDKMDEPQHYGK 17
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TELEFAX: (415) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.3
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-060-692-56
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-060-692-56
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Search completed: January 29, 2002, 10:24:09 Job time: 515 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein . protein search, using sw model

; Search time 144.96 Seconds January 29, 2002, 10:26:43 Run on:

(without alignments)
9.459 Million cell updates/sec

US-09-763-397A-17

102 1 GNAEKYDKMDEPQHYGKS 18 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apical membrane an	66K merozoite surf	apical membrane an	hypothetical prote			probable splicing	hypothetical prote	outer membrane ush	hypothetical prote	M protein precurso	ribonuclease inhib	methionine aminope	vacuolar ATP synth	methionine aminope	methionine aminope	hypothetical prote	att	L1 protein - human	apical membrane an	pectic enzyme secr	hypothetical prote	probable glycine d	hypothetical prote	hypothetical prote				
SUMMARIES	ID	A32499	C44986	D44986	B44986	A44986	A39238	A44944	T34410	E71620	B42983	T40312	T29682	A49891	T24866	860797	C69973	A81531	T41656	F86616	E72008	D83136	S54484	JE0295	A44964	B47021	D64527	S62435	338	T32452
	DB	7	~	~	~	7	~	7	~	~	~	7	~	Н	~	N	-	~	~	7	~	7	-	7	7	~	7	~	~	7
	Query Match Length	622	622	622	622	622	563	562	371	508	188	379	384	835	971	99	91	266	282	291	291	294	384	203	558	712	813	1017	1110	1635
œ	Query	100.0	97.1			88.2		48.0	43.1	•	•	41.2	41.2	41.2	41.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2
	Score	102	66	66	93	06	26		44	43	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
	Result No.	1	7	e	4	2	9.	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

hypothetical prote	hypothetical prote	bib protein - frui	molybdopterin-cont	nifu protein homol	outer membrane pro	interleukin-2 rece	eha protein VC1798	hypothetical prote	sensor histidine k	hypothetical prote	cytochrome-c3 hydr	hypothetical 129.5	gonadoliberin prec	hypothetical prote	
H70034	T27533	66960S	G81444	G81441	A43592	149280	B82157	T17868	F72324	C64377	S08199	T40778	RHMSG	T19724	D86272
7	7	7	~	7	7	۲,	~	7	~	7	7	~	Н	7	7
170	687	700	838	323	344	369	383	443	489	206	564	973	90	148	155
39.7	39.7	39.7	39.7	39.2	39.2	39.2	39.2	39.2	39.2	39.2	39.5	39.2	38.2	38.2	38.2
40.5	40.5	40.5	40.5	40	40	40	40	40	40	40	40	40	39	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

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apical membrane antigen 1 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum.
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Cybre: 12-ort-1989 #sequence_revision 12-oct-1989 #text_change 09-Jun-2000 Cybre: 12-ort-1989 #sequence_revision 12-oct-1989 #sext_change 09-Jun-2000 Cybression: A32499 #sequence_revision 12-oct-1989 #sequence_revision 12-oct-1989 #sequence_reson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; A Mol. Cell. Biol. 9, 3151-3154, 1989 A; Fitle: Integral membrane protein located in the apical complex of Plasmodium falcip A; Accession: A32499; MUID:89384584 A; Accession: A32499; MUID:89384584 A; Accession: A32499; MID:89384584 A; Molecule type: DNA; mRNA A; Molecule type: DNA; Molecul

ö Gaps ö Length 622; Indels Score 102; DB 2; Pred. No. 1.8e-08; ; Mismatches 0; 0; Mismatches 100.0%; 100.0%; Query Match 100. Best Local Similarity 100. Matches 18; Conservative

1 GNAEKYDKMDEPQHYGKS 18 δ

571 GNAEKYDKMDEPQHYGKS 588 g

7 C44986

apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain FCR 3) C;Species: Plasmodium falciparum C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000

C;Accession: C44986
R;Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Blochem. Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate
A;Reference number: A44986; MUID:91101665
A;Accession: C44986

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: DNA A;Residues: 1-622 <THO> A;Cross-references: GB:M34554 C;Keywords: membrane protein; surface antigen

Gaps ö 97.1%; Score 99; DB 2; Length 622; 94.4%; Pred. No. 5.4e-08; ive 1; Mismatches 0; Indels Query Match 97.1 Best Local Similarity 94.4 Matches 17; Conservative

ö

1 GNAEKYDKMDEPQHYGKS 18 δ

571 GNAEKYDKMDQPQHYGKS 588 q

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A44944
apical membrane antigen 1 precursor - Plasmodium fragile
C;Species: Plasmodium fragile
C;Species: Plasmodium fragile
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: A44444
R;Peterson, M.G.; Nguyen-Dlnh, P.; Marshall, V.M.; Elliott, J.F.; Collins, W.E.; Ande Mol. Blochem. Parasitol. 39, 279-284, 1990
A;Title: Apical membrane antigen of Plasmodium fragile.
A;Reference number: A44944; MUID:90205978
                                                                                                                                                                                                                                              A39238
66K merozoite surface antigen precursor - Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C;Accession: A39238
R;Waters, A.P.; Thomas, A.W.; Deans, J.A.; Mitchell, G.H.; Hudson, D.E.; Miller, L.H.
J Biol. Chem. 265, 17974-17979, 1990
A;Title: A merozoite receptor protein from Plasmodium knowlesi is highly conserved an A;Reference number: A39238; MUID:91009268
A;Accession: A39338
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-oct-1999
C;Accession: T34410
R;Du, Z.; Goela, D.
Submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid F07E5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Length 622
                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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  Score 90; DB 2; I
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 2;
Pred. No. 0.39;
4; Mismatches
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                                                  1; Mismatches
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  88.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%;
60.0%;
                                                                                                                             1 GNAEKYDKMDEPQHYGKS 18
                                                  16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563 <WALN
A;Cross-references: GB:J05631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 60.0
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514 DKYDKMDQAEAYGKT 528
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A;Cross-references: GB:M29898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 EKYDKMDEPQHYGKS 18
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514 DKYDKMEQADGYGK 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
The 8; Conserv?
  Query Match
Best Local Similarity
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A:Molecule type: DNA
A:Residues: 1-562 <PET>
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Matches 9
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C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 28.Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: A44986
R:Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Blochem, Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti
A;Reference number: A44986; WUID:91101665
                                                                 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain 7GB)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 28 Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: D4986
R;Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 268-288, 1990
A;Title: Analysis of variation in PP83, an erythrocytic merozoite vaccine candidate anti
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Mol. Blochem. Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti
A;Reference number: A44986; MUID:91101665
A;Accession: B44986
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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5e-07;
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Pred. No. 5e-07;
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Pred. No. 5e-07
0; Mismatches
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A;Cross-references: GB:M34553.
C;Keywords: membrane protein; surface antigen
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A;Cross-references: GB:M34552
C;Keywords: membrane protein; surface antigen
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A, Residues: 1-622 <THO>
A, Cross-references: GB:M34555
C; Keywords: membrane protein; surface antigen
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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A;Cross-references: EMBL:AL078627; PIDN:CAB44757.1; GSPDB:GN00067; SPDB:SPBC365.05c A;Experimental source: strain 972h-; cosmid c365 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U64848; PIDN:AAB04891.1; GSPDB:GN00023; CESP:C50E3.13
A;Experimental source: strain Bristol N2; clone C50E3
                                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29682
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C;Species: Bscherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49891
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                                                                                                                                                                                             probable splicing factor - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                C;Accession: T40312
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, submitted to the EMBL Data Library, June 1999
A;Reference number: 221920
A;Accession: T40312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Superfamily: Arabidopsis thaliana hypothetical protein F16L2.160
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submitted to the EMBL Data Library, July 1996
A; Description: The sequence of C. elegans cosmid C50E3.
A; Accession: T29682
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2; Mismatches
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Pred. No.
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Pred. No.
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50.0%;
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llarity 50.0%;
Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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175 ERYEKLDELQNKGE 188
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A; Introns: 13/3; 47/3; 79/3
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                                                    YDKMDEPQHYGK 17
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-384 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PFB0225c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: E71620
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
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C.Species: Lactobacillus casei
C.Species: Lactobacillus casei
C.Species: Lactobacillus casei
C.Accession: B4298
R:Heaton, M.P.; Neuhaus, F.C.
J. Bacteriol. 174, 4707-4717, 1992
A:Title: Biosynthesis of D-alanyl-lipoteichoic acid: cloning, nucleotide sequence, and 4.8 Reference number: A42983; MUID:92325063
A:Reference number: A42983
A:Residues: preliminary
A:Molecule type: DNA
A:Residues: 1-188 cHEA>
A:Residues: 1-188 cHEA>
A:Cross-references: GB:M83993; NID:9149534; PIDN:AAA25235.1; PID:9149536
A:Rocs - reference extracted from NCBI backbone (NCBIN:108162), NCBIP:108166)
C:Reywords: transmembrane protein
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                                                                                            A;Cross-references: EMBL:U80837; PIDN:AAB37904.1; GSPDB:GN00020; CESP:F07E5.5
A;Experimental source: strain Bristol N2; clone F07E5
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A:Introns: 76/3; 134/3; 167/3; 227/2; 276/1; 293/1; 326/1
                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Regidues: 1-371 <DUZ>
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Pred. No. 42;
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21;
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Pred. No.
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47.1%;
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53.8%;
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200 NEQENNKMDENQHIDKN 216
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Best Local Similarity 53.8
Matches 7; Conservative
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Matches 5; Conserva
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Matches 8; Conserv
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A; Accession: T34410
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Gaps

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Length 68; 3; Indels

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Score 41; DB 2 Pred. No. 10; 1; Mismatches

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A;Reference number: S60784; MUID:95198537
A;Accession: S60797
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-68 <WHA>
A;Cross-references: EMBL:U11932; NID:9533541; PIDN:AAA99548.1; PID:91235802
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Superfamily: M5 protein
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Job time: 655 sec
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Best Local Similarity 63.6%;
Matches 7; Conservative
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560797
M protein precursor - Streptococcus pyogenes (serotype M17) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M17
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S60797
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
    R:Schifferli, D.M.; Alrutz, M.A.
J. Bacteriol. 176, 1099-1110, 1994
A. Bacteriol. 176, 1099-1110, 1994
A. Stitle: Permissive linker insertion sites in the outer membrane protein of 987P fimbria A. Reference number: A49891; MUID:94148769
A. Accession: A49891
A. Status: preliminary
A. Status: preliminary
A. Residues: 1-835 < SCH>
A. Residues: 1-835 < SCH>
A. Cross-references: GB:L22659; NID:9437334; PIDN:AAA21827.1; PID:9437336
C; Genetics:
A. Genetics:
A. Genetics:
A. Status: preliminary
A. Cross-references: GB:L22659; NID:9437334; PIDN:AAA21827.1; PID:9437336
C; Superfamily: outer membrane usher protein fimD
C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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A; Reference number: 219944
A; Accession: T24866
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-971 <WIL>
A; Cross-references: EMBL:281120; PIDN:CAB03350.1; GSPDB:GN00021; CESP:T12D8.9
A; Experimental source: clone T12D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted to the EMBL Data Library, December 1996
A; Reference number: 220008
A; Accession: T25274
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-971 <WIZ>
A; Construction: PRISON SERIES (1997) <WIZ>
A; Residues: 1-971 <WIZ>
A; Construction: Cast (1996) Submitted from GB/EMBL/DDBJ
A; Construction: Cast (1996) Submitted from GB/EMBL/DDBJ
A; Construction: Cast (1996) Submitted from GB/EMBL/DDBJ
C; Genetics: Clone T25C8
C; Genetics: Cast (1996) Submitted from GB/EMBL/DDBJ
C; GB/EMBL/
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T24866; T25274
R;McMurray, A.
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57.1%;
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Best Local Similarity , 53.8
Matches 7; Conservative
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A;Introns: 148/2; 929/1
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Search time 80.65 Seconds (without alignments) 8.183 Million cell updates/sec
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2000
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102
1 GNAEKYDKMDEPQHYGKS 18
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Perfect score:
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100059 Total number of hits satisfying chosen parameters:

100059 segs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_39:* Database :

	Description							P22622 plasmodium		P46000 escherichia		Q9z6q0 chlamydia p		P16445 plasmodium	-	Q09785 schizosacch	P23645 drosophila	054713 cavia porce	P29721 treponema p	_	_	P18188 desulfovibr	_	_	_	_	lactoco	_	P55019 pseudopleur	_	Q03264 saccharomyc	P48235 saccharomyc	0321 canis fam	P21062 vaccinia vi
SUMMARIES	ΩI	AMA1_PLAFF	AMA1_PLAFG	AMA1_PLAF8	AMA1_PLAFH	AMA1_PLAFC	PK66_PLAKU	AMA1_PLAFR	DLTB_LACCA	FASD_ECOLI	VATD_SCHPO	AMPM_CHLPN	SCS7_YEAST	AMA1_PLACH	GSPD_ERWCH	GCSP_SCHPO	BIB_DROME	GON1_CAVPO	TMPA_TREPH	CYRG_MOUSE	Y619_METJA	PHNL_DESFR	DPOD_ORYSA	GON1_MOUSE	GON1_TUPGB	TRPC_HALVO	RPOA_LACLA	CAG5_CHICK	TSCC_PSEAM	ALLA_SCHPO	YM80_YEAST	YG3K_YEAST	CYRG_CANFA	VA39_VACCC
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1; ALTAINGEMBRANE ANTIGEN.

1 24 APLCAL MEMBRANE ANTIGEN 1.

25 622 APLCALLULAR (POTENTIAL).

26 622 CYTOPLASMIC (POTENTIAL).

27 66 E22 CYTOPLASMIC (POTENTIAL).

28 162 N-LINKED (GLCNAC...) (POTENTIAL).

29 65 N-LINKED (GLCNAC...) (POTENTIAL).

21 421 N-LINKED (GLCNAC...) (POTENTIAL).

22 422 N-LINKED (GLCNAC...) (POTENTIAL).

23 422 N-LINKED (GLCNAC...) (POTENTIAL).

24 620 N-LINKED (GLCNAC...) (POTENTIAL).

25 422 N-LINKED (GLCNAC...) (POTENTIAL).

26 422 N-LINKED (GLCNAC...) (POTENTIAL).

27 407 N-E (IN REF. 1; AAA29476).

38 312 I-> N (IN REF. 1; AAA29476).

39 439 H-> N (IN REF. 1; AAA29476).

30 496 I-> M (IN REF. 1; AAA29476).

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DOMAIN TRANSMEM DOMAIN CARBOHYD

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Q57706 methanococc P24764 vaccinia vi Q01532 saccharomyc Q59714 pseudomonas P94132 acinetobact P27902 streptomyce P31780 aeromonas P41428 autographa P45778 aeromonas s P41428 drosophila Q09750 schizosacch P53886 saccharomyc) TE SURFACE ANTIGEN).	um. Lev of ES.	yright. It is produced through a collaboration of Bioinformatics and the BMBL outstation notitite. There are no restrictions on its tions as long as its content is in no way is not removed. Usage by and for commercial asperement (See http://www.isb-sib.ch/announce/isb-sib.ch).
Y258_METJA VA39_VACCV BLH1_YEAST CATA_PSEPU ETFD_ACICA DNAA_STRCO GSPD_AERHY GSPD_AERHY GSPD_AERHY GSPD_AEREA Y023_NPVAC TTKA_DROME PST1_SCHPO	T 1 PLAFF PAM1_PLAFF STANDARD; PRT; 622 AA. P22621; 01-A0G-1991 (Rel. 19, Created) 20-A0G-2001 (Rel. 9, Last sequence update) 20-A0G-2001 (Rel. 40, Last annotation update) APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE	AMA-1 OR PF83. Blasmodium falciparum (isolate FC27 / Papua New Guinea). Blasmodium falciparum (isolate FC27 / Papua New Guinea). Blasmodium falciparum (isolate FC27 / Papua New Guinea). BLASMOTIUE 5837; [1] SEQUENCE FROM N.A. MEDLINE-89384584; Pubmed-2701947; MEDLINE-89384584; Pubmed-2701947; MEDLINE-89384584; Pubmed-2701947; MEDLINE-89384584; Pubmed-2701947; SILVA A., Anders R.F., Kemp D.J.; "Integral membrane protein located in the apical complex of Plasmodium falciparum."; "Integral membrane protein located in the apical complex of Plasmodium falciparum."; "Integral membrane protein located in the apical complex of Plasmodium falciparum."; "Integral membrane Protein located in the apical complex of Plasmodium falciparum."; "Integral membrane Protein located in the apical complex of Plasmodium falciparum."; "Integral membrane Protein located in the apical complex of Plasmodium falciparum."; "Integral membrane PROTEIN."; "Integral membrane PROTEIN."	This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricted by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.lsb-silor send an email to license@isb-sib.ch). EMBL: M27957; AAA29475.1;
37.3 404 1 1 37.3 441 1 1 37.3 454 1 1 37.3 454 1 1 37.3 570 1 37.3 656 1 37.3 658 1 37.3 690 1 37.3 1522 1 37.3 1748 1	STANDARD; STANDARD; (Rel. 19, Created) (Rel. 19, Last son (Rel. 40, Last son AME ANTIGEN 1 PREC	AMA-1 OR PF83. Plaamodium falciparum (isolate FC27 Plaamodium falciparum (isolate FC27 BUKBTYOTA: Alveolata; Apicomplexa; INCBL_TAXID=5837; [1] MEDLINE-89384584; Pubmed=2701947; MEDLINE-89384584; Pubmed=2701947; Peterson M.G., Marshall V.M., Smyth Silva A., Anders R.F., Kemp D.J.; "Integral membrane protein located Plasmodium falciparum."; MOLUTION: INVOLVED IN PARKSITE -: FUNCTION: INVOLVED IN PARKSITE -: SUBCELLULAR LOCATION: TYPE I ME: -: SUBCELLULAR LOCATION: TYPE I ME: -: SUBCELLULAR LOCATION: TYPE I ME: -: SUBCERLULAR LOCATION: TYPE I ME: -: SIMILARITY: STRONG TO AMA-1 FROITED	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bloinformatics Institute use by non-profit institutions as lomodified and this statement is not remmodified and this statement is not send an email to license agreement or send an email to license@isb-sib.ch. EMBL; M27133; AAA29475.1;
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LT 1 PLAFF AMA1 PLAFF P22621; 01-AUG-1991 (20-AUG-1991 (APTICAL MEMBRR	OR Odiu yota yota NCE Son A., graj odiu Cell UNCT UBCE	This SWISS-PROT entry is between the Swiss Instit the European Bioinformatiuse by non-profit instandified and this statemeentities requires a licen or send an email to licen created and mail to licen EMBL; MAZ133; AAA29475.1; EMBL; MAZ133; AAA29475.1; EMBL; MAZ999; A32499; InterPro; IPR003298; Apme Pfam; PF02430; AMA-1; 1. Mallaria; signal; Transmem SIGNAL
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                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-001-1996 (Rel. 34, Created)
01-001-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                   Plasmodium falciparum (isolate 7G8).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate thtn / Thailand).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93; DB 1; Length 622; Pred. No. 2e-07;
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CYTOPLASMIC (POTENTIAL).
                   622 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=91101665; PubMed=2270110;
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InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
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                                               (Rel. 34, Created)
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94.4%;
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                                                                                                                                                 NCBI_TaxID=57266;
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                                                                                                       AMA-1, OR PF83
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                                             01-OCT-1996
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P50491;
                 AMA1_PLAF8
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                                P50492;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                        ·.
                                                   Score 102; DB 1; Length 622;
Pred. No. 7e-09;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum (isolate FCR-3 / Gambia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
  N -> R (IN REF. 1; AAA29476).
7D41335E249FA18F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APICAL MEMBRANE ANTIGEN 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKED (GLCNAC. . .) (PO 089336BE0464695C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99; DB 1; Le
Pred. No. 2.1e-08;
1; Mismatches 0;
                                                                                                                                                                                                                   622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                PRT;
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 503 N
72009 MW;
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100.0%;
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94.48;
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                                                                                     Conservative
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Best Local Similarity
"Thes 17; Conserve
503
622 AA;
                                                        Query Match
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5838;
                                                                                                                                                                                                                                                                                                     AMA-1 OR PF83
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CONFLICT
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TRANSMEM
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Gaps

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1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas A.W., Waters A.P., Carr D.;
"Analysis of variation in PPB3, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum.";
MOI. Blochem. Parasitol. 42:285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (isolate Camp / Malaysia).
Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                       APICAL MEMBRANE ANTIGEN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1FDFA53593C94CC5 CRC64;
                                                                                                                                                                                                                                                                            Pfam; PF02430; AMA-1; î. — .
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 1;
Pred. No. 2e-07;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (
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                                                                                                                                                                                                                                                             InterPro; IPR003298; Apmem_Ag1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      622 AA;
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Best Local Similarity
Matches 17; Conserv
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P50489;
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DOMAIN
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"Intra-generic conservation and limited inter-strain variation in a protective minor surface antigen of Plasmodium knowlesi merozoites.";

Mol. Blochem. Parasitol. 44:141-144(1991).

-I- Blochem. Parasitol. 44:141-144(1991).

-I- FUNCTION: MEROZOITE RECEPTOR PK66 IS A SURFACE ANTIGEN INVOLVED

IN PARASITE INVASION OF ERYTHROCYTES.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CONCENTRATED AT THE APICAL END PRIOR TO RUPTURE, FOLLOWING WHICH IT CAN DISTRIBUTE

ITSELF ENTIRELY ACROSS THE SURFACE OF THE FREE MEROZOITE. DURING INVASION PR66 IS EXCLUDED FROM THE ERYTHROCYTE AT, AND BEHIND, THE INVASION INTERFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- MISCELLANEOUS: PK66 EXPRESSED IN MATURE SCHIZONTS IS RAPIDLY PROCESSED AS THE SCHIZONT RUPTURES. YIELDING A 42/44 KDA DOUBLET ASSOCIATED WITH THE SURFACE MEROZOITE.
-i- SIMILARITY: STRONG TO AMA-1/PF83 OF P.FALCIPARUM, P.CHABAUDI, AND
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1991 (Rel. 18, Created)
1-MOS-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MEROZOITE RECEPTOR PK66 PRECURSOR (66 KDA PROTECTIVE MINOR SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LINE W1;
MEDLINE-91009268; PubMed-2211675;
Waters A.P., Thomas A.W., Deans J.A., Mitchell G.H., Hudson D.E.,
Miller L.H., McCutchan T.F., Cohen S.;
Miller Lott, McCutchan T.F., Cohen S.;
Mercosolite receptor protein from Plasmodium knowlesi is highly
conserved and distributed throughout Plasmodium.";
J. Biol. Chem. 265:17974-17979(1990).
                                                                                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                           Score 90; DB 1; Length 622;
Pred. No. 6.1e-07;
1; Mismatches 1; Indels
                                                                                             POTENTIAL.
APICAL MEMBRANE ANTIGEN 1.
                                                                                                                              EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                           26CE8CF76D07C637 CRC64;
                                                                                Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 AA
                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium knowlesi (strain nuri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91187058; PubMed-2011149;
                                              InterPro; IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
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M
                                                                                                                                                                                                                                                                                                                             88.2%;
88.9%;
                              EMBL; M58545; AAA29718.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                               1 GNAEKYDKMDEPQHYGKS 18
                                                                                                                                                                                                                                                                             71943
                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                              622
546
567
622
162
186
286
421
421
422
                                                                                                                                                                                                                                                                             622 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5852;
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P21303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINSNURI
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                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                               DOMAIN
                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                            Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90205978; PubMed=2181309; Peterson M.G., Nguyen-Dinh P., Marshall V.M., Elliott J.F., Peterson M.G., Anders R.F., Kemp D.J.; Anders R.F., Anders R.F., Anders R.F., Remp D.J.; Aplical membrane antigen of Plasmodium fragile."; Mol. Biochem. Parasitol. 39:279-284(1990).
-i-FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-i-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i-SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FALCIPARIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                 EXTRACELLURR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-K (IN STRAIN LINE WI).
N -> K (IN STRAIN LINE WI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AuG-1991 (Rel. 19, Created)
01-AuG-1991 (Rel. 19, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN I PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium fragile.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                            Antigen; Glycoprotein.
                                                                                                                                                                                         POTENTIAL.
MEROZOITE RECEPTOR PK66
                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.17
4; Mismatches
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                                                                                                                             EMBL; M61097; AAA29728.1; -
InterPro; IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
                                                                                                                                                                         Malaria; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                               M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M29898; AAA29474.1; -. PIR; A44944; A44944.
                                                                                                                  EMBL; M58317; AAA63444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         54.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO PK66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                               64680
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.9
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 DKYDKMDQAEAYGKT 528
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563
4487
508
563
107
176
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14
88
509
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107
176
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P22622;
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                                                                                                                                                                                                                                                                       CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID=1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97302479; PubMed-9158726;
Wenbaus F.C., Headron M.P., Debabov D.V., Zhang Q.;
"The dlt operon in the biosynthesis of D-alanyl-lipoteichoic acid
Lactobacillus casei.";
                                   POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

WP. 9FAB72D437EA7164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heaton M.P., Neuhaus F.C.; "Biosynthesis of D-alanyl-lipoteichoic acid: cloning, nucleotide sequence, and expression of the Lactobacillus casei gene for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alanine-activating enzyme.";
J. Bacteriol. 174:4707-4717(1992).
-!- FUNCTION: COULD BE INVOLVED IN THE TRANSPORT OF ACTIVATED
-LALANINE THROUGH THE MEMBRANE.
-!- PATHWAY: BIOSYNTHESIS OF D-ALANINE LICENTIAL).
                                                                                                                                                                                                      ;
                                                                                                                                                                         Length 562;
                                                                                                                                                                                                      3; Indels
          APICAL MEMBRANE ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                           Score 49; DB 1;
Pred. No. 2.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-007-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DLTB PROTEIN (BASIC MEMBRANE PROTEIN) (BMP).
                                                                                                                                                                                                                                                                                                                                 405 AA
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POTENTIAL
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STRAIN-ATCC 7469;
MEDLINE-92325063; PubMed-1385594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U43894; AAB17658.1; -. EMBL; M83993; AAA25235.1; -.
                                                                                                                                                                              48.0%;
57.1%;
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TRANSMEM 11 31
TRANSMEM 34 54
TRANSMEM 55 75
TRANSMEM 90 110
                                                                                                                                      64488
                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
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514 DKYDKMEQADGYGK 527
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                                                                                                                                      562 AA;
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                                                                                                                                                                                            Best Local Similarity
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P35855;
             CHAIN
DOMAIN
TRANSMEM
                                                                    CARBOHYD
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DLTB_LACCA
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MEDLINE=99206606; PubMed=10192388;
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                                                                   VATD_SCHPO
059823;
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                                 RESULT 10
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 405;
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2FECE6E2305274E1 CRC64;
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2
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                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0UTER MEMBRANE USHER PROTEIN FASD PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                             835 AA.
                                                                                                                                                                                                        Pred. No. 21;
5; Mismatches
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                                                                                                                                                                                      41.28;
                                                                                                                                      47758
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425 ANKYDKIHSGQSYG 438
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174 YDRVPDPEHYAQ 185
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835 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                   405 AA;
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Best Local Similarity
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P46000;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                        15-DEC-1998 (Rel. 37, Last sequence update)
COAGG-20001 (Rel. 40, Last annotation update)
VACUOLAR APP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT)
(VACUOLAR PROTOW PUMP D SUBUNIT).
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092600; 0930D4; Q9KIXI.
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2010 (Rel. 39, Last sequence update)
20-AdG-2001 (Rel. 40, Last annotation update)
METHIONINE AMINOPEPTIDASE (EC 3.4.11.18) (MAP) (PEPTIDASE M).
MAP OR CPN1009 ON CP0844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%; Score 41; DB 1; Length 285; 47.1%; Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL023590; CAA19063.1; -.
InterPro; IPR002699; ATP-synt_D.
Pfam; PF01813; ATP-synt_D: 1.
Probom; PD004122; ATP-synt_D: 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 285 AA; 32219 MW; 5B95DF17D1887DD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi: Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
285 AA.
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PRT;
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Best Local Similarity 4/...
Best Local Similarity 6/...
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STANDARD;
                                                    15-DEC-1998 (Rel. 37, 15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Last annotation update)

Last sequence update)

(Rel. 35, (Rel. 35, 1) (Rel. 35, 1)

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Mitchell A.G., Martin C.E.; "Fahlp, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
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"Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C) ascorbaromyces cerevisiae requires Scs7p, a protein with both a cytochrome b5-like domain and a hydroxylase/desaturase domain.";
Yeast 14:311-321(1998).
                                                                                              INOSITOLPHOSPHORYLCERAMIDE-B C-26 HYDROXYLASE (EC 1.-.-.) (IPC-B
                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                 Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                            SCS7 OR FAHI OR YMR272C OR YM8156.14C
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98220296; PubMed-9559540;
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STRAIN=S288C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                 [2]
CHARACTERIZATION.
                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                        20-AUG-2001
                          01-NOV-1997
01-NOV-1997
                                                                                                                      HYDROXYLASE)
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TRANSMEM
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                                                                                                                                                                                     Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Eisen J., Fraser C.M., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24A; ALSO KNOWN AS THE
MAP FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:231-2314(2000).
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEINS (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE
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A) 094F6D6E17F23DE9 CRC64;
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EMBL; AP002548; BAA99216.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002467; MAP_1.
InterPro; IPR001714; Methamino_PTase.
InterPro; IPR000994; Peptidase_M24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                               MEDLINE=20150255; PubMed=10684935;
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                   SEQUENCE FROM N.A.
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THE C26-FATTY

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its Arabidopsis thaliana homolog that lacks the cytochrome b5 domain both function in the alpha-hydroxylation of sphingolipid-associated very long chain fatty acids.";
-1. Biol. Chem. 272:3828-19288 (1997).
-1. FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY ACIDS. HYDROXYLATES THE C26-FATTY ACIDS. HYDROXYLATES THE C26-FATTY. ACID OF INOSITOLPHOSPHORILCENAIDE-B (IPC-B) TO FORM IPC-C.
-1. COFACTOR: IRON (BY SIMILARITY).
-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1. DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL 10N BINDING.
-1. SIMILARITY: CONTAINS A CYTOCHROME B5 FAMILY, HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGD: $00044885, SCS7.

InterPro: IPR001199; Cyt_B5.

InterPro: IPR001541; Sterol_desat.

Pfam; PF00173; heme_1: 1.

PR0SITE: PS00191: CYTOCHROME_B5_1; 1.

PR0SITE: PS00255; CYTOCHROME_B5_2; 1.

Oxidoreductase; Fatty acid biosynthesis; Iron; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 384;
Pred. No. 29;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IME LIGAND (BY SIMILARITY). DF4BA5F2E0EA2218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; Heme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEME-BINDING
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Best Local Similarity
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STANDARD:

SCS7_YEAST

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RESULT 12 SCS7_YEAST

KKYDAIAAPFHYG 100 4 EKYDKMDEPQHYG 16

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EKYDKMDEPQHYGKS 18
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Q09785;
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GCSP_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: STRONG TO AMA-1/PF83 FROM P.FALCIPARUM, P.FRAGILE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APICAL MEMBRANE ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                           Marshall V.M., Peterson M.G., Lew A.M., Kemp D.J.; \rm ``Structure\ of\ the\ apical\ membrane\ antigen\ I\ (AMA-1)\ of\ Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
9773873E56A439A972 CRC64;
                                                                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                   Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                             MEDLINE-96333375; PubMed-8757869;
Crewther P.E., Matthew M.L., Flegg R.H., Anders R.F.;
"Protective immune responses to apical membrane antigen 1 c
Plasmodium chabaudi involve recognition of strain-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; Glycoprotein.
                                                                                   558 AA.
                                                                                                                                                                                                                                                                                              Mol. Blochem. Parasitol. 37:281-284(1989)
                                                                                   PRT;
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                                                                                                                                                                                                                                             MEDLINE-90114335; PubMed-2608101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A4964; A44964.
InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
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             170 DQIHRPRHYGK 180
7 DKMDEPQHYGK 17
                                                                                                                                                                     Plasmodium chabaudi
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                   AMA1_PLACH
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi: sequence comparison with secretion genes from other gram-negative bacteria.";
J. Bacteriol. 174.7385-7397(1992).
-I- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROPEIDINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.
-I- SUBCELLULAR LOCATION: OUTER MEMBRANE (PROBABLE).
-I- SIMILARITY: BELONGS TO THE EXED/OUTD/PULD/XPSD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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; 8A065D9ADAE24888 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
NCBL_TaxID=556;
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 32, Last sequence update)
PUTATIVE GLYCINE DEHYDROGENASE [DECARBOXYLATING], MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
SECRETION PROTEIN OUTD).
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InterPro; IPR00016; Bac_GSPprotein.
Pfam; PF00263; Bac_GSPproteins; 1.
PRINTS; PR00811; BCTERIALGSPD.
PROSITE; PS00875; T2SP_D; 1.
Transport; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93054355; PubMed-1429461;
                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
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712 AA;
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Matches 7; Conser
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Best_Local Similarity Matches 7; Conserv

Query Match

40.2%; Score 41; 46.7%; Pred. No. 4

DB 1; Length 558;

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REPL: 254308; CAA91099.1;
Refine: Proc. 1 Proc. 1 Coc. P.
R. Pfan: Proc. 1 Protein; Oxidoreductase; Mitochondrion;
KW Pyridoxal phosphate; Transit peptide.
RW Pyridoxal phosphate; Transit peptide.
RT TRANSIT ? 1017 PUTATIVE GLYCINE DEHYDROGENASE
FT TRANSIT ? 1017 PUTATIVE GLYCINE DEHYDROGENASE (DECARBOXYLATING).
FT CHAIN ? 769 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                          Odell C., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-1-FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF
GLYCINE. THE PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE
THROUGH ITS PYRIDOXAL PHOSPHATE COFACTIOR; CO(2) IS RELEASED AND
THE REMAINING METHYLAMINE MOIETY IS THEN TRANSFERRED TO THE
LIPOAMIDE COFACTIOR OF THE H PROTEIN.
-1-CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                           DIHYDROLIPOYLPROTEIN + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
-!- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

40.2%; Score 41; DB

Best Local Similarity 42.1%; Pred. No. 84;

Matches 8; Conservative 5; Mismatches
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                                                                                                                            Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                         SPAC13G6.06C
                                                                                                                                                                                                               STRAIN=972;
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Search completed: January 29, 2002, 11:13:46 Job time: 822 sec

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Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
Marshall v.M., Zhang L.X., Anders R.F., Coppel R.L.;
"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 77:109-113(1996).
EMBL; U33279; AAC47109-1; -
Interpro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Last sequence update)
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100.0%; Pred. No. 7.5e-08;
iive 0; Mismatches 0;
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098H00
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098HP7
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ID Q25746 P.
AC 025746;
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Compugen Ltd
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Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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sp_unclassified:*
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sp_phage:*
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seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
MOL. Blochem. Parasitol. 77:109-113(1996).
EMBL: U33277; AAC47107.1;
InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kocken C.H.M., Dubbeld M.A., Herrera S., Thomas A.W.;
"Diversity of Apical Membrane Antigen 1 sequence in Plasmodium falciparum FVO strain.".
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277646; CAC05390.1; -..
InterPro; IPR003398; Apmem_A91.
     Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                              Score 99; DB 5; Length 604; Pred. No. 2.3e-07;
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Pred. No. 2.3e-07;
1; Mismatches 0; Indels
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604 AA; 69886 MW; 791620C3B24D342B CRC64;
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69897 MW; F6D89F02F7690C19 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Plasmodium falciparum (isolate kf1916).
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                                                                                                       MEDLINE=96379227; PubMed=8784778;
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PRINTS; PR01361; MEROZOITESA.
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94.48;
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94.48;
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Best Local Similarity 94.45
Matches 17; Conservative
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Best Local Similarity 94.4
Matches 17; Conservative
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                                        NCBI_TaxID=5833;
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01-JUN-2001 (
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STRAIN-VI:
MEDLINE-96379227; PubMed-8784778;
Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
MOI. Blochem Parsaitol. 77:109-113(1996).
EMBL; 033276; AAC47106.1;
InterPro: IPR003298; Apmem_Ag1.
Pfam; PF02430; AMA-1; 1.
NOW_TER 604
NOW_TER 604
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"Cloning and structure of apical membrane antigen I (AMA-1) gene of
Plasmodium falciparum isolate FCC1/HN.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IRR003298; Agmem_Agl.
Pfam; PF0240; AMA-1; I.
PRINTS; PR01361, MEROZOTIESA.
SEQUENCE 622 AA; 72045 MW; 69045E66776C3BBB CRC64;
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                                      Plasmodium falciparum (isolate v1).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5847;
                                                                                                                                                                                                                                                                                                                                               Length 604;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-JUN-2001.(TrEMBLrel. 17, Last annotation update) APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1.
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U-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 102; DB 5;
100.0%; Pred. No. 7.7e-08;
Live 0; Mismatches 0;
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100.0%; Pred. No. 7.9e-08;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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025747;
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Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
Mol. Blochen. Parasitol. 77:109-113(1996).
EMBL; U65407; AAB36701.1;
EMBL; U33274; AAC47104.1;
                                                                                       Kocken C.H.M., Dubbeld M.A., Thomas A.W.;

Kocken C.H.M., Dubbeld M.A., Thomas A.W.;

"Aptical membrane antigen 1 of Plasmodium reichenowi: molecular characterisation, comparison with Plasmodium falciparum AMA-1 and antibody-mediated inhibition.";

Submitted (DEC.1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ252087: CAB66387.1; -.

InterPro; IPR003298; Apmem_Agl.

PFam: PFC2430; AMA-1: 1.

PRINTS; PR01361; MEROZOITESA.

NON_TER 605 605

SEQUENCE 605 AA; 70072 MW; E4959A99D5C880C6 CRC64:
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STRAIN=3D7;
Tine J.A., Lanar D.E., Smith D.M., Wellde B.T., Schultheiss P.,
Ware L.A., Kauffman E.B., Wirtz R.A., de Taisne C., Hui G.S.N.,
Chang S.P., Church P., Hollingdale M.R., Kaslow D.C., Hoffman S.,
Guito K.P., Ballou W.R., Sadoff J.C., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.2%; Score 93; DB 5; Length 622; 94.4%; Pred. No. 2e-06; 1: Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (APICAL MEMBRANE ANTIGEN-1)
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Pred. No. 2e-06;
1; Mismatches
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STRAIN-3D7;
MEDLINE-96379227; PubMed-8784778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 91.2%;
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 94.4'
Matches 17; Conservative
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Plasmodium reichenowi.
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"The immunogenicity and protective efficacy of Plasmodium falciparum AMA-1 DNA vaccines.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U84348; AAD03790.1; -.
InterPro; IPR003298; Apmem_Ag1.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-57269;
                                                                                                                                                                                                                   Eisen Dr., Marshall V.M., Billman-Jacobe H., Coppel R.L.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; 90276; AAB50405.1; -. EMBL; AF064132; AAC1573.1; -. InterPro; IPR03298; Apmem_Agl., Fam: PF02430; AMA-1; 1. NON. TER. SEQUENCE 620 AA; 71721 MW; 9194F06A0D138677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99; DB 5; Length 620;
Pred. No. 2.3e-07;
1; Mismatches 0; Indels
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Pred. No. 2.3e-07;
1; Mismatches 0; Indels
                                                                                                            Eisen D., Billman-Jacobe H., Marshall V.M., Coppel R.L.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN I (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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94.4%;
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Best Local Similarity 94.4<sup>†</sup>
Matches 17; Conservative
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Best Local Similarity
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Best Local Similarity 100.
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437 AA;
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MARDLINE=96379227; PubMed=8784778;
Marshall V.M., Zhang L.X., Anders R.F., Coppel R.L.;
"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
MMI. Biochem. Parasitol. 77:109-113(1996).
EMBE; U33275; AAC47105.11
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MEDLINE=96147889; PubMed=8556798;
Zhang L.X., Zhan B., Wang J., Feng X.;
Chung Kuo Chi Sheng Chung Hsueh Yu Chi Sheng Chung 13:203-208(1995).
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STRAIN-NIGERIAN 015;
Polley S.D., Conway D.J.;
"Diversilfying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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NCBL_TaxID=5833;
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
  592 AA.
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Pfam; PF02430; AMA-1; 1.
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PRELIMINARY;
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592 AA;
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STRAIM-NIGERIAN 029;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, A4408306; CAC34747.1; -.
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STRAIN-WIGERIAN 030;
POLIDES S.D., CONWAY D.J.;
POLIDES S.D., CONWAY D.J.;
PLIVETSITYING SElection in domains of Plasmodium falciparum Apical
Membrane Antigen 1 (AMA).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, A4408307; CAC34748.1;
NON_TER 437 437
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                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50247 MW; 8C6C4F7A87139B70 CRC64;
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                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-NIGERIAN 034A;
Polley S.D., Conway D.J.;
Diversifying selection in domains of Plasmodium falciparum Apical
Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408308; CAC34749.1; -.
NON_TER 1 1 1
NON_TER 437 A37
SEQUENCE 437 AA; 50217 MW; 68A4IFEE41C3271C CRC64;
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STRAIN-NIGERIAN 034B;
POLIEY S.D., CONWAY D.J.;
Poliey S.D., CONWAY D.J.;
Poliey S.D., CONWAY D.J.;
Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408309; CAC34750.1; -.
NON_TER 1 1
NON_TER 437 437
SEQUENCE 437 AA; 50206 MW; EB05396E7D92AC98 CRC64;
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                                                                                        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=5833;
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            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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Best Local Similarity 100.
Matches 13; Conservative
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Q9BHR5;
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Search completed: January 29, 2002, 11:12:14 Job time: 770 sec

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Zea mays protein f
Zea mays protein f
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Breast and ovarian
Rabbit HBI protein
Human FK506 bindin
Tetratricopeptide
Human protein kina
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hYAK3-2 polypeptid Human YAK3b (hYAK3 Human protein kina hYAK3-2 alpha poly

Human protein kina

Human protein sequ S. epidermidis ope Multiple drug resi Malarial PfEMP3 ep

B. licheniformis b Human secreted pro Human transport pr

Peptide #464 encod

Plasmodium falcipa Plasmodium falcipa

S. epidermidis ope S. epidermidis ope Eucalyptus grandis Chlamydia pneumoni

Minimum DB s Maximum DB s

Database

Searched:

OM protein

Run on:

Sequence:

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T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; mSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum AMA-1 antigenic epitope, P602.
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AAB72682
AAW03515
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AAR46608
AAB18161
AAB46484
AAG01304
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AAG19095
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AAW54038
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AAG81810
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AAB94564
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 (NAIM-) NAT INST IMMUNOLOGY
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WO200011179-A1.
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RESULT
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Plasmodium falcipa
Plasmodium knowles
Plasmodium vivax 6
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Human SGP039 phosp
Mouse serine/threo
Novel protein kina
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Recombinant vaccin
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4.528 Million cell updates/sec
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                    Compugen Ltd.
                                                                                                                                                                                                                    hits satisfying chosen parameters:
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          GenCore version
Copyright (c) 1993 - 2000
                                                                         January 29, 2002, 10:21:49
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAR27532
AAR68840
AAR10551
AAR10935
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AAE02843
                                                                                                                   US-09-763-397A-18
105
1 DQPKQYEQHLTDYEKIKEG 19
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Gapop 10.0 , Gapext 0.5
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WPI; 2000-237654/20.

Result Š.

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AAP91632
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                                                                              The present sequence is the antigenic epitope P602, derived from a procal membrane antigen. (AMA-1) of the asexual blood stage of Plasmodium falciparum. It is used in the construction of recombinant protein CDC/NIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melitin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein. (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein. (MSP-1), MSP-2, apical membrane antigen-1 (RAP-1) and gamete specific antigen. PfG27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
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                                                                                                                                                                                                                                                                                                                                                 Gaps
          Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
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100.0%; Pred. No. 7.9e-09;
Live 0; Mismatches 0;
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                           detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant vaccine CDC/NIIMALVAC-1.
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                         Claim 2; Page 17; 52pp; English.
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                   19 AA;
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (RAP-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
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                                                                                                                                                                                                                             Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 350;
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100.0%; Pred. No. 1.7e-07;
ive 0; Mismatches 0;
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NAT INST IMMUNOLOGY.
US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                        plasmodium falciparum life cycle
                                                                                   Shi YP, Hasnain SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100. Best Local Similarity 100. Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SARA ) SARAMANE PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-263714/36.
N-PSDB; AAN90703.
                                                                                                                                            WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA;
                                                                                                                                                                          N-PSDB; AAZ51336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peterson MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W08907645-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP91632;
(NAIM-) (USSH )
                                                                                   Lal AA,
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AAQ80910 encodes AAR68840 the P. falciparum AMA-1 gene product. New recombinant poxviruses containing either the SERA, ABRA, Pfhsp70, AMA-1, Pfs25, Pfs16, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1, MSA-1 (N-terminal pp3 or C-terminal pp42) genes, or a combination of these in non-essential regions of their genomes are claimed. These poxviruses (pref. with a virulence reducing genomic deletion or disruption) can be used as vaccines against malaria and for the prodn. of Plasmodium immunogens. These viruses provide multicomponent, multistage vaccines due to their expression of sporozite, liver stage, blood stage and sexual stage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant poxvirus contg. Plasmodium DNA in non-essential region - useful in vaccines against malaria and for prodn. of Plasmodium immunogens
                                                                                                                                                                                                                                                                        Plasmodium falciparum AMA-1 gene; recombinant poxvirus; multicomponent multistage malarial vaccines; immunogens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium knowlesi 66kD merozoite antigen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; .Score 105; DB 16;
ilarity 100.0%; Pred. No. 3e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium merozoite antigens; malaria vaccine.
                                                                                                                                                                                                                  Plasmodium falciparum AMA-1 gene protein.
                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tine JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR10551 standard; Protein; 563 AA.
                                                   AAR68840 standard; Protein; 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 5; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (3D7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DQPKQYEQHLTDYEKIKEG 19
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94US-0257073
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                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoletti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-036113/05.
N-PSDB; AAQ80910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                              malaria diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           De Taisne C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1994;
                                                                                                                                                            24-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9428930-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR10551;
                                                                                                         AAR68840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
5
                         AAR68840
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                                                                            80 kD.
                                                   immune response to malaria, and antibodies which the parasite. RMA-1 initially has mol. wt. 80 \rm ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        before being inserted into the vaccinita virus to be used in a vaccine to stimulate an antimalarial immunological response, or for in virro prodn. of gene prods. for use as immunogens. As plasmodium egenes are conserved among P. falciparum strains, they are widely effective in a vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant poxvirus; antimalarial vaccine; malaria; immunise;
                                                                                                                                                                                                                  622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 622;
                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - contg. Plasmodium DNA, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the Plasmodium falciparum AMA1 antigen. cDNA encoding it was cloned into vaccinia donor plasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 105; DB 13;
llarity 100.0%; Pred. No. 3e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                               100.0%; Score 105; DB 10;
100.0%; Pred. No. 3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum AMA1 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoletti E, Tine JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR27532 standard; Protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 5; 74pp; English.
Claim 1; Fig 3; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 dgpkqyeqhltdyekikeg 366
                                                                                                                                                                                                                                                                                                                                                          91US-0672183
92US-0852305
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                                                                                                                                                                                                                                                                                                                           1 DQPKQYEQHLTDYEKIKEG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant pox:virus antimalarial vaccine
                                                   RMA-1 can generate an
can inhibit growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-349203/42.
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les 19; Conserv
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                  622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ29189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  De TAISNE C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR27532;
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                                                                                                                                     Sequence
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Length 622; Indels 4

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                                                                                                the complete P.vivax merozoite antigen gene and e.g. a purely or vaccinia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. It is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells.
Plasmodium merozoite antigen proteins and DNA sequences - useful in vaccine prodn., anti-malarial drug design, and in diagnostics
                                                                                   This protein is encoded by a recombinant DNA molecule comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Predicted mol. wt. is 63901 D. This shows great similarity to P. falciparum RMA-1 protein (sequence in specification-claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.6%; Score 72; DB 10; Length 561;
68.4%; Pred. No. 0.017;
ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                           Length 489;
                                                                                                                                                                                                                                                                        Score 79; DB 12; Length 452
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marshall VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhoptry membrane antigen of Plasmodium falciparum - used for producing antibodies and in immunisation, diagnostic and treatment methods for malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malaria; rhoptry membrane antigen-1; antibodies.
                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smythe JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP91588 standard; protein; 561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig. 3; 46pp; English.
                                                  Disclosure; fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                        75.2%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                               111:|||: :|||::|
219 dqprqyeeemtdyqkiqqg 237
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                                                                                                                                                                                                                                                                                                                                                            1 DQPKQYEQHLTDYEKIKEG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhoptry membrane antigen-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium chabaudi adami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SARA ) SARAMANE PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-263714/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                         489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            561 AA;
                                                                                                                                                                                                        See also AAQ10418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1990
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                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                          Query Match
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ID AAP9
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                                                                                                                                                                                                                                                                                                          Plasmodium merozoite antigen proteins and DNA sequences - useful in vaccine prodn., anti-malarial drug design, and in diagnostics
                                                                                                                                                                                                                                                                                                                                                                                          This protein is encoded by a recombinant DNA molecule comprising the complete P.knowlesi merozoite antigen gene and e.g. a pUC19
                                                                                                                                                                                                                                                                                                                                                                                                                         or vaccinia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. It is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR10935 standard; Protein; 489 AA.
                                                                                                                                                                                                                                                                                                                                                        Disclosure; fig 1; 31pp; English.
                                                                                                                    90US-0483516.
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293 dqprqyeeeltdyekiqeg 311
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                                                                                                                                                                                      (USSH ) NAT INST OF HEALTH.
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                                                                                                                                                                                                                        McCutchan TF;
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                                                                                                                                                                                                                                                        WPI; 1991-044381/06.
N-PSDB; AAQ10418.
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                Plasmodium knowlesi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAQ10869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium vivax.
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                                                                                                                    22-FEB-1990;
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                                                US7483516-A.
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Matches 15;
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Sequence

Query Match

AAR10935

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sequence is classified as serine phosphatase, STP and PP2C.

360 AA;

Sequence

Soxx

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sequences encoding them, as well as various products and methods useful for the diagnosis and treatment of various phosphatase-related diseases and conditions. Substance that modulates the activity of phosphatase cardiovascular disease, brain or neuronal-associated diseases and cardiovascular disease, brain or neuronal-associated diseases and methobolic disorders, including cancers of tissues, cancers of methobolic disorders, including cancers of tissues, cancers of methobolic disorders, including cancers of tissues, cancers of system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, system, Alzheimer's disease, Parkinson's disease, miltiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias and organ transplant rejection. The present amino acid sequence is human SGP039 phosphatase polypeptide. This
                                                                                                                                                                                                                                                Human; SGP039 phosphatase polypeptide; phosphatase-related disease; infamune-related disorder; ocular disease; organ transplant rejection; infection; diabetes; pain; sexual dysfunction, Alzheimer* disease; metabolic disorder; haematopoletic cancer; mood disorder; cardiant; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; cardiovascular disease; multiple sclerosis; amyotrophic lateral sclerosis; attention disorder; cognition disorder; psychotic disorder; cytostatic; neurological disorder; virucide; nootropic; cerebroprotective; therapy; neuroprotective; antibacterial; vulnerary; trandulliser; antiasthmatic; hypotensive; immunosuppressive; antipsoriatic; analgesic; hypotrensive; antifungal; migraine; serine phosphatase; STP; PP2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel phosphatase polypeptide useful for treating cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hill RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to phosphatase polypeptides, nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martinez R, Whyte D, Manning G, Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91..344
/label- Phosphatase_domain
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/label- Catalytic_domain
                                                                                                                                                                                                                     Human SGP039 phosphatase polypeptide.
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                                                                                                AAE04841 standard; Protein; 360 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0173255.
99US-0175766.
2000US-0178078.
2000US-0179301.
293 dgpkgyekhledtakirrg 311
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                                                                                                                                                                            (first entry)
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31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                              10-SEP-2001
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                                                                                                                                     AAE04841;
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Domain
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                                                                              AAE04841
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The present sequence is mouse serine/threonine kinase, YAK3. The YAK3 is useful for screening compounds which inhibit or stimulate the function of YAK3. The identified agonists and antagonists are useful in treatment of human diseases including neutropenia, cytopenia, anaemias including anaemias due to renal insufficiency or due to chronic disease such as autoimmunity or cancer, polycythaemia, myelosuppression, inflammatory diseases such as adult respiratory disease syndrome, rheumatoid arthritis, psoriasis, dermatitis, asthma, allergies, rheumatoid arthritis, psoriasis, dermatitis, asthma, allergies, particularly infections caused by HIV and other immunodeficiency diseases, pain, injury, anorexia, Parkinson's disease, cardiovascular
                                                                                                                                                                                                                                                                                                                                                               Mouse; serine/threonine kinase; YAK3; therapy; neutropenia; cytopenia; anaemia; renal insufficiency; chronic disease; autoimmunity; cancer; polycythaemia; myelosuppression; infertility; testicular cancer; bone loss; osteoporosis; inflammatory disease; rheumatoid arthritis; psoriasis; adult respiratory disease syndrome; dermatitis; asthma; allergy; infection; human immunodeficiency virus; HIV; pain; injury; infercion; disease; anorexia; parkinson's disease; hypotension; atherosclerosis; cardiovascular disease; hypertension; ulcer; psychotic; myocardial infarction; neurological disorder; anxiety; schizophrenia; dementia; delirium; dyskinesias; Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel murine serine/threonine kinase polypeptides and polynucleotides for identifying agonists, antagonists useful for treating anemia, cancer, rheumatoid arthritis, psoriasis, psychotic and neurological
                                          Gaps
                                        ö
    Length 360;
                                        4; Indels
  Score 53; DB 22;
Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                              Mouse serine/threonine kinase, YAK3 version #1.
                                        2; Mismatches
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                                                                                                                                                                                                            AAE02843 standard; Protein; 551 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 24; 34pp; English.
  50.5%;
62.5%;
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|144 pealkghlqdyekdke 159
Query Match 50.5
Best Local Similarity 62.5
Matches 10; Conservative
                                                                          3 PKOYEOHLTDYEKIKE 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-335832/35.
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                                                                                                                                                                                                                                                                                        10-AUG-2001
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diseases including atherosclerosis, hypotension, hypertension, myocardial infarction, ulcers, psychotic and neurological disorders including anxiety, schizophrenia, dementia, delirium and dyskinesias such as Huntington's disease. The YAK3 is also used as a probe to screen suitable libraries to obtain murine YAK3 genomic DNA clone and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies expression and activity. Diseases related to kinase expression and activity. Diseases related to kinase expression and activity. Diseases related to kinase expression and activity. Diseases related to myocardial infarction, disorders, complications of organ transplantation, myocardial infarction, timmune disorders, cardiomyopathias, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -
                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                 22; Length 551;
                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                               Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel protein kinase, SEQ ID NO: 189.
                                                                                                                                                                                                                                                                                                                                                                                                            AAB65662 standard; Protein; 553 AA.
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                                                                                                                                                                                             50.5%;
64.3%;
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                                                                                                                                                                                                                                     Conservative
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112 kgykhhltayekle 125
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                                                                                                  localisation studies.
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                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                    551 AA;
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                                                                                                                                        Sequence
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chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein kinase; hVAK-beta; human; bone loss; osteoporosis; inflammation; acute respiratory distress syndrome; osteoarthritis; rhemmation bowel disease; psoriasis; rhemmatidis atthritis; inflammatory bowel disease; psoriasis; cachexia; septic shock; pain; injury; cancer; testicular cancer; anorexia, bulimia; Parkinson's disease; cardiovascular disease; restenosis; atherosclerosis; heart failure; myocardial infarction; hypotension; hypertension; uthary retention; angla pectoris; ucer; benign prostatic hypertrophy; psychosis; schizophrenia; anxiety; mantc depression; delixium; severe mental retardation; dementia; Huntington's disease; dilles de la Tourette syndrome; dyskinesia; diagnosis; therapy; vaccine.
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                                                                                                                                                                                                                                           Length 553;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                           50.5%; Score 53; DB 22;
64.3%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW75791 standard; Protein; 568 AA.
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97US-0040618.
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                                                                                                                                                                                                                                                                                                                  Conservative
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||113 kgykhhltayekle 126
                                                                       reproductive disorders.
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                       553 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP870825-A1.
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                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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diagnosing a disease related to expression or activity of hYAK3, and methods for identifying agonist and antagonist compounds. hYAK3 polypeptides and polynucleotides can be used to treat and diagnose
                                                                                                                                                                                                                                                             schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles
                                                      bone loss (e.g. osteoporosis), inflammatory diseases (e.g. ARDS), rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, psorlasis, dermatitis, asthma, allergies, infections (e.g. bacterial, fungal, protozoal and viral infections such as HIV, associated cachexia and other immunodeficiency disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human YAK3-2; hVAK3-2; serine/threonine kinase; kinase; phosphorylation; signal transduction; antisense; suppression; bone marrow; foetal liver; testis; prevention; treatment; diagnosis; anaemia; neutropaenia; cytopaenia; polycythaemia; myelosuppression; bone loss; osteoporosis; inflammatory disease; adult respiratory disease syndrome; ARDS; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; IBD; psoriasis;
                                                                                                                                             septic shock, pain, injury, cancers (e.g. testicular cancer), anorexia, bulimia, Parkinson's disease, cardiovascular disease (e.g. restenosis, atherosclerosis, acute heart failure and myocardial infarction), hypotension, hypertension, urinary retention, angina pectoris, ulcers, benign prostatic hypertrophy and psychotic and neurological disorders (e.g. anxiety,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dermatitis; asthma; allergies; infection; the man immunodeficiency virus; HIV; HIV-associated cachexia; septic shock; pain; injury; cancer; anorexia; bulimia; Parkinson's disease; cardiovascular disease; restenosis; atherosocierosis; acute heart failure; myocardial infarction; hypotension; urinary retention; anginal pectoris; ulcers; benign prostatic hypertrophy.
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                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB 19; Length 568;
Pred. No. 9.5;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               50.5%;
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99US-0371674.
99US-0440236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                    de la Tourette syndrome).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 kgykhhltayekle 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KOYEQHLTDYEKIK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hYAK3-2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-499340/44.
N-PSDB; AAA47745.
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                         568 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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15-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB00059;
                                                                                                                                                                                                                                                                                                                                         Sequence
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cellular effects through a signal transduction pathway. Transduction of signals from the celli surface receptors to intracellular effectors from the celli surface receptors to intracellular effectors frequently involves phosphorylation or dephosphorylation of specific protein substrates by regulatory protein serine/threonine kinases (PSTK) and phosphatases. Aberrant protein serine/threonine kinases activity has been implicated in a number of pathologies and disease activity has been implicated in a number of pathologies and disease activity has been implicated in a psTK with sequence homology to CDK's (cyclin dependent kinases, which have a role in cell cycling). It was originally identified in yeast where it can act as a cell cyclin supressor. Novel human homologues of yeast YAKI designated YAK3-2 have been described. YAK3-2 is expressed predominantly in heamatopoietic tissues such as bone marrow, foetal liver and in the testis. Inhibitors of hYAK3-2 is expressed to stimulate expression of cells in which it is expressed. The use of antisense oligonucleotides to achieve such ends is described. Nucleic acids encoding the HYAK3-2 and the HYAK3-2 protein may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate HYAK3-2 expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; YAK3b; serine/threonine protein kinase; STPK; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; bone loss; osteoporosis; inflammatory disease; osteoarthritis; adult respiratory disease syndrome; ARDS; rheumatoid arthritis; allergy; inflammatory bowel disease; IBD; psoriasis; dermatitis; asthma, cachexia; human immuno deficiency virus; HTV; immunodeficiency disorder; psychotic; septic shock; restenosis; pain; cancer; anorexia; bulimia; hypotension; attherosclerosis; parkinson's disease; cardiovascular disease; anxiety; acute heart failure; myocardial infarction; hypertension; cutinary retention; angina pectoris; ulcer; benign prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARDS)), rheumatoid arthritis, osteoarthritis, inflammatory bowel disease (IBD), psoriasis, dermatitis, asthma, allergies, infections described, fungal, protozoan and viral infections, particularly infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, HIV-associated cachexia and other immunodeficiency disorders), septic shock, pain, injury, cancers (e. g. testicular cancer), anorexia, bulimia, Parkinson's disease, cardiovascular disease (e.g. restenosis, atherosclerosis, acute heart failure and myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                     hYAK3-2 protein serine kinases polypeptides and nucleic acids useful for treating e.g. anemia, neutropenia and cytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides include heamatopoietic cellular deficiency (either anaemia, neutropaenia, cytopaenia, polycythaemia, myelosuppression, They may also be used to treat bone loss including osteoporosis, inflammatory diseases (e.g. adult respiratory disease syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infarction), hypotension, hypertension, urinary retention, anginal pectoris, ulcers, benign prostatic hypertrophy and psychotic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 21; Length 568; Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                             Claim 12; Page 40-41; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE02013 standard; Protein; 568 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.5%;
64.3%;
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128 kqykhhltayekle 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disorders.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE02013;
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restenosis; atherosclerosis; heart failure; myocardial infarction; hypotension; hypertension; urinary retention; angina pectoris;

anorexia, bulimia; Parkinson's disease; cardiovascular disease

ulcer; benign prostatic hypertrophy; psychosis; schizophrenia; anxiety; manic depression; delirium; severe mental retardation; dementia; Huntington's disease; Gilles de la Tourette syndrome; dyskinesia; diagnosis; therapy; vaccine.

Homo sapiens.

EP870825-A1. 14-OCT-1998.

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The present sequence is human YAK3D (hYAK3D) serine/threonine protein
Xinase (STPK). YAK polypeptides are involved in the signal transduction
Xinase (STPK). YAK modulators are used to treat bone loss such as
Seteoporosis, inflammatory diseases such as adult respiratory disease
Seteoporosis, inflammatory diseases such as adult respiratory disease
Caydrome (ARDS), rheumatoid arthritis, osteoarthritis, inflammatory bowel
disease (IBD), psoriaais, dermatitis, asthma and allergies, bacterial,
fungal and viral infections such as human immunodeficiency virus-1
changed and viral infections such as human immunodeficiency virus-1
changed and viral infections such as human immunodeficiency virus-1
changed and viral infections of disease, cardiovascular diseases such as
restenosis, atherosclerosis, acute heart failure, myocardial infarction,
hypotension, hypertrophy and psychotic and neurological disorders
Such as anxiety, schizophrenia, manic depression, delirium, dementia,
severe mental retardation and dyskinesias such as Huntington's disease or
cilles dela Tourette's syndrome and proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for YAK polypeptide kinase activity comprising contact with a candidate peptide to detect molecules useful for treating disorders including the treatment of bone loss -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
neurological disorder; depression; delirium; dementia;
Huntington's disease; mental retardation; proliferative disease;
Gilles dela Tourette's syndrome;
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Pred. No. 9.5;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 29-30; 49pp; English.
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BEECHAM PLC.
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03-NOV-2000; 2000US-0706426.
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64.3%;
                                                                                                                                                                                     06-NOV-2000; 2000WO-US30542.
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128 kgykhhltayekle 141
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                                                                                                                                                                                                                                                                                                                                   S, Annan RS,
                                                                                                                                                                                                                                                                                                                                                                     2001-335837/35
                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE (SMIK ) SMITHKLINE
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Best Local Similarity
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                                                                                                             WO200132918-A1.
                                                                                                                                                                                                                       05-NOV-1999;
                                                                             Homo sapiens
                                                                                                                                                 10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                     Kassis
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New DNA encoding hYAK3 human protein kinase polypeptides - used to treat and diagnose e.g. osteoporosis, inflammatory diseases, inflammatory bowel disease, psoriasis, dermatitis, asthma, allergies, infections, septic shock, anorexia and cancer

Claim 15; Fig 1; 23pp; English.

(SMIK) SMITHKLINE BEECHAM CORP.

Xie W;

Creasy CL,

WPI; 1998-523155/45. N-PSDB; AAV57439.

97US-0040618. 97US-0835170. 98EP-0301641

05-MAR-1998; 07-APR-1997; 05-MAR-1997;

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This is the amino acid sequence of hYAK-alpha, a novel human protein kinase that is expressed predominantly in skeletal muscle. The sequence was deduced from a full-length cDNA clone (see AAV57439) isolated from a skeletal muscle cDNA library. Another clone (see AAV57440), from a testis cDNA library, codes for a shorter form (see Splicing. The invention provides host cells and methods for producing hYAK3 polypeptides, as well as methods for treating producing hYAK3 polypeptides, as well as methods for treating subjects having need to enhance or inhibit hYAK3 activity for diagnosing a disease related to expression or activity of hYAK3, and methods for identifying agonist and antagonist compounds. HYAK3 and methods for identifying agonist and antagonist compounds. hYAK3 polypeptides and polynucleotides can be used to treat and diagnose bone loss (e.g. osteoporosis), inflammatory diseases (e.g. ARDS), rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, containist, dermatitis, asthma, allergies, infections (e.g. Dacterial, fungal, protozoal and viral infections such as HIV), HIV-Associated dachexia and other immunodeficiency disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    septic shock, pain, injury, cancers (e.g. testicular cancer), anorexia, bulimia, Parkinson's disease, cardiovascular disease, (e.g. restenosis, atheroselerosis, acute heart failure and myocardial infarction), hypotension, hypertension, urinary retention, angina pectoris, ulcers, benign prostatic hypertrophy and psychotic and neurological disorders (e.g. anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de la Tourette syndrome).
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148 kgykhhltayekle 161
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Matches 9; Conserv
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inflammation; acute respiratory distress syndrome; osteoarthritis; hebumatory bowel disease; psoriasis; dermatitis; asthma; allergy; infection; HIV; immunodeficiency; cachexia; septic shock; pain; injury; cancer; testicular cancer;

Protein kinase; hYAK-alpha; human; bone loss; osteoporosis;

Human protein kinase hYAK3-alpha.

(first entry)

21-DEC-1998

AAW75790;

AAW75790 standard; Protein; 588 AA.

15

AAW75790

Search completed: January 29, 2002, 10:21:50 Job time: 426 sec

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GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, Jane, Charles
APPLICANT: Tine, MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08257073
Patent No. 5766597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 840-333
TELEFAX: (212) 840-0712
TELEX: 42506 CURTWS
INFORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 628 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                      US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: N
STATE:
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                                                                                         (without alignments)
3.210 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, 1
Sequence 33, 1
Sequence 24, 1
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Sequence 16,
                                                                           Search time 133.18 Seconds
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Sequence 13,
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Sequence 26
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/AB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-835-170-4

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US-08-897-340-33

US-08-897-340-33

US-08-336-618-24

US-08-336-618-24

US-08-336-618-24

US-08-336-618-26

US-08-315-29-4

US-08-979-260-4

US-08-971-988-2

US-08-971-111
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US-09-328-320-2
US-08-897-340-34
US-09-252-329-34
US-08-961-083-96
                                                                                                                                                                                                                       212252 seqs, 22503292 residues
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                                                                           January 29, 2002, 10:24:09
                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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1 DQPKQYEQHLTDYEKIKEG 19
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                                                                                                                              US-09-763-397A-18
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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UNITED STATES OF AMERICA

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US-08-18-582-11
US-08-18-582-11
US-09-314-242-2
US-07-998-003A-95
US-08-453-2748-95
US-08-453-695A-95
US-08-453-702A-95
US-08-263-161A-95
US-09-099-639-95
PCT-US95-08071-95
US-09-099-639-95
US-08-95-08071-95
                                                                          US-08-453-274B-103
US-08-453-695A-103
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ALIGNMENTS

Caretha

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APPLICANT: Creasy,
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                                                                                                    Indels
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Pred. No. 1.2;
3; Mismatches · 2;
                                                                                                                                                                                                                                                                                                          APPLICANT: Creasy, Caretha
APPLICANT: Wei Xie
TITLE OF INVENTION: Human Protein Kinases hYAK3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                  Score 105; DB 1;
Pred. No. 9.9e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOCFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,170
FILING DATE: 26-FBB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GH50004
                                                                                                                                                                                                                                                        Sequence 4, Application US/08835170 Patent No. 5965420 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09359257; Patent No. 6165766; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Han, William
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEPHONE: 610-270-4026
                                                                  100.0%;
100.0%;
                                                                                                                                                        348 DQPKQYEQHLTDYEKIKEG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                      1 DOPKOYEQHLTDYEKIKEG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 amino acids
                                                                Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  King of Prussia
 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-835-170-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||: ||| |||::
| 128 KQYKHHLTAYEKLE 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
; FRAGMENT TYPE:
US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
COUNTRY: US
ZIP: 19406
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US-09-359-257-4
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1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Wei Xie
TITLE OF INVENTION: Human Protein Kinases hYAK3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
TITLE OF INVESTION: HUMAN PROTEIN KINASES HYAKS FILE REFERENCE: GH5000AX1D1
CURRENT APPLICATION NUMBER: US/09/359,257
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: 08/835,170
EARLIER FILING DATE: 1997-04-07
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEO ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA!
FILLING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 568
                                                                                                                                                                                                                                                                                                                                 Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GH50004
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; Sequence 2, Application US/08835170
; Patent No. 5965420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                 50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-835-170-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   128 KQYKHHLTAYEKLE 141
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                            4 KOYEQHLTDYEKIK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                      ) ORGANISM: Human
US-09-359-257-4
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US-09-252-329-33
Sequence 33, Application US/09252329
Sequence 34, Application US/09252329
Sequence 34, Application US/09252329
Sequence 34, Application US/09252329
Sequence 34, Application US/09252329
SEREMAL INFORMATION: Weight Control Pathway Genes and Uses TITLE OF INVENTION: Therefor NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                          Score 44; DB 2; Length 308;
Pred. No. 16;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match ,41.9%; Score 44; DB 4; Length 308; Best Local Similarity 53.8%; Pred. No. 16; Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,329
               REFERENCE/DOCKET NUMBER: MNI-005CP
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNI-005CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
APPLICATION NUMBER: 08/897,340
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TELEFAX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 39,030
                                                                                                                                                                                                                                                                                                              41.9%;
53.8%;
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TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                            Query Match 41.9
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide FRAGMENT TYPE: internal
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270 EQYEEAVRDYEKV 282
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                                                                                                                                                                                                                                                US-08-897-340-33
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STATE: MA
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Sequence 33, Application US/08897340
Patent No. 5955306
GENERAL INFORMATION:
APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.
TITLE OF INVENTION: Weight Control Pathway Genes and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                 DB 2; Length 588;
1.2;
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                                                            2; Indels
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                                                                                                                                                                                                                                                                                                 APPLICANT: Creasy, Caretha
APPLICANT: Creasy, Caretha
TITLE OF INVENTION: HUMAN PROTEIN KINASES HYAK3
FILE REFERENCE: GHSO004X1D1
CURRENT APPLICATION NUMBER: US/09/359,257
CURRENT FILING DATE: 1999-077-22
EARLIER APPLICATION NUMBER: 08/835,170
EARLIER PILING DATE: 1997-04-07
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Mindows Version 3.0
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                 Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/715,032 FILING DATE: 17-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    US-09-359-257-2

Sequence 2, Application US/09359257

Patent No. 6165766

GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%;
64.3%;
            Query Match
Best Local Similarity 64.3°
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                          148 KQYKHHLTAYEKLE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||: ||| |||:
|148 KQYKHHLTAYEKLE 161
                                                                                                4 KOYEQHLTDYEKIK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human
US-09-359-257-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 588
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ISOLATION OF AN Mr 52,000 FK506 BINDING PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN CDNA
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Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
TITLE OF INVENTION: CDNA
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Pred. No. 24;
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                                                                                                                                            Smith and Reynolds, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton, Brook, Smith and Reynolds, P.C.
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NDATA:

APPLICATION NUMBER: US/08/336,618

FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/777,752
PRIOR APPLICATION NUMBER: US 07/777,752
PRIOR APPLICATION NUMBER: CT 1991
PRIOR APPLICATION NUMBER: PCT/FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
                     TITLE OF INVENTION: ISOLATION OF TITLE OF INVENTION: ESOLATION OF TITLE OF INVENTION: CDNA NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ADDRESSE: Hamilton, Brook, STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 459 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 5/...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                              Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-336-618-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| || :| || 244 KYELHLKSFEKAKE 257
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STATE: Massachusetts
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                                                                                                                                                                                                                                                     ZIP: 02173
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                                                                                                                                                                                      CITY: Lex
STATE: Ma
COUNTRY:
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                                                                                                                                                                                                                       APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
NUMBER OF SEQUENCES: 32
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ADDRESSE: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STRATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 1; Length 458; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-0CT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPI91-06A
                                                                                                                                                   Sequence 24, Application US/08336618 Patent No. 5763590 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/0833618
Patent No. 5763590
GENERAL INFORMATION:
APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFRENCE/POCKET NUMBER: VP19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 458 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.9
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-336-618-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| || :|| || 244 KYEVHLKSFEKAKE 257
                         :|||: : ||||:
270 EQYEEAVRDYEKV 282
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4 KQYEQHLTDYEKI 16
                                                                                                                                   US-08-336-618-24
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
AP
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                                                                                                                                                                                                                                                                                                                                                                                         Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
0609.4260001/JAG/SRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Porter Dr. CITY: Palo Alto
STATE: CA
COUNTRY: USA
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APPLICATION NUMBER: 08/977,816
FILING DATE:
                   TELECOMMUNICATION INFORMATION:
TELEPAX: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
WOLECULE TYPE: protein
US-08-879-260-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09231529 Patent No. 6096308
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                               41.9%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 53.87
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-416b
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||: : ||||:
332 EQYEEAVRDYEKV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KQYEQHLTDYEKI 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: COLL...
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US-09-231-529-4
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Pred. No. 24;
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N.W., Suite 600
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION DATA:
APPLICATION DATE: US-OT-1992
APPLICATION DATE: US-OT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION PROPARATION:
APPLICATION PROPARATION:
APPLICATION PROPARATION:
APPLICATION PROPARATION:
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Patent No. 593881
GENERAL INFORMATION:
APPLICANT: MULTHY, Anita E.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: TPR-Containing Genes NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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STREET: 1100 New York Ave, N.W.,
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20JUN1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VPI9
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-336-618-26
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 QYEQHLTDYEKIKE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-879-260-4
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RESULT 15
US-08-971-988-2
; Sequence 2. Application US/08971988
; Patent No. 5786461
; GENERAL INFORMATION:
; APPLICANT: Michiyuki MATSUDA et al.
; TITLE OF INVENTION: CDNA OF DOCK180 GENE AND DOCK180 PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ....eveckE: Wenderoth, Lind & Ponack
           CDNA OF DOCK180 GENE AND DOCK180 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 1865;
Pred. No. 1.1e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:

ORIGINAL SOURCE: spleen cell of homo sapiens

US-08-588-985-2
                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                           ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,985
                                                                                                                                                                                                                                                                                                               January 19, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                         FILING DATE: January 19, 71
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITED M. Cheek, JF.
REGISTRATION NUMBER: 33,36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.98;
46.78;
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1865 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1302 EQYENEMFDYEQLSE 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KQYEQHLTDYEKIKE 18
                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: Si
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20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                           Gaps
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                                                                                                                                                                                   Sequence 4, Application US/08977816
Patent No. 6194186
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEIN KINASE AND KINASE INHIBITORS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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Pred. No. 26;
4; Mismatches 2; Indels
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: In Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,816
FILING DATE: Filed Herewith
CLASSIFFCATION: 435
PROS APPLICATION 1435
PROGRAPLICATION NUMBER:
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0429 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.9%;
53.8%;
   53.8%;
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                   7; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.8
Matches 7; Conservative
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COMPUTER READABLE FORM:
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332 EQYEEAVRDYEKV 344
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332 EQYEEAVRDYEKV 344
                                                       4 KOYEQHLTDYEKI 16
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CLONE: 701698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CLONE: 7
US-08-977-816-4
                                                                                                                                                                     US-08-977-816-4
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Gaps

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                                                                                                                                                                                                                                                                                  TELEX:
TELEX:
TELEX:
TELEX:
SEQUENCE CHARACTERISTICS:
LENGTH: 1865 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOUNCE: spleen cell of homo sapiens
US-08-971-988-2
APPLICATION NUMBER: US/08/971,988
FILING DATE: 17-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/588,985
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELECHONE: 202-371-8850
```

Search completed: January 29, 2002, 10:24:10 Job time: 516 sec

:||| : |||: | Db 1302 EQYENEMFDYEQLSE 1316 4 KOYEQHLTDYEKIKE 18

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(without alignments)
9.984 Million cell updates/sec
                                                                                                          January 29, 2002, 10:26:44; Search time 144.96 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                     US-09-763-397A-18
105
1 DQPKQYEQHLTDYEKIKEG 19
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                    Scoring table:
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Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

apical membrane an 66k merozoite surf apical membrane an hypothetical prote probable integral botulinum neurotox hypothetical prote cytochrome-c oxida ribonucleotide red DNA (cytosine-5)-MMC class II alpha ketol-acid reducto lectine like oxidiz hypothetical prote hypothetical prote hypothetical prote hsp 90-binding pro hypothetical prote developmental prot cis-Golgi matrix p ro-3 protein - Neu hypothetical prote immunophilin FKBP5 Description SUMMARIES JE0111 E82912 T17406 H64355 F75216 A83700 A46372 T10754 T18364 E82895 D44986 B44986 A44986 A44986 C44986 A44944 A44944 A44964 T131570 T10733 T10733 T10733 A44964 T131570 T10733 A44964 T131570 T10644 T131573 T10644 T1064 T10644 Query Match Length DB 463 333 372 1165 222 222 319 696 1573 332 362 1022 256 281 299 Score Result Š

hypothetical prote hypothetical prote satl protein - fis	Satlp - fission ye hypothetical prote hypothetical prote conserved hypothetical	CT144 hypothetical conserved hypothet ketol-acid reducto	hypothetical prote iron-sulfur cluste hypothetical membr Ll protein - human	glucose inhibited hypothetical prote
T27372 T19872 T43544	T39942 H70377 D71453 R72099	H86522 F86865 H75044	D84079 H69393 B82931 P1WL5	D82942 E96558
000	0000	777	7777	0 0
320 329 441	550 169 279	289 307 332	337 363 394 516	614 765
41.4	41.4 41.0 41.0	41.0 41.0 41.0	41.0 41.0 41.0	41.0
443.5 43.5 5.5	43.5 43.5 43.5	4 4 4 6 6 6 6	4 4 4 4 w w w w	43
30 31 32	33 35 35	37 38 39	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44

ALIGNMENTS

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Discal membrane antigen 1 precursor - Plasmodium fragile
C; Species: Plasmodium fragile
C; Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C; Accession: A4494#
R; Peterson, M.G.; Nguyen-Dinh, P.; Marshall, V.M.; Elliott, J.F.; Collins, W.E.; Ande Mol. Blochem Parasitol. 39, 279-284, 1990
A; Title: Apical membrane antigen of Plasmodium fragile.
A; Reference number: A44944; MUID:90205978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Plasmodium knowlesi
C.Species: Plasmodium knowlesi
C.Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C.Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C.Accession: A39238
B.Waters, A.P.; Thomas, A.W.; Deans, J.A.; Mitchell, G.H.; Hudson, D.E.; Miller, L.H.
J. Biol. Chem. 265, 17974-17979, 1990
A.Title: A merozoite receptor protein from Plasmodium knowlesi is highly conserved an A.Reference number: A39238
A.Fatus: preliminary
A.Accession: A39238
A.Status: preliminary
A.Wolecule type: mRNA
A.Residues: 1-563 <a href="Mailto-WAT">Mailto-WAT</a>
A.Coss.references: GB:J05631
C.Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prical membrane antigen 1 - Plasmodium chabaudi adami
C;Species: Plasmodium chabaudi adami
C;Species: Plasmodium chabaudi adami
C;Dacession: A44964
R;Marshall, V.M.; Peterson, M.G.; Lew, A.M.; Kemp, D.J.
Mol. Blochem: Parasitol. 37, 281-283, 1989
A;Fitle: Structure of the apical membrane antigen I (AMA-1) of Plasmodium chabaudi.
A;Reference number: A44964; MUID:90114335
                                                                    Gaps
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        Length 622;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66K merozoite surface antigen precursor - Plasmodium knowlesi
        Score 105; DB 2;
Pred. No. 3.7e-08;
Mismatches 0;
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0.00015;
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Pred. No. (
                                                                    0;
           100.0%;
100.0%;
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                                                                                                                                                             348 DQPKQYEQHLTDYEKIKEG 366
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293 DQPTQYEEELTDYQKIQEG 311
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293 DQPRQYEEELTAYEKIQEG 311
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                                                                                                                            1 DOPKOYEQHLTDYEKIKEG 19
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Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Accession: A44944
A Status: preliminary
A Molecule type: DNA
Residues: 1-562 < PFIP
A Cross-references: GB:M29898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 77.1
Best Local Similarity 73.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 73.7
Matches 14; Conservative
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                                                                                                                C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 12-oct-1889 #sequence_revision 12-oct-1989 #text_change 09-Jun-2000
C; Accession: A32499
B; Peterson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; Ande Mol. Cell. Biol. 9, 3151-3154, 1989
A; Title: Integral membrane protein located in the apical complex of Plasmodium falciparu A; Reference number: A32499; MUID:89384584
A; Reference number: A32499; MUID:89384584
A; Molecule type: DNA; mRNA
A; Molecule type: DNA; mRNA
A; Residues: 1-622 < PET>
A; Cross-references: GB:M27133; NID:g160072; PID:g160073
C; Keywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain CAMP)
C;Species: Plasmodium falciparum
C;Satecies: Plasmodium falciparum
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C;Accession: A44986
R;Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti A;Cession: A44986
A;Accession: A44986
A;Accession: A44986
A;Accession: A44986
A;Accession: A44986
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-62, CTHO>
A;Cross-references: GB:M34552
C;Keywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
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C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C; Accession: C44986
R; Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A; Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate
A; Reference number: A44986; MUID:91101665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain FCR 3)
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                                                                                              malaria parasite (Plasmodium falciparum)
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Pred. No. 3.7e-08;
0; Mismatches 0;
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ilarity 100.0%; Pred. No. 3.7e-08;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 19; Conservative 0;
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A; Cross-references: GB:M34554
C; Keywords: membrane protein:
                                                                                              antigen 1
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Contacts and the grain membrane protein Cj1662 [imported] - Campylobacter jejuni (strain N C Species: Campylobacter jejuni (Species: Campylobacter) (Species: Campylobacter) (Species: Campylobacter) (Species: Campylobacter (Campylobacter Jejuni reveals (Campylobacter Jejuni reveals (Campylobacter Jejuni reveals (Campylobacter Jejuni reveals (Campylobacter) (Species: Campylobacter Jejuni reveals (Campylobacter) (Campylob
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A:Molecule type: DNA
A:Rolecule type: DNA
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A;Cross-references: EMBL:X71086; NID:9509740; PIDN:CAA50404.1; PID:9509741
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993 C;Genetics:
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Pred. No. 52;
2; Mismatches
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Pred. No. 1
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nilarity 61.1%;
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ilarity 57.1%;
Conservative
     211 EKPKEHEKHEVEYPKIPE 228
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257 DVPKVFEKHKNDYE 270
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Best Local Similarity
Matches 11; Conserv
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C;Species: Gossypium barbadense (sea-island cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Mar-2000
C;Accession: T10738
R;Rinehart, J.; Petersen, M.; John, M.E.
Bubmitted to the EMBL Data Library, August 1995
A;Description: Tissue-specific and developmental regulation of cotton mRNA, FbLate-2: Pr
A;Reference number: 217108
A;Accession: T10738
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y105c5A.m - Caenorhabditis elegans
C;Secies: Caenorhabditis elegans
C;Secies: Caenorhabditis elegans
C;Secies: Oscort.1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31570
R;McMurray, A.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21045
A;Accession: T31570
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T31570
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-463 <WIL>A;Residues: 1-463 <WIL>A;Cross-references: EMBL:AL117193; NID:e1549703; PIDN:CAB54993.1; CESP:Y105C5A.m
A;Residues: 1-463 <WIL>A;Residues: 1
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A; Cross-references: EMBL:U34401; NID:g1143223; PID:g1143224
A; Experimental source: cv. Sea Island
C; Genetics:
                                                                                     A;Molecule, type: DNA
A;Residues: 1-558 <MAR>
A;Cross-references: GB:M25248; NID:g160076; PID:g160077
C;Reywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 2;
Pred. No. 0.0036;
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Pred. No. 3.3;
6; Mismatches
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Pred. No. 3.3;
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C;Superfamily: proline-rich protein 3
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60.0%;
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Best Local Similarity 68.4%;
Matches 13; Conservative
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64 KEYEMHLTDTTKLEE 78
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A; Accession: A44964
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hypothetical protein At2g07520 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: E84.86
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD: 20083487
A; Molecule type: DNA
A; Residues: 1-222 <STO>
A; Cross-references: GB: AE002093; NID: 94895172; PIDN: AAD32760.1; GSPDB: GN00139
C; Genetics:
A; Gene: At2g07520
A; Map position: 2
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-319 <SEE>
A; Residues: 1-319 <SEE>
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A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: cox; SCOEDB:SC6G10.29c
C; Superfamily: cytochrome-c oxidase chain II; cytochrome-c oxidase chain II homology
C; Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp
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R.Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A; Reference number: A70300; MUID:99196666 A; Accession: A70431 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: A70431
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Feb-2000
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Pred. No. 18;
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282 PERYEQHLQDLAK 294
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A: Residues: 1-696 <AQF>
A; Cross-references: GB:AE000743; NID:g2983875; PIDN:AAC07431.1; PID:g2983879; GB:AE00 A; Experimental source: strain VF5
C; Genetics:
A; Gene: nrdF
Query Match
Best Local Similarity 75.0%; Pred: No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Bot Local Similarity 75.0%; Pred: No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 72 KQYETVLSDYEK 15
Search completed: January 29, 2002, 10:26:45
Job time: 656 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 11:13:46; Search time 80.65 Seconds (without alignments) 8.638 Million cell updates/sec Run on:

US-09-763-397A-18 105 1 DOPKOYEOHLTDYEKIKEG 19 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	riptio	1								O43781 homo sapien		P93779 solanum mel	Q57890 methanococc	P27124 oryctolagus	homo	Q99615 homo sapien	Q62839 rattus norv	Q01397 neurospora			Q9uz09 pyrococcus	_	_	Q57588 methanococc		-	_	Q9pre0 ureaplasma	P40053 saccharomyc	O14286 schizosacch	Q21974 caenorhabdi	_	900	067453 aquifex aeo
SUMMARIES	ΩI	AMA1_PLAF8	AMA1_PLAFC	AMA1_PLAFF	AMA1_PLAFG	AMA1_PLAFH	PK66_PLAKU	AMA1_PLAFR	AMA1_PLACH	DYR3_HUMAN	ILVC_ARCFU	RL5_SOLME	Y448_METJA	FKB4_RABIT	FKB4_HUMAN	TTC2_HUMAN	GM13_RAT	DYNA_NEUCR	Y416_UREPA	YQG1_CAEEL	ILVC_PYRAB	VL1_HPV05	GIDA_UREPA	Y124_METJA	IM9A_HUMAN	IM9A_MOUSE	Y142_UREPA	RF1_UREPA	YERO_YEAST	YETI_SCHPO	UNC8_CAEEL	SRP_DROME	BACA_BACLI	YE76_AQUAE
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100.0%; Score 105; DB 1; Length 622;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels

1 DQPKQYEQHLTDYEKIKEG 19

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218 223 385 385 457 457 692 897 1006 1103 1103	AFB STANDARD; PRT; 62 1996 (Rel. 34, Created) 1996 (Rel. 34, Last sequence upd 2001 (Rel. 40, Last annotation u 1997 (Rel. 40, Last annotation u 1997 (Rel. 40, Last annotation u 105-5726; 23, Alveolata; Apicomplexa; Haem 105-5726; 24, Alveolata; Apicomplexa; Haem 105-5726; 25 FROM N.A. 29 Hold65; Pubmed-2270110; 24 Auters A.P., Carr D.; 25 FROM N.A. 29 Hold65; Pubmed-2270110; 20 Variation in PFB3, an eryt 20 eantigen of Plasmodium falcipa 20 of variation in PFB3, an eryt 20 eantigen of Plasmodium falcipa 20 of variation in PFB3, an eryt 21 eantigen of Plasmodium falcipa 22 copyright. It 24 Autitude 25 G22 Apical MEM 26 Apical MEM 27 SAG SAG SAG SAG SAG SAG 28 EXTRACELLU 28 Apical MEM 29 Apical MEM 20 Apical MEM 21 Apical MEM 22 Apical MEM 23 Apical MEM 24 Apical MEM 25 Apical MEM 26 Apical MEM 27 Apical MEM 28 Apical MEM 28 Apical MEM 29 Apical MEM 21 Apical MEM 21 Apical MEM 22 Apical MEM 23 Apical MEM 24 Apical MEM 25 Apical MEM 26 Apical MEM 27 Apical MEM 28 Apical MEM 28 Apical MEM 29 Apical MEM 20 Apical MEM 20 Apical MEM 21 Apical MEM 22 Apical MEM 23 Apical MEM 24 Apical MEM 25 Apical MEM 26 Apical MEM 27 Apical MEM 28 Apical MEM
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SEQUENCE FROM N.A.
MEDLINE=91101665; PubMed=2270110;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
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                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate Camp / Malaysia).
Bukaryota, Alveolata, Apicomplexa; Haemosporida, Plasmodium.
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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SIGNAL 1 24 norman
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01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                        622 AA.
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Pfam; PF02430; AMA-1; 1.
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348 DOPKOYEQHLTDYEKIKEG 366
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Matches 19; Conservative
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P50489;
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01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-N (IN REF. 1; AAA29476).

I -> M (IN REF. 1; AAA29476).

I -> M (IN REF. 1; AAA29476).

N-N (IN REF. 1; AAA29476).

N-N (IN REF. 1; AAA29476).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5838;
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SEQUENCE FROM N.A.
MEDLINE=89384584; Pubmed=2701947;
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Pfam; PF02430; AMA-1; 1.
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72009 MW;
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EMBL; M27957; AAA29476.1; -.
EMBL; A08267; CAA00764.1; -.
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                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Thomas A.W., Waters A.P., Carr D.;
"Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum.";
Mol. Blochem. Parasitol. 42:285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PR66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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N.LINKED (GLCNAC. .) (POTENTIAL).
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01-ocT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 1; Length 622;
Pred. No. 7e-08;
Mismatches 0; Indels
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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InterPro; IPR003298; Apmem_Ag1.
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286
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Best Local Similarity
Matches 19; Conserv
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P50491;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waters A.P., Thomas A.W., Mitchell G.H., McCutchan T.F.;
Waters A.P., Thomas A.W., Mitchell G.H., McCutchan T.F.;
"Intra-generic conservation and limited inter-strain variation in a protective minor surface antigen of Plasmodium knowlesi merozoites.";
Mol. Biochem. Parasitol. 44:141-144(1991).
-I- FUNCTION: MEROZOITE RECEPTOR PK66 IS A SURFACE ANTIGEN INVOLVED IN PARASITE INVASION OF ENTHROCYTES.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CONCENTRATED AT THE APICAL END PRIOR TO RUPTURE, FOLLOWING WHICH IT CAN DISTRIBUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITSELF ENTIRELY ACROSS THE SURFACE OF THE FREE MEROZOTTE. DURING INVASION PK66 IS EXCLUDED FROM THE ERYTHROCYTE AT, AND BEHIND, THE INVASION INTERFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANBOUS: PK66 EXPRESSED IN MATURE SCHIZONTS IS RAPIDLY PROCESSED AS THE SCHIZONT RUPTURES, YIELDING A 42/44 KDA DOUBLET ASSOCIATED WITH THE SURFACE MEROZOITE SIMILARITY: STRONG TO AMA-1/PP83 OF P.FALCIPARUM, P.CHABAUDI, AND
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MEROZOITE RECEPTOR PK66 PRECURSOR (66 KDA PROTECTIVE MINOR SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91009268; PubMed=2211675; Waters A.P., Thomas A.W., Deans J.A., Mitchell G.H., Hudson D.E., Waller L.H., McCutchan T.F., Cohen S.; A merozoite receptor protein from Plasmodium knowlesi is highly conserved and distributed throughout Plasmodium."; J. Biol. Chem. 265:17974-17979(1990).
                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                      Score 105; DB 1; Length 622;
Pred. No. 7e-08;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                              Antigen; Glycoprotein
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                                              EMBL; M58547; AAA29720.1;
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Best Local Similarity 100.
Matches 19, Conservative
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                                                                             Pfam; PF02430; AMA-1; 1.
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P21303;
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                                                                InterPro:
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              the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Swiss Institute of Bioinformatics and the EMBL outstation
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MEDLINE-90205978; PubMed=2181309;

MEDLINE-90205978; PubMed=2181309;

Peterson M.G., Nguyen-Dinh P., Marshall V.M., Elliott J.F.,

Collins W.E., Anders N.F., Kemp D.J.;

"Aploal membrane antiqen of Plasmodium fragile.";

Mol. Biochem. Parasitol. 39:279-284(1990).

-i FUNCTION: INVOLEDE IN PARASITE INVASION OF ENTHROCYTES.

-i SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FALCIPARIUM, AND

TO PR66 FROM P.KNOWLESI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-X (IN STRAIN LINE WI).
N-> K (IN STRAIN LINE WI).
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01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMMRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.9%; Score 87; DB 1; Length 563; 78.9%; Pred. No. 2.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                             MEROZOITE RECEPTOR PK66.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A44944; A44944.
Interpro; IPR003298; Apmem_Ag1.
Priem; PF03430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                          Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
SIGNAL 1 13 POTENTIAL.
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                                                                                                                                       EMBL; M61097; AAA29728.1; -.
InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            64680 MW;
                                                                                                                      EMBL; M58317; AAA63444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29898; AAA29474.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DOPKOYEQHLTDYEKIKEG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
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P22622;
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Infect. Immun. 64:3310-3317(1996).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SUBCELLULAR: STRONG TO AMA-1/PF83 FROM P.FALCIPARUM, P.FRAGILE AND
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90114335; PubMed=2608101;
Marshall V.M., Peterson M.C., Lew A.M., Kemp D.J.;
"Structure of the apical membrane antigen I (AMA-1) of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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Plasmodium chabaudi involve recognition of strain-specific
                                                                                                                                                                                                                                                                                                                                              Score 81; DB 1; Length 562;
Pred. No. 0.00019;
3; Mismatches 2; Indels
                           APICAL MEMBRANE ANTIGEN 1. EXTRACELLULAR (POTENTIAL).
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APICAL MEMBRANE ANTIGEN 1.
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Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
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  POTENTIAL
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                                                                                                                                                                                                                                                                   64488 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 DOPTQYEEELTDYQKIQEG 311
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SEQUENCE OF 38-377 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.7
Matches 14; Conservative
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21
562
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  1 22 22 22 22 508 508 84 84 05 64 05 64 17 6
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P16445;
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D43D897D34C29D9E CRC64;

65812 MW;

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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).

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PROTEIN KINASE

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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam; PP000069; pkinase; 4.
Pfam; PP000020; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00100; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonlane-protein kinase; ATP-binding; Phosphorylation.
 HSSP; Q16539; 1A9U.
                MIM; 603497;
                                                                                                                                                                                               ACT_SITE
SEQUENCE
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BINDING
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                                                                                                                                                                                                             Gaps
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Xia J., Yang X., Ruan Q., Pan Q., Liu C., Xie W., Deng H.;
"Molecular cloning and characterization of novel protein kinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence characteristics, subcellular localization, and substrate specificity of DYRK related Kinases, a novel family of dual specificity protein kinases "; J. Biol. Chem. 273:25893-25902(1998).
                  CYTOPLAIN.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Fetal brain;
MEDINE-98421512; Pubmed-9748265;
Becker W., Weber Y., Wetzel K., Elrmbter K., Tejedor F.J.,
Joost H.-G.;
                                                                                                                                                                                Score 72; DB 1; Length 558;
Pred. No. 0.0038;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
 EXTRACELLULAR (POTENTIAL).
                                                                                                                          N-LINKED (GLCNAC. . .) (PC
9773F3E6A439A972 CRC64;
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                            5;
                                                                                                                                          63973 MW;
                                                                                                                                                                                  68.6%;
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                                                                                                                                                                                                                                                        68.48;
                                                                                                                                                                                                                                        1 DOPKQYEQHLTDYEKIKEG 19
                                                                                                                                                                                Query Match 68.65
Best Local Similarity 68.45
Matches 13; Conservative
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480
503
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CARBOHYD
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                                                                                                                                       SEQUENCE
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DYR3_HUMAN
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or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049343; PubMed=980475;
MELON D. C. C. C. Winn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.L., Woreli L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Overbeek R., Gorayne T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- CARTALYTIC ACTIVITY: (R)-2,3-DIHYDROXY-3-METHYLBUTANOATE + NADP(+)
-!- FS)-2-HYDROXY-2-METHYL-3-OXOBUTANOATE + NADPH.
-!- PATHWAY: VALINE AND ISOLEUCINE BIOSYNTHESIS; SECOND STEP.
-!- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
                                            Gaps
                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Last sequence update)
Co.NdG-2001 (Rel. 40, Last annotation update)
KETOL-ACID REDUCTOTSOMERASE (E.C. 1.1.1.86) (ACETOHYDROXY-ACID
ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-
                                            ö
50.5%; Score 53; DB 1; Length 588; 64.3%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                            2; Indels
                                                                                                                                                                                                                                                     332 AA.
                       Pred. No. 2.3;
3; Mismatches
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Query Match 50.5
Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                 148 KQYKHHLTAYEKLE 161
                                                                                       4 KOYEQHLTDYEKIK 17
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Matches

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20-AUG-2001 (Rel. 40, Last annotation update)
ES9 PROTEIN (HSP BINDING IMMUNOFHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (FKBP52 PROTEIN) (52 KDA FKS06 BINDING PROTEIN) (FKBP59).
                                                                                                        MEDLINE=9633799; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lebeau M.-C., Massol N., Herrick J., Faber L.E., Renoir J.-M., Radanyl C., Baulieu E.-E.; "PS9, an hsp 90-binding protein. Cloning and sequencing of its cDNA and preparation of a peptide-directed polyclonal antibody."; J. Biol. Chem. 267:4281-4284(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92335279; PubMed=1631118; Callebaut I., Renoir J.-M., Lebeau M.-C., Massol N., Burny A., Baulieu E.-E., Mornon J.-P.; "An immunophilin that binds M(r) 90,000 heat shock protein: main
          Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 256; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein; Complete proteome.
256 AA; 29409 MW; 0A4773E57FDECCEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996).
-!- SIMILARITY: TO M.JANNASCHII MJ0301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
MEDLINE=92165768; PubMed=1537818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.9%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U67496; AAB98437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 PREYEYEMEEFQCIKDG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PKQYEQHLTDYEKIKEG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 6; Conserv
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                   NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; MJ0448;
Hypothetical
                                                                                                                                                                                                                                                                                                                                             jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKB4_RABIT
P27124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Matches
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          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum melongena (Eggplant) (Aubergine).
Wakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Momiyama T., Kayano T., Takaiwa F., Takayanagi K.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIBP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                       5;
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0
                                                              Oxidoreductase; Branched-chain amino acid biosynthesis; NADP;
                                                                                                                                                                                            DB 1; Length 332;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 121; Pred. No. 9.3;
                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                      POTENTIAL.; 598EF6AB3E2B000F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
13979 MW; DOCBBF76A71FF02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update) 60S RIBOSOMAL PROTEIN L5 (FRACMENT).
TIGR; AF1985; -.
InterPro; IPR000506; Acetohydrxac_isomrdctse.
Pfam; PF01450; IlvC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                          Score 45; DB 1
Pred. No. 18;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                            37212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
15-DEC-1998 (Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB001583; BAA19415.1; -.
                                                                                                                                                                                          42.9%;
50.0%;
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                                                                                                                                                                                                                                                                                                               87 OPAVYREHIOD -- KLKEG 102
                                                                                                                                                                                                                                                                         2 QPKQYEQHLTDYEKIKEG 19
                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                            332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA;
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Best Local Similarity
                                                                                 Complete proteome.
ACT_SITE 109
SEQUENCE 332 AA;
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Cotyledon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y448_METJA
ID Y448_METJA
AC Q57890;
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9
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P93779;
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SEQUENCE
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Indels

457 AA.

Matches

ò g 243 KYEVHLKSFEKAKE 256

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RESULT 14
FKB4_HUMAN
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                                                                                                                                                                                                                                                                                                             ŝ
                                                                      MEDLINE-96154240; PubMed-8579335; Deshpande K.L., Seubert P.H., Tillman D.M., Farkas W.R., Katze J.R.; "Cloning and characterization of cDNA encoding the rabbit tRNN-guanine transqlycosylase 60-kilodalton subunit."; Arch. Biochem. Biophys. 326:1-7(1996).
                                                                                                                                                                                                                                                        BLOCHEMISTRY 35:11045-11052(1996).

-I- FUNCTION: BINDS TO HSP90 AND IS ASSOCIATED WITH IT, INCLUDING WHEN HSP90 PARTICIPATES IN HETBRO-OLIGOMERIC COMPLEXES OF UNTRANSFORMED MAMMALLIAN STEROID RECEPTORS THAT SEDIMENT AT 8-10 P59 MAY HAVE A ROTAMASE ACTIVITY WHICH MAY APPLY TO BOUND HSP90 AND THUS BE IMPLIED IN THE INTRACELLULAR TRAFFICKING OF HETERO-OLIGOMERIC FORMS OF STEROID HORMONE RECEPTORS.

-I- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                MEDLINE-96374215; PubMed-8780506; Craescu C.T., Rouviere N., Popescu A., Cerpolini E., Lebeau M.-C., Baulieu E.E., Mispelter J.; "Three-dimensional structure of the immunophilin-like domain of FKBP59 in solution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: INTERACTS WITH PEROXISOMAL PHYTANOYL-COA ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKBP-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00453; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_2; 2.
PROSITE; PS50059; FKBP_PPIASE_3; 2.
ISOMerase; Rotamase; TPR repeat; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> T (IN REF. 3).
EC58CC4BCF66A44A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> H (IN REF. 3).
structural features of a mammalian p59 protein."; Proc. Natl. Acad. Sci. U.S.A. 89:6270-6274(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKBP-TYPE 1.
FKBP-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB :
Pred. No. 35;
2; Mismatches
                                                            STRAIN-NEW ZEALAND WHITE; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S -> H (I
EG -> FI
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TPR 1.
TPR 2.
TPR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001179; FKBP_PPIase.
InterPro; IPR001440; TPR.
Pfam; PF00254; FKBP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M84474; AAA31438.1; -. EMBL; M84988; AAA31439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.9%;
ilarity 57.1%;
Conservative
                                                                                                                                                                     STRUCTURE BY NMR OF 1-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
252
302
351
385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A42386; A42386.
PDB; IROT; 07-DEC-96.
PDB; IROU; 07-DEC-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
166
269
318
353
14
20
20
25
                                            SEQUENCE OF 1-25
                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D-structure.
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                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
PSP PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL
CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPTASE) (ROTAMASE) (FKBP52 PROTEIN)
(52 KDA FK506 BINDING PROTEIN) (P52) (FKBP59) (HSP56).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 93066366; PubMed-1279700;
Peattie D.A., Harding M.W., Fleming M.A., Decenzo M.T.,
Lippke J.A., Livingston D.J., Benasutti M.;
Expression and characterization of human FKBP52, an immunophilin
that associates with the 90-kDa heat shock protein and is a component
of steroid receptor complexes.";
Proc. Natl. acad. Sci. U.S.A. 89:10974-10978(1992).
I-FUNCTION: BINDS TO HSP90 AND IS ASSOCIATED WITH IT, INCLUDING
WHEN HSP90 PARTICIPATES IN HETERO-OLIGOMERIC COMPLEXES OF
UNTRANSPORMED MAMMALIAN STEROID RECEPTORS THAT SEDIMENT AT 8-10 S.
P59 MAY HAVE A ROTAMASE ACTIVITY WHICH MAY APPLY TO BOUND HSP90
AND THUS BE IMPLED IN THE INTRACELLULAR TRAFFICKING OF HETERO-
OLIGOMERIC FORMS OF STEROID HORMORE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- TISSUE SPECIFICITY: WIDELY EXPRESSED.
-i- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          MEDLINE-92147620; PubMed-1371107;
Yem A.W., Tomasselli A.G., Heinrikson R.L., Zurcher-Neely H., Ruff V.A., Johnson R.A., Delbel M.R.;
"The Hsp56 component of steroid receptor complexes binds to immobilized FK506 and shows homology to FKBP-12 and FKBP-13.";
J Biol. Chem. 267:2868-2871(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: INTERACTS WITH PEROXISOMAL PHYTANOYL-COA ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00453; FKBP_PPIASE_1; 1.
PROSITE; PS00454; FKBP_PPIASE_2; 2.
PROSITE; PS50059; FKBP_PPIASE_3; 2.
ISOMERASE; ROTAMASE; Repeat; TPR repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROXYLASE.
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPIASE, FKBP-TYPE 1. PPIASE, FKBP-TYPE 2.
  459 AA
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001179; FKBP_PPlase.
InterPro; IPR001440; TPR.
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00254; FKBP; 2.
Pfam; PF00515; TPR; 3.
                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A46372; A46372.
HSSP; P27124; 1ROU.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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FKB4_HUMAN
002790;
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DOMAIN
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Gaps

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Indels

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5 OYEQHLTDYEKIKE 18

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Length 457;

DB 1;

Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWIss Institute of Bioinformatics and the EMBL outstation—the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           ö
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96433003; PubMed=8836031; Murthy A.E., Bernards A., Church D., Wasmuth J., Gusella J.F.; "Identification and characterization of two novel tetratricopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                           ;
0
                                                                                                                    DB 1; Length 459; 36;
                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last annotation update)
TETRATRICOPEPTIDE REPEAT PROTEIN 2 (TPR REPEAT PROTEIN 2).
                                                                                                                                                         Indels
                                                         6A498105418D9435 CRC64;
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4147EBDB0CE50DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat-containing genes.";
DNA Cell Biol. 15:727-735(1996).
-!- SUBUNIT: INTERACTS WITH THE GAP DOMAIN OF NF1.
-!- SIMILARITY: CONTAINS 9 THE REPEATS.
-!- SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                            484 AA.
                                                                                                                  Score 44; DB Pred. No. 36; 2; Mismatches
   TPR 1.
TPR 2.
TPR 3.
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PROSITE; PS50076; DNAJ_2; 1.
Repeat; TPR repeat; Chaperone.
18 51 TPR 1.
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TPR 2.
TPR 4.
TPR 5.
TPR 6.
TPR 6.
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 303 TP
352 TP
386 TP
51804 MW;
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ilarity 57.1%;
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InterPro; IPR001440; TPR.
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Pfam; PF00515; TPR; 8.
SMART; SM00271; DnaJ; 1.
SMART; SM00028; TPR; 7.
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270
319
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459 AA;
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Best Local Similarity
Matches 8; Conserv
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Q99615;
                                                           SEQUENCE
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TTC2_HUMAN
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41.9%; Score 44; DB 1; Length 484;

Query Match

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Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 4; Mismatches 2; Indels 0;
Qy 4 KOYEQHLTDYEKI 16
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Search completed: January 29, 2002, 11:13:47 Job time: 823 sec

(OTASU) NNALB 3DA9 SIHT

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Goel V.K., Chishti A.H., Oh S.S.;
Goel V.K., Chishti A.H., Oh S.S.;
"Plasmodium falciparum apical membrane antigen-1 (AMA-1) gene, partial
"DNA sequence.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352829; AAK26116.1;
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099hq3
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09bh26
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 402;
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402 402
402 AA; 46227 MW; 06DAE211FD596275 CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEROZOITE ANTIGEN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 105; DB 5; 100.0%; Pred. No. 3.4e-07;
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098H01
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Matches 19; Conservative
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                                Plasmodium falciparum.
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Q9BHS1;
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01-JUN-2001 (
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9.739 Million cell updates/sec
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                                                      Search time 285.36 Seconds
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                             473505 seqs, 146272329 residues
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                                                      January 29, 2002, 11:12:14
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
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sp_phage:*
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seq length: 200000000
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Query Match

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09BHS0

RESULT Q9BHS0

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Gaps
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                  SEQUENCE FROM N.A.

STRAIN-NIGERIAN 015;
Polley S.D., Conway D.J.;
Polley S.D., Conway D.J.;
Pliversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ40833; CAC34744.1; -.
NON_TER 1
NON_TER 437 437
SEQUENCE 437 AA; 50243 MW; 28D9E9E5165A39EE CRC64;
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SEQUENCE FROM N.A.
STRAIN S.D.; CONWAY D.J.;
Poiley S.D.; Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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50243 MW; 28D9E9E5165A39EE CRC64;
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Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN I (FRAGMENT).
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                                                                                                                                                                                                  100.0%; Score 105; DB 5; 100.0%; Pred. No. 3.7e-07;
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Pred. No. 3.7e-07;
; Mismatches 0;
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100.0%;
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Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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STRAIN=NIGERIAN 029;
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01-JUN-2001
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SEQUENCE 1
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                                                                                                                Polley S.D., Conway D.J.;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408300; CAC34741.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-NIGERIAN 006;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408302; CAC34743.1; -.
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                       Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                          50218 MW; C043561972E8D49F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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Pred. No. 3.7e-07;
0; Mismatches 0;
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Pred. No. 3.7e-07;
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APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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437 AA; 50137 MW;
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100.0%;
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Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                     SEQUENCE FROM N.A.
STRAIN-NIGERIAN 002;
                                                                                                                                                                                                                          437 AA;
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SEQUENCE
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NON_TER
SEQUENCE
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Q9BHR9; Q9BHR9

ID DI DI OX

RESULT Q9BHR9

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EB05396E7D92AC98 CRC64;

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100.0%;
100.0%;
    50206 MW;
                                                         Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
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437 AA;
    437 AA;
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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Q9BHR4
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Diversifying selection in domains of Plasmodium falciparum Apical
Membrans Afying selection in domains of Plasmodium falciparum Apical
Membrans Antigen 1 (AMA).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BEBL; AJ408309; CAC34750.1;
NON TER 437 437
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SEQUENCE FROM N.A.
THAIN-WILDERIAN 034A;
POLLEY S.D., CONWAY D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical
"Membrane Antigen I (AMA1).";
Submitted (JAN-2001) to "BL/GenBank/DDBJ databases.
EMBL; AJ408308; CAC34749.1; '.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodíum.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408307; CAC34748.1; -.
NON_TER 437 437
SEQUENCE 437 AA; 50275 MW; 2973536F47E387EB CRC64;
                                                                         437 AA; 50275 MW; 2973536F47E387EB CRC64;
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437 AA; 50217 MW; 68A41FEE41C3271C CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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100.0%; Pred. No. 3.7e-07;
tive 0; Mismatches 0;
                                                                                                                                                           Score 105; DB 5;
Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 AA.
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ilarity 100.0%;
Conservative 0
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STRAIN-NIGERIAN 034B;
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Best Local Similarity
Matches 19; Conserv
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Matches 19; Conser
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Q9BHR6
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Q9BHR5
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STRAIN—NIGERIAN 035;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408310; CAC34751.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-NIGERIAN 036;
Polley S.D., Conway D.J.;
The selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408311; CAC34752.1; -.
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Length 437;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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                                          Indels
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437
437 AA; 50205 MW; AA9096AD6FD63AA2 CRC64;
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                                                                                                                                                                                                                                                          Q9BHR4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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100.0%; Pred. No. 3.7e-07;
tive 0; Mismatches 0;
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Pred. No. 3.7e-07;
Score 105; DB 5;
Pred. No. 3.7e-07;
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                                          Mismatches
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100.0%;
                                                                                                            202 DQPKQYEQHLTDYEKIKEG 220
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Gaps

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Indels

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Mismatches

0;

Conservative

19;

Matches

RESULT 11

Q9BHR2

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"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen 1 (AMA1).";
Submitted (JAN-201) 10. BMBL/GenBank/DDBJ databases.
EMBL; AJ408315; CAC34756.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 437;
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                                                                                                                                                    Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408316; CAC34757.1;
                                                                                                                                                                                                                                                                                                                                                                            50039 MW; 625A5E6F26E01064 CRC64;
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                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 105; DB 5;
100.0%; Pred. No. 3.7e-07;
iive 0; Mismatches 0;
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01-JUN-2001 (TrEMBLrel. 17, Last anno
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
                                                                       Created)
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STRAIN-NIGERIAN 050;
Polley S.D., Conway D.J.;
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Best Local Similarity 100.
Matches 19; Conservative
                                  PRELIMINARY;
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STRAIN=NIGERIAN 035;
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Q9BHQ8
ID Q9BHQ8
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STARAIN-NIGBRIAN 039;
POLICY S.D., Conway D.J.;
Policy S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical Membrane Antigen I (AMA1).";
Submitted (JAN-2001) to He EMBL/GenBank/DDBJ databases.
EMBL; AJ408312; CAC34753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polley S.D., Conway D.J.;
Polley S.D., Conway D.J.;
"Diversifying selection in domains of Plasmodium falciparum Apical
Membrane Antigen 1 (AMA1).";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ408314; CAC34755.1; -..
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          50356 MW; 734A74080D1BAC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50232 MW; BA3061373049C9CE CRC64;
                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105; DB 5;
Pred. No. 3.7e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105; DB 5;
Pred. No. 3.7e-07;
; Mismatches 0;
                                                                                                                   437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 AA.
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                   202 DQPKQYEQHLTDYEKIKEG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 DQPKQYEQHLTDYEKIKEG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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1 DÓPKQYEQHLTDYEKIKEG 19
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                    Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                            437
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STRAIN-NIGERIAN 044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 AA;
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NON_TER
SEQUENCE
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SEQUENCE
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RESULT 12 Q9BHR1

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Gaps

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AC 09BH08:
DT 01-JUN-2001 (TrEMBLrel: 17, Created)
DT 01-JUN-2001 (TrEMBLrel: 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel: 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel: 17, Last annotation update)
DT AAA1.

OS Plasmodium falciparum.
OC ENARYCEA Alvolata; Aplcomplexa; Haemosporida; Plasmodium.
OX NCBI_TAXID-583;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MIGERIAN 050;
RA POlley S.D., Conway D.J.;
RT TOLVERSITYING Selection in domains of Plasmodium falciparum Apical
RT Membrane Antigen 1 (AAM1).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; A4408317; CAC34758.1; -..
RF NON_TER 437 437
SQ SEQUENCE 437 AA: 50144 MW; 991DB6652BD8134F CRC64;
Best Local Similarity 100.0%; Pred. NO. 3.7e-07;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 19, Conservative 0, Mismatches 0; Indels 0; Gaps 0;
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Search completed: January 29, 2002, 11:12:14 Job time: 770 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Plasmodium falcipa	Recombinant vaccin	Rhoptry membrane a	Plasmodium falcipa	Plasmodium falcipa	Antirrhinum majus	Torenia hybrida fl	ABN-A from A. nige	Arabidopsis thalia	Arabidopsis thalia	Human formin bindi
SUMMARIES	ΠD	AAY70295	AAY70278	AAP91632	AAR27532	AAR68840	AAB20572	AAB20573	AAR27576	AAG08691	AAG42699	AAW94252
	DB	21	21	10	13	16	21	21	13	21	21	20
	Query Match Length DB	22	350	622	622	622	206	512	346	133	133	151
æ	Query	100.0	100.0	100.0	96.2	96.2	39.7	37.4	35.5	35.1	35.1	35.1
	Score	131	131	131	126	126	52	49	46.5	46	46	46
	Result No.	г	7	e	4	S	9	7	œ	6	10	11

(NAIM-) NAT INST IMMUNOLOGY. (USSH) US DEPT HEALTH & HUMAN SERVICES.

99WO-US18869 98US-0097703

02-MAR-2000. 19-AUG-1999; 21-AUG-1998;

Plasmodium falciparum.

WO200011179-A1.

Lal AA, Shi YP, Hasnain SE;

WPI; 2000-237654/20.

	12.		35.1	230	21	AAG08690	
	13	9	35.1	230	21	AAG42698	lopsis tr
	14	ဖ	35.1	255	22	AAB92532	Human protein sequ
	15		35.1	262		AAY76587	Human ovarian tumo
	16		34.4	124		AAU14709	. Novel bone marrow
	17	2	34.4	168		AAB74619	Human matrilysin c
	18	45 3	34.4	168	22	AAB68683	72 kDa gelatinase
	19	2	34.4	171		AAW24980	Recombinant human
	20	S	34.4	474		AAR14676	
	21	ر د	34.4	631		AAP91139	Human type IV coll
	22	ı L		631		AAP96143	Sequence of human
,	23	ر د		631		AAY07350	Human type IV matr
	24	ഹ		631		AAR07969	Complete type IV c
	25	Ωl		631		AAW4 1 2 2 6	Human mature matri
	970	ກ u	4.4	644		AAB20490	Human matrix metal
	7 0	n u		000		AAKU0420	Type IV collagenas
	300	ח ע	7. 4.	000		AAB6460/	Chickon matrix mot
	0 0	ר ער	t . v.	663		AAM*1111	Chicken matrix met
	5 5) <	7.7.7	5 -		AAV07369	Matrix metalloprot
	33	* =	9.0	2 5		AN10/303	Schizochytrium en
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	3.4	. 4	2.0	140		AAW85128	A nutative partial
	• LC		9.0	7 7		AAV84696	Amino acid compon
	7	,	33.0	7 7		AA104030	L
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	n <		02.0	07.0	77	AAB95200	Auman process segu
	•	# L		, r	77	AAG04131	Himan Open Open 200
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						ST. TONMENTS	
RES	RESULT 1						
g a	AAY70295		standard;	peptide;		22 AA.	
XX				•			
AC	AAY70295	95;					
XX		0		•			
Z ×	-NOC-90	0007-NOC-	(Ilrst entry)	entry	<u>-</u>		
ΒŒ	Plasmod	lium fa	Plasmodium falciparum AMA-1	um AMP		antiqenic epitope, P603	
XX							
KW	Recombi	inant F	Recombinant protein;	CDC/	'NIIN'		malaria; vaccine;
KW	T-cell	epitor	oe; teta	anus t	oxo	antigenic epitope;	treatment;
K.	circums	poroze	circumsporozoite protein; CSP;	otein;	CSI	sporozoite surface p	۲.
Z D	TIVET :	ncaye c	ancident	1, 100	, .	merozorte surrace pro	
XX	FRA-175	rhor	שבי סווב	1000	֓֞֞֞֜֞֜֞֜֞֓֓֓֓֓֓֟֝֟֝֓֟֟֓֓֓֓֓֟֟ ֓֓֞֞֞֞֞֞֞֓֞֞֞֞֞֞֞֞֓֓֞֞֞֞֩֞֞֩֞	n i, elythiolyte bindi	g ancigen 1/3, s specific antigen:
K	Pfq27;	antipa	rasitio	bre.	vent	Pfq27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.	anti-CDC/NIIMALVAC-1 antibody.
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10-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO8907645-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP91632;
                                                                                                                                                                                                                                                                                                                                                                            Sequence
              (NAIM-)
                                                      Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP91632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the antigenic epitope P603, derived from apical membrane antigen-1 (AMA-1) of the asexual blood stage of Plasmodium falcibarum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (H18) fag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-1 (KSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (KMS-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), roperty associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for catecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; reall epitope; treatment; recall epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; herozoite surface protein-1; MSP-1; metozoite surface protein-1; MSP-1; EBA-175; rhoptry associated protein-1; RAP-1; cychrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; qamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                             Gaps
           Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23..350
/label- Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                   Length 22;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 131; DB 21;
100.0%; Pred. No. 7.9e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                               Claim 2; Page 17; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70278 standard; Protein; 350
                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                    1 EFTYMINFGRGQNYWEHPYQKS 22
                                                                                                                                                                                                                                                                                                                                                                                                  98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 22; Conservative
                                                                                                                                                                                                                                                                                              22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200011179-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY70278;
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70278
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag, T-cell epitope from tetanus toxoid and 21 antigent epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage matigen-1 (LGA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBB-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, PfG27. These epitopes were obtained at different stages of the life cycle of activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 vaccine has antiparasitic bilections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marshall VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhoptry membrane antigen of Plasmodium falciparum - used for producing antibodies and in immunisation, diagnostic and treatment methods for malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 131; DB 21;
100.0%; Pred. No. 1.9e-12;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malaria; rhoptry membrane antigen-1; antibodies.
NAT INST IMMUNOLOGY.
US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smythe JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP91632 standard; protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 43-44; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
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                                                                                              Shi YP, Hasnain SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SARA ) SARAMANE PTY LTD.
                                                                                                                                                           WPI; 2000-237654/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
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Plasmodium falciparum AMA-1 gene; recombinant poxvirus; multicomponent multistage malarial vaccines; immunogens; malaria diagnosis.
                                                                                     Plasmodium falciparum AMA-1 gene protein.
                                                                                                                                                                                                                                                                          Paoletti E, Tine JA;
                           AAR68840 standard; Protein; 622 AA.
                                                                                                                                              Plasmodium falciparum (3D7).
                                                                                                                                                                                                       94WO-US06652
                                                                                                                                                                                                                         93US-0075783.
                                                                  (first entry)
                                                                                                                                                                                                                                                       (VIRO-) VIROGENETICS CORP.
                                                                                                                                                                                                                                                                                            WPI; 1995-036113/05.
N-PSDB; AAQ80910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           622 AA;
                                                                                                                                                                                                                                                                          De Taisne C,
                                                                                                                                                                                                     10-JUN-1994;
                                                                                                                                                                                                                         11-JUN-1993;
                                                                                                                                                                                                                                   09-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-2000
                                                                  24-AUG-1995
                                                                                                                                                                WO9428930-A.
                                                                                                                                                                                    22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                              AAR68840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                          immune response to malaria, and antibodies which the parasite. RMA-1 initially has mol. wt. 80 kD.
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the Plasmodium falciparum AMA1 antigen.

CDNA encoding it was cloned into vaccinia donor plasmids
before being inserted into the vaccinia virus to be used in a
vaccine to stimulate an antimal immunological response, or for
in vitro prodn. Of gene prods. for use as immunogens. As plasmodium
genes are conserved among P. falciparum strains, they are widely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                       ö
                                                                                                                                                                                                                                                                          Recombinant poxvirus; antimalarial vaccine; malaria; immunise;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 622;
                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant pox:virus - contg. Plasmodium DNA, useful as
                                                                                   Score 131; DB 10;
Pred. No. 3.6e-12;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 126; DB 13;
Pred. No. 2.2e-11;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tine JA;
                                                                                                                                                                                                                                                       Plasmodium falciparum AMA1 antigen.
                                                                                                                                                                                            AAR27532 standard; Protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 5; 74pp; English.
                                                                                                       ö
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                                                                                                                          1 EFTYMINFGRGONYWEHPYOKS 22
        Claim 1; Fig 3; 46pp; English.
                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.2%;
llarity 95.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                  910S-0672183.
920S-0852305.
                                                                                                                                                                                                                                                                                                                                                                92WO-US02207
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Paoletti E,
                                                                                                                                                                                                                                                                                                                                                                                                                (VIRO-) VIROGENETICS CORP.
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a vaccine.
                          RMA-1 can generate an can inhibit growth of
                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimalarial vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-349203/42.
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 AA;
                                                        622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ29189
                                                                                                                                                                                                                                                                                                                                                                                                                                   De TAISNE C,
                                                                                                                                                                                                                                   08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                19-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1992;
                                                                                                                                                                                                                                                                                                                         W09216616-A.
                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                             01-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Si
Matches 21;
                                                                                                                                                                                                                                                                                     immunogen
                                                                                                                                                                                                                AAR27532;
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                                                        Sequence
                                                                                                      Matches
X & X C C X & S
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                                                                                                                                                                              AAQ80910 encodes AAR68840 the P. falciparum AMA-1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
Recombinant poxvirus contg. Plasmodium DNA in non-essential region - useful in vaccines against malaria and for prodn. of Plasmodium immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flavone; flavanone; flavone synthase; plant; flower colour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.2%; Score 126; DB 16;
95.5%; Pred. No. 2.2e-11;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antirrhinum majus flavone synthase SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20572 standard; Protein; 506
                                                                                                                      Claim 3; Fig 5; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BETYMINEGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XX DX DX XX
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Gaps

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The present sequence represents a protein which has flavone synthase activity for converting flavanone directly into flavone. Flavone synthase can be used in the production of plant varieties with modified flower colour, improved resistance to bacteria, improved interaction with nitrogen flixing bacteria, or increased protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endo 1,5-alpha-L-arabinase A; arabinan; juice; fruit; vegetable; haze; yield; wood pulp; lignins; terpenoids; paper processing.
                                                    Gene encoding a flavone synthase for production of Antirrhinum and other plants with modified flower colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The protein sequence was deduced from the DNA sequence obtd. by screening an A. niger N400 genomic library with a probe which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabinan-degrading enzymes and genes - isolated from fungi and having lower pH optima than arabinan-degrading enzymes of bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coutel Y, De Graaff LH, Flipphi MJA;
Van Heuvel M, Visser J;
                                                                                                                                                                                                                                              Score 49; DB 21; Length 512;
Pred. No. 19;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //note= "signal peptide"
20.346
/note= "mature protein"
                                                                                        Claim 3; Page 38-40; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       AAR27576
ID AAR27576 standard; Protein; 346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 16; Fig 20; 75pp; English.
                                                                                                                                                                                                                                                                                                               396 fvniwsigrnpnywespme 414
                                                                                                                                                                                                                                                                                              2 FTYMINFGRGONYWEHPYQ 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KONN ) GIST-BROCADES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bakhuis JG,
der Veen P,
                                                                                                                                                                                 ultraviolet radiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hardera, Van der Veen
              WPI; 2000-543394/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN-A from A. niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-325492/40.
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                         512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus niger.
                           N-PSDB; AAA87997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PDSB; Q29231
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                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                             AAR27576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                              The present sequence represents a protein which has flavone synthase activity for converting flavanone directly into flavone. Flavone synthase can be used in the production of plant varieties with modified flower colour, improved resistance to bacteria, improved interaction with nitrogen fixing bacteria, or increased protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                   Gene encoding a flavone synthase for production of Antirrhinum and other plants with modified flower colour \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
bacterial resistance; nitrogen fixing bacteria; protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavone; flavanone; flavone synthase; plant; flower colour; bacterial resistance; nitrogen fixing bacteria; protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                       Akashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torenia hybrida flavone synthase SEQ ID NO:4.
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                                                                                                                                                                                                       Ayabe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB;
Pred. No. 6.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                      Claim 3; Page 31-34; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB20573 standard; Protein; 512 AA.
                                                                                                                                                                                                      Kusumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.78;
42.18;
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                                                                                                               28-JAN-2000; 2000WO-JP00490
                                                                                                                                                    99JP-0205229
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                                                                                                                                        99JP-0022427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.7
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                      Tanaka Y,
              ultraviolet radiation
                                                                                                                                                                                                                                                                                                                                                                                              ultraviolet radiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ultraviolet radiation.
                                                                                                                                                                                                                              WPI; 2000-543394/49.
                                                                                                                                                                           (SUNR ) SUNTORY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                     506 AA;
                                   Antirrhinum majus
                                                                                                                                                                                                                                           N-PSDB: AAA87996
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                                                             WO200044907-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200044907-A1.
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19-JUL-1999;
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                                                                                      03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20573;
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990S-0134218.
990S-0134219.
990S-0134221.
990S-0134370.
99US-0134768.
                                                                                               990S - 0.135124
990S - 0.135124
990S - 0.135629
990S - 0.136722
990S - 0.137724
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990S - 0.137724
990S - 0.139452
990S - 0.139454
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990S - 0.139455
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990S - 0.139457
990S - 0.139460
990S - 0.139463
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990S-0141842.
990S-0142154.
990S-0142154.
990S-0142055.
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99US-0143542.
99US-0143624.
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99US-0144086.
99US-0144325.
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99US-0145086.
99US-0145088.
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99US-0142920
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99US-0145089
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08-70L-1999

08-70L-1999

13-70L-1999

13-70L-1999

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15-70L-1999

16-70L-1999

16-70L-1999

19-70L-1999

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20-70L-1999

20-70L-1999

21-70L-1999

21-70L-1999
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28-JUN-1999;
        obtd. from a primary screen of A. niger DNA with anti-ABN A antibodies.

ABN-A has arabinan-degrading activity and has the ability to cleave
(1-2), (1-3) alof a L-arabinosidic linkages and can cleave the
1-6 linkage between the terminal arabinofuranosyl unit and the
intermediate glucosyl unit of monterpenyl alpha-L-arabinofuranosyl
glucosides. The enzyme has a lower pH optimum than those of bacterial
crigin. The enzyme may be used in the produ. of concd. juices, e.g.
fruit or vegetable, to eliminate arabinan haze, to increae the yield
of juice from pulp, to improve the filterability and reduce the
cof juice from pulp, to improve the liberation of aroma copds. from
substrates such as juices or wines, to improve the in vivo uptake and
utilisation of plant nutrients by animals, to provide more efficient
removal of both lignins and terpenoids in wood pulp and paper processing
and in the hydrolysis of sugar beet pulp, sycamore or gum arabic or
agricultural residues such as wheat-straw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                             DB 13; Length 346;
                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 6329.
                                                                                                                                                                                                                                                                          Score 46.5; DB
Pred. No. 30;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          AAG08691 standard; Protein; 133 AA
                                                                                                                                                                                                                                                                           35.5%;
50.0%;
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990S-0123180.
99US-0123548.
99US-0125788.
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990S-0127462.
990S-012834.
990S-0128714.
990S-0130845.
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99US-0131449.
99US-0132048.
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99US-0132484.
99US-0132485.
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99US-0132863
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                                                                                                                                                                                                                                                                                                                                 3 TYMINFGRGQNYWEHPYQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                     346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
119-APR-1999;
21-APR-1999;
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PR 27-10L-1999 9905-0145218
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PR 12-MG-1999 9905-0149726
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                                                                                                                                  4; Mismatches
                                                                                                                                                                                                            AAG42699 standard; Protein; 133 AA,
                 990S-0161404.
990S-0161405.
990S-0161369.
990S-0161359.
990S-0161361.
990S-0161920.
990S-0161992.
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990S-0123180.
990S-012348.
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99US-0134221.
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 99US-0160981.
99US-0160989.
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99US-0134941
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13 gsgeafwehewek
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Matches 6; Conserv
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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06-APR-1999;
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16-APR-1999;
11-APR-1999;
23-APR-1999;
23-APR-1999;
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04-MAY-1999;
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                                                                                                                                                                                                                                                                         Formin binding protein; FBPhu; human; developmental disorder; anaemia; renal tubular acidosis; Cushing's syndrome; epilepsy; spina bifida; glaucoma; cancer; tumour; leukaemia; lymphoma; immune suppression; autoimmunity; inflammation; acquired immune deficiency syndrome; AIDS; allergy; asthma; ulcerative colitis; multiple sclerosis; osteoporosis; microbial; viral; infection; chromosomal mapping.
                                                                                       Gaps
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                                                                21; Length 133;
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12;
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                                                                 Score 46;
Pred. No.
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                                                                                                                                                                                                                                                        Human formin binding protein (FBPhu).
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                                                                                                                                                                                      AAW94252 standard; Protein; 151 AA
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         990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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46.2%;
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                                                                        Local Similarity
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29-OCT-1999;
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for diagnosis and monitoring, to detect FBPhu-encoding nucleic acid (in standard hybridisation and/or amplification assays); as therapeutic antisense, triplex-forming or ribozyme molecules; to identify genetic variation, mutations etc., and for chromosomal mapping.
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                                                                                                                                                            2; Mismatches
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47.1%;
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99US-0123180.
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99US-0125788.
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                                                                                151 AA;
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25-MAY-1999;
27-MAY-1999;
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01-APR-1999;
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18-MAY-1999;
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25-MAR-1999;
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                                           Gaps
                                          0;
              Score 46; DB 21; Length 230;
Pred. No. 22;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 53279.
                                                                                                                                                                AAG42698 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0121825.
990S-0123180.
990S-0125788.
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990S-0126785.
990S-0126785.
990S-0128234.
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990S-0132486.
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990S-0137502.
990S-0137724.
990S-0138094.
              Query Match 35.1%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                                                                                                                                                                      18-OCT-2000 (first entry)
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110 gsgeafwehewek 122
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 10692; 2537pp + CD ROM; English.
                                                                                        Human protein sequence SEQ ID NO:10692.
                                        AAB92532 standard; Protein; 255 AA
                                                                                                                                                                                                                                                               Wakamatsu
                                                                                                                                                                                                                                                      ogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                      29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                         (first entry)
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 110 gsgeafwehewek 122
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                                                                                                                                                                                                                                                                                                                      full-length cDNAs
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                                                        AAB92532;
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Pred. No.
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990S-0153070.
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25 - AUG - 1999;
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26 - AUG - 1999;
27 - AUG - 1999;
31 - AUG - 1999;
31 - AUG - 1999;
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24-SEP-1999;
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04-OCT-1999;
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08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
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15-SEP-1999;
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26-OCT-1999
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Yamamoto J;

Saito K, Ye Otsuki T;

Hayashi K, S A, Nagai K,

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The present invention describes primer sets to synthesising your comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide omprises a 1'-end sequence, where the complementary to a polynucleotide comprises a 3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs represent human cDNA sequences; AAB92446 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632. The present complement invention
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present invention describes primer sets for synthesising 5602
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Pred. No. 25;
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Matches 8; Conserv
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Gaps

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Indels

Mismatches

Conservative

Job time: 426 sec

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have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of covarian cancer. (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY76505-Y76638 represent protein fragments encoded by the human overlan tumor cDNA library derived EST fragments represented in AAZ77450-Z77572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences expressed in ovarian, and some other, canceitissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel nucleic acid (cDNA) sequences (A) which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian tumor EST fragment encoded protein 83.
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2 FTYMINFGRGONYWEHP 18
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N-PSDB; AAZ77485.
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Query Match
Best Local Similarity 47.1%; Pred. No. 26;
Matches , 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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Search completed: January 29, 2002, 10:21:50

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APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
PRIOR APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                      US-08-836-325-15
US-08-836-325-16
US-08-836-325-10
US-08-836-325-11
US-08-836-325-12
US-08-937-326-8
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US-08-937-972-1
US-08-001-711-2
              US-09-211-704A-9
US-08-561-521-13
PCT-US95-01219-13
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US-08-158-682A-2
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                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Curtis, Morris & Safford, STREET: 530 Fifth Avenue, 25th Floor CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08257073
Patent No. 5766597
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TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 628 amino acids
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1969
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TYPE: amino a STRANDEDNESS:
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                                                                                               January 29, 2002, 10:24:10 ; Search time 133.18 Seconds
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Sequence 17,
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Sequence 32,
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Sequence 13
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-914-848-24

US-08-872-783-1

US-08-444-628-9

US-08-357-820-9

US-08-357-820-9

US-08-357-820-9

US-08-74-11A-18

US-08-74-713-3

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US-08-113-113-113

US-08-128-809-8

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                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein – protein search, using sw model
                                                                                                                                                                                       1 EFTYMINFGRGONYWEHPYOKS
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                             US-09-763-397A-19
                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Score

Result Ş

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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                      US-08-914-848-24
                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-914-848-24
                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-872-783-1
                                                                                                       APPLICANT
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                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENCODING ARABINAN-DEGRADING ENZYMES OF FUNGAL ORIGIN
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                                                                   Score 126; DB 1; Length 628;
Pred. No. 4.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/07/952,853
FILING DATE: 19921125
CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION:
NAME: MURABANIGE, Rate H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 246152003500
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-813-5600
                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONING AND EXPRESSION OF DNA MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46.5; DB 2;
Pred. No. 8.4;
3; Mismatches 3;
                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                               Harder, Abraham
De Graaff, Leendert H.
Flipphi, Michel J. A.
Van Der Vener, Peter
Visser, Jacob
                                                                                                                                                                                                                                                                                                 Van Heuvel, Margaretha
Bakhuis, Janna G.
Coutel, Yves
                                                                                                                                                                                                                                                 Sequence 24, Application US/07952853 Patent No. 5863783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                      14 EFTYMINFGRGONYWEHPYONS 35
                                                                                                                                   1 EFTYMINFGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                Andreoli, Peter M.
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                                                                   96.2%;
95.5%;
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50.0%;
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                                                              Query Match
Best Local Similarity 95.5%
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
; FRAGMENT TYPE: internal US-08-257-073-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-07-952-853-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CTITLE OF INVENTION: BY TITLE OF INVENTION: BY TITLE OF INVENTION: OF UMBER'OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abc...
STREET: 755 ...
CITY: Palo Alto
marge: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                                                                                                                     RESULT 2
US-07-952-853-24
                                                                                                                                                                                                                                                                                                 APPLICANT:
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CLONING AND EXPRESSION OF DNA
MOLECULES ENCODING ARABINAN-DEGRADING ENZYMES OF FUNGAL
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08872783
; Patent No. 5858717
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN FORMIN BINDING PROTEIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46.5; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MUTASAIJG, KATE H.
REGISTRATION NUMBER: 29,959
REFRERENCE/POCKET NUMBER: 246152003500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFRAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,853
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                             Van Heuvel, Margaretha
Bakhuis, Janna G.
Coutel, Yves
Harder, Abraham
                                                                                                                                               De Graaff, Leendert H.
Flipphi, Michel J. A.
Van Der Veen, Peter
Visser, Jacob
; Sequence 24, Application US/08914848
; Patent No. 5989887
                                                                                                                                                                                                                                                                                                                                                                E: MORRISON & FOERSTER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                       Andreoli, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24:
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 346 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TYMINFGRGQNYWEHPYQ 20
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               APPLICANT: Visser, Jacob
APPLICANT: Andreoli, Pet
TITLE OF INVENTION: CLON
TITLE OF INVENTION: MOLE
TITLE OF INVENTION: ORIG
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: California
ZIP: 94304-1018
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Matches 9; Conserv
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                                       GENERAL INFORMATION:
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Gaps
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Patent No. 6194189

GENERAL INFORMATION:

APPLICATT: Senior, Robert M.

TITLE OF INVENTION:

CARASPONENCES: 9

CORRESPONDENCES: 9

CORRESPONDENCES: 9

CORRESPONDENCES: 50-014 J. Meyer, Monsanto/Searle, A3SG

STREET: 800 N. Lindbergh Blvd.

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

LIPE 63167
                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,820
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meyer: Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-2855
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU-2855
TELECOMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
  APPLICATION NUMBER: US/08/357,820
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.4%;
Best Local Similarity 58.8%;
Matches 10; Conservative
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LENGTH: 168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (314)694-5435 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EFTYMINFGRGONYWEH 17
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-628-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-357-820-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-357-820-9
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APPLICANT: Senior, Robert M.
TITLE OF INVENTION: Catalytically-active Gelatinase Mutant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 2; Length 151;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,628
                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,783
FILING DATE: Herewith
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/872,783
FILING DATE: Herewith
RPLICATION NUMBER: APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/CORKET NUMBER: PF-0317 US
TELEMBONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
    AUDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-444-628-9; Sequence 9, Application US/08444628; Patent No. 6184021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 35.1%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 151 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FTYMINFGRGQNYWEHP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TESTTUT02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LIBRARY: TESTTU
; CLONE: 2345085
US-08-872-783-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63167
                                                                                                   COUNTRY:
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Gaps
                                                              ; OTHER INFORMATION: Description of Unknown Organism: Known Member of COTHER INFORMATION: Matrix Metalloproteinase Family US-08-448-489-17
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, HOIST
APPLICANT: HINDMANN Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                     4
                                                                                                                                                                                      Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%; Score 45; DB 3; Length 660; 58.8%; Pred. No. 30;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FIPOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BY PAGE FIPOPY
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
FILING PAPLICATION DATE: WO PCT/DE95/00357
PROFILE TOWN NUMBER: WO PCT/DE95/00357
PRILING DATE: 21-OCT-1994
PRIOR APPLICATION NUMBER: DE 4438838.1
PRILING DATE: 21-OCT-1994
PRIOR APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                      Score 45; DB 4
Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: GRANADOS, Patricia D. REGISTRATION NUMBER: 33,683
                                                                                                                                                                                      34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               137 EADIMINFGR----WEH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 660 amino acids
amino acid
                                                                                                                                                                                                                                                                       1 EFTYMINFGRGQNYWEH 17
                                                                                                                                                                                      Ouery Match 34.4
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 34.4
Best Local Similarity 58.8
Matches 10; Conservative
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US-08-704-711A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
                       TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           US-08-704-711A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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APPLICANT: SATO, Hiroshi
APPLICANT: SHINGAMA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                APPLICANT: Ye, Qi-Zhuang
APPLICANT: Johnson, Linda L.
APPLICANT: Hupe, Donald J.
TITLE OF INVENTION: Process for the Production of
TITLE OF INVENTION: Gelatinase Catalytic Domain Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Warner-Lambert Company
STREET: 2800 Plymouth Rd.
CITY: Ann Arbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5120-FJT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-448-489-17; Sequence 17, Application US/08448489; Patent No. 6184022; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Tinney, Francis J.
REGISTRATION NUMBER: 33,069
REFERENCE/DOCKET NUMBER: 5120-
TELECOMMUNICATION INFORMATION:
TELEFAX: 313 996-7295
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         Sequence 1, Application US/08303270 Patent No. 5646027 GENERAL INFORMATION:
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58.8%;
                       60 EADIMINFGR----WEH 72
EFTYMINFGRGONYWEH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EFTYMINFGRGQNYWEH 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-303-270-1
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 48105
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                                                                                                                        US-08-303-270-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hawkins, Phillip R.
APPLICANT: Hallman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: California COUNTRY: USA
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/741,437
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: PF-0148 US
REGISTATION NUMBER: PF-0148 US
TELEFHONE: (415) 855-0555
TELEFHONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/741,437
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-593-3
; Sequence 3, Application US/09134593
; Patent No. 5981232
; GENERAL INFORMATION:
              3174 Porter Drive
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 114 amino acids
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8 YIWNYGTLPQTWEDPHEK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide IMMEDIATE SOURCE:
        STREET: 31/.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: GenB
CLONE: 727225
                                                                                                 94304
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                                                                                                                                                    Sequence 3, Application US/08872783
Patent No. 5658717
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HOWN FORMIN BINDING PROTEIN
ITITLE OF INVENTION: HUMAN FORMIN BINDING PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN PYROPHOSPHATASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,783
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB ;
Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.8%;
                                      1 EFTYMINFGRGONYWEH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FTYMINFGRGONYWEHP 18
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51 YTYYNTETGESKWEKP 67
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Best Local Similarity 41.2
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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CLONE: 1255023
                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
COUNTRY: US,
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; CLONE: 1
US-08-872-783-3
                                                                                                                  RESULT 10
US-08-872-783-3
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                                                                                      Score 43; DB 2; Length 219;
Pred. No. 18;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.8%; Score 43; DB 3; Length 219; 38.9%; Pred. No. 18; ive 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,887
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0186 US
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/773,368
                                                                                                                                                                                                                                                                            Sequence 3, Application US/09199887
Patent No. 6071874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                        32.8%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                161 FICNYGPGGNYPTWPYKR 178
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                                                                                                                                                           4 YMINFGRGQNYWEHPYQK 21
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CLONE: 847722
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                                                                                                    Best Local Similarity
Matches 7; Conserv
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      ; LIBRARY: GenB:
; CLONE: 847722
US-08-773-368-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                            RESULT 14
US-09-199-887-3
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                                             Score 43; DB ;
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
ATTORNEY/AGENT INFORMATION:

NAME: Bilings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0148 US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 114 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: Alinear

MOLECULE TYPE: peptide

INMEDIATE SOURCE:

LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
- SEQUENCE CHARACTERISTICS:
- LENGTH: 219 amino acids
- TYPE: amino acid
- STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            Query Match 32.8%;
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    8 YIWNYGTLPQTWEDPHEK 25
                                                                                                                                                                                                                                                                                                                                                                                                             4 YMINFGRGONYWEHPYOK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                           US-09-134-593-3
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Score 43; DB 2; Length 266;
Pred. No. 22;
5; Mismatches 6; Indels
Sequence 4, Application US/08773368
Patent No. 5856130
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 314 POTTER PROTEIN
NUMBER OF SEQUENCES: 6
COUNTRY: Palo Alto
STATE: CA
COUNTRY: USA
COMPUTER: Instance Libration
OPERATING SYSTEM: DATA:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DATA:
MEDIUM TYPE: BASESO for Windows Version 2.0
SOFTWARE: FastESO for Windows Version 2.0
CLASSIFICATION UNBER: US/08/773,368
FILING DATE:
APPLICATION UNBER: US/08/773,368
FILING DATE:
FILING DATE:
APPLICATION UNBER: 35,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: BF-0186 US
TELECOMMUNICATION INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 266 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
LIBRARY: GenBank
CLONE: 1030053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.8%;
Best Local Similarity 38.9%;
Matches 7; Conservative
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Search completed: January 29, 2002, 10:24:10 Job time: 516 sec

:: |:| | || ||:: 171 FICNYGPGGNYPTWPYKR 188 4 YMINFGRGONYWEHPYOK 21

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Gaps ; WASH AND THE FORM WATER

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January 29, 2002, 10:26:45; Search time 144.96 Seconds (without alignments) 11.561 Million cell updates/sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    219241 seqs, 76174552 residues
                                                                                                                                                                          US-09-763-397A-19
131
1 EFTYMINFGRGQNYWEHPYQKS 22
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                     Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	88	ID	Description
П	131	100.0	622	~	D44986	apical membrane an
7	131	100.0	622	~	A32499	apical membrane an
m	131	100.0	622	7	C44986	apical membrane an
4	126	96.2	622		B44986	
S	126	96.2	622		A44986	
9	53.5	40.8	631	~	T40189	probable biotin-pr
7	51	38.9	2658		A86216	protein T23G18.2 [
8	49	37.4	218		T10522	ribonuclease (EC 3
6	49	37.4	808		T39059	probable mannosyl-
10	47	35.9	452		C85024	probable polygalac
11	47	35.9	1620		E83261	conserved hypothet
12	46		116		T42412	FMRFamide-like pep
13	46	35.1	230	~	A84443	probable ribonucle
14	46	35.1	466	N	F84139	beta-glucosidase B
15	46	35.1	476	•	SGMSV	vitronectin precur
16	4	35.1	502	7	T07141	cytochrome P450 CY
17	45.5	34.7	2100	7	T38128	t7i23.15 protein -
18	45	34.4	28	7	PH1911	T-cell receptor al
19	45	34.4	140		C49829	T-cell receptor va
20	45	34.4	193	•	T17952	hypothetical prote
21	45	34.4	459	•	JC5139	vitronectin precur
22	45	34.4	465		D69785	beta-glucosidase h
23	45	34.4	475	•	A38340	66K glycoprotein p
24	45	34.4	478		SGHUIV	vitronectin precur
25	45	34.4	504		F70813	hypothetical prote
56	45	34.4	649		T27232	_
27	45	34.4	099		A28153	Ø
28	45	34.4	662		424	A (EC
53	45	34.4	662		S34780	ď

gelatinase A (EC 3	gelatinase A (EC 3	probable ribosomal	self-incompatibili	hypothetical prote	probable transposa	cytochrome P450 (C	ATPase - Erwinia a	CWH41 protein - ye	hypothetical prote	hypothetical prote	synaptojanin 2 alp	hypothetical prote	formin binding pro	hypothetical prote	glioma pathogenesi
S70365	S46492	A72570	PD0004	B86276	877650	862899	S52141	S62136	T25635	T25634	JW0105	G70918	S64714	G85867	JC4131
~	П	7	7	~	ņ	7	~	7	~	~	~	~	~	N	~
662	663	104	196	228	474	509	726	833	1129	1175	1216	379	67	80	219
34.4	34.4	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.2	32.8	32.8	32.8
					-	4	4	7	4	7	14	'n.	3	m	3
45	45	44	44	44	4	4	4	7	7	•	•	43	43	4	4

ALIGNMENTS

219241

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

RESULT 1 D4496 apical membrane antigen 1 - malaria paras C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Accession: D44966 R;Thomas, Aw.; Waters, A.P.; Carr, D. Mol. Biochem. Parasitol. 42, 285-288, 199 A;Title: Analysis of variation in PR83, a A;Reference number: A44986; MUD:91101665 A;Accession: D44986 A;Accession: D44986 A;Accession: D44986 A;Cross-references: GB:M34555 C;Reywords: membrane protein; surface and Query Match Best Local Similarity 100.0%; pred. Matches 22; Conservative 0; Miss Oy 1 EFTYMINFGRGONYWEHPYOKS 22 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 1 D44986 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain 7G8) C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Species: Plasmodium falciparum C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000 C; Accession: D44986 R; Thomas, A.W.; Waters, A.P.; Carr, D. Mol. Biochem. Parasitol. 42, 285-288, 1990 A; Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate a A; Reference number: A44986; MUID: 91101665 A; Accession: D44986 A; Accession: D44986 A; Accession: D44986 A; Accession: D44986 A; Residues: 1-622 < THO> A; Residues: 1-622 < THO> A; Residues: 1-622 < THO> C; Keywords: membrane protein; surface antigen	Juery Match 100.0%; Sest Local Similarity 100.0%; datches 22; Conservative 1 EFTYMINFGRGONYWEHPYOKS 14 EFTYMINFGRGONYWEHPYOKS	RESULT 2 A32499 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jun-2000 C;Accession: A32499 R;Peterson, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; A MOI. Cell. Biol. 9, 3151-3154, 1989 A;Title: Integral membrane protein located in the apical complex of Plasmodium falcip A;Reference number: A32499 A;Sttus: preliminary A;Sctus: preliminary A;Stetus: DNA; mRNA A;Residues: 1-622 <pet> A;Cross-references: GB:M27133; NID:g160072; PID:g160073 C;Keywords: membrane protein; surface antigen</pet>	uery Match 3est Local Similarity 100.0%; datches 22; Conservative 1 EFTYMINEGRGONVWEHPYOKS 14 FFTYMINEGRGONVWEHPYOKS 14 FFTYMINEGRGONVWEHPYOKS
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Gaps

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RESULT C44986

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protein T23G18.2 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (Speciession: A86216 (Speciession: A862216 (Speciession: A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable biotin-protein ligase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40189
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A submitted to the EMBL Data Library, February 1998
A;Reference number: 221910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-631 <WOO>
A;Cross-references: EMBL:297992; PIDN:CAB10802.1; GSPDB:GN00067; SPDB:SPBC30D10.07c
A;Experimental source: strain 972h-; cosmid c30D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE005172; NID:g6579214; PIDN:AAF18257.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 631;
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         Length 622;
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    Score 126; DB 2;
Pred. No. 3.6e-11;
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Pred. No. 33;
4; Mismatches
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 FTVLGNYQTAGRGRGGNMWVSPY 405
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                                                                                            ;
                                                                                                                                                                                                                                      14 EFTYMINFGRGONYWEHPYONS 35
                                                                                                                                                                                   1 EFTYMINFGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%;
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50.0%;
Query Match 96.2%;
Best Local Similarity 95.5%;
Matches 21; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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1039 VMTFKRGMNFWEYP 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: SPDB:SPBC30D10.07c
A;Map position: 2
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Best Local Similarity
Matches 11; Conserv
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                                                                                                              aprical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain FCR 3) (Species: Plasmodium falciparum (C;Species: Plasmodium falciparum (C;Species: Plasmodium falciparum (C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000 (C;Accession: C498ers, A.P.; Carr, D. Mol. Blochem. Parasitol. 42, 285-288, 1990 Mol. Blochem. Parasitol. 42, 285-288, 1990 ArTitle: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti A;Reference number: A4986; MUID:91101665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A;Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti
A;Reference number: A44986; MUID:91101665
A;Accession: A44986
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A;Molecule type: DNA
A;Residues: 1-622 <THO>
A;Cross-references: GB:M34553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not shown; not compared with conceptual tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain CAMP) C;Species: Plasmodium falciparum C;Date: 28-Apr-1993 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
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Pred. No. 3.6e-11;
0; Mismatches 1; Indels
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100.0%; Pred. No. 6.4e-12;
tive 0; Mismatches 0;
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C;Keywords: membrane protein; surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Residues: 1-622 <THO>A)Cross-references: GB:M34554
C;Keywords: membrane protein; surface antigen
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95.5%;
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Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 22; Conserv
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C; Species: "Freudomonas aeruginosa C; Species: "Freudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: B83261 B3261 B326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA3068 [imported] - Pseudomonas aeruginosa (strain PAO
                           A; Accession: C85024
A; Status: preliminary
A; Mocession: C85024
A; Status: preliminary
A; Mocession: C85024
A; Mocession: C85024
A; Mocession: C85024
A; Cross-references: GB:NC_001268; NID:g7268573; PIDN:CAB80682.1; GSPDB:GN00140
C; Genetics:
A; Gene: AT4g01890
A; Map position: 4
C; Superfamily: polygalacturonase
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T42412
R;Li, C; Nelson, L.S.; Memmott, J.M.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z22162
A;Recession: T42412
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 6.8;
1; Mismatches
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Pred. No. 20;
2; Mismatches
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C;Genetics:
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Pred. No. 79;
3; Mismatches
A; Reference number: A85001; MUID:20083488
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70.0%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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Matches 7; Conserv
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A; Residues: 1-116 <LIC>
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Gene: flp-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable mannosyl-oligosaccharide glucosidase (EC 3.2.1.106) - fission yeast (Schizosacc Species: Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Species: Obloc-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: 739059
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
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                                                                                                                                                                                                                                                            R;Norioka, S.
submitted to the EMBL Data Library, August 1995
A;Description: Molecular cloning and nucleotide sequences of S-RNases and non-S-RNase A;Reference number: Z17069
A;Accession: T10522
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A;Accession: T39059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-808 <OLI>A;Cross-references: EMBL:298603; PIDN:CAB11295.1; GSPDB:GN00066; SPDB:SPAC6G10.09
A;Experimental source: strain 972h-; cosmid c6G10
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                                                                                                                                 ribonuclease (EC 3.1.27.-) precursor - Persian tobacco
C;Species: Nicotiana alata (Persian tobacco)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T10522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Experimental source: style from unopened and induces C:Superfamily: Enterobacter ribonuclease C:Keywords: hydrolase F:1-22/Domain: signal sequence #status predicted <SIG>F:23-218/Product: ribonuclease #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-218 <NOR>
A;Cross-references: EMBL:D63888
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Pred. No. 4.7;
1; Mismatches
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Pred. No. 19;
2; Mismatches
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A;Introns: 80/1
C;Keywords: glycosidase; hydrolase
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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711 VYFGTGENYWRGP 723
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Best Local Similarity
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A; Accession: JT0662
A; Molecule type: DNA
A; Rocal and A; Z56-434, S', 435-476 (SEI>
A; Molecule type: DNA
A; Cross-references: GB:X72091; NID:9441465; PIDN:CAA50981.1; PID:9441466
B; Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatohgo, T.; Ogawa, H.; Uchibori, H.; Ma
Biochim. Biophys. Acta 1120, 1-10, 1992
A; Title: Vitronectin diversity in evolution but uniformity in ligand binding and size
A; Reference number: S21768; MUID:92207982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics: A: 116/1; 222/3; 273/1; 324/1; 439/1
A:Introns: 22/1; 62/1; 176/1; 222/3; 273/1; 324/1; 439/1
C:Superfamily: vitronectin; hemopexin repeat homology; somatomedin B homology
C; Seywords: cell adhesion; glycoprotein; heparin binding; phosphoprotein; sulfoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>F:20-476/Product: vitronectin #status predicted <MAT>
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: 819894; JT0662; S22224, A56398
R;Ehrlich, H.J; Richter, B.; von der Ahe, D.; Preissner, K.T.
Submitted to the EMBL Data Library, November 1991
A;Description: Molecular cloning and expression in E. coli of mouse vitronectin. A;Reference number: 819894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues, D; XxxF', 25-34,'X', 36-37,'X', 39,'X',41,'X',43,'X'
A; R; Selffert, D.; Reeton, M.; Eguchi, Y.; Sawdey, M.; Loskutoff, D.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 9402-9406, 1991
A; Title: Detection of vitronectin mRNA in tissues and cells of the mouse.
A; Reference number: A56398; MUID:92052101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-255,'A',256-382,385-414,'K',416-434,'S',435-476 <SE2>
A;Cross-references: GB:M77123; NID:g202371; PIDN:AAA40558.1; PID:g202372
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F;20-62/Domain: somatomedin B homology <SBH>
F;20-62/Domain: somatomedin B homology <SBH>
F;40-66/Fegion: cell attachment (R-G-D) motif
F;40-66/Fegion: hemopexin repeat homology #status atypical <PX1>
F;286-471/Domain: hemopexin repeat homology *PX2>
F;365-398/Region: hemopexin repeat homology *Px2>
F;57-8/Binding site: sulfatte (Tyr) (covalent) #status predicted
F;86.168.241/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;291-430/Disulfide bonds: #status predicted
F;397/Binding site: phosphate (Ser) (covalent) #status predicted
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30;
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Pred. No. 30;
6; Mismatches
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Job time: 657 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poenninger, J.; Binder, B.R. 34, 1993
                                                                                                                                                                                                                                                                                         A.Accession: S19894
A.Molecule type: mRNA
A.Residues: 1.476 A.Cross-references: EMBL:X63003
R.Seiffert, D.; Poenninger, J.; Bi
Gene 134, 303-304, 1993
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37.5%;
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Best Local Similarity 37.5
Matches 6; Conservative
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R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: F84139
A;Accession: F84139
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-466 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
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A; Status: preliminary
A; More action of the control of the 
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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N;Alternate names: complement protein S
N;Centains: somatomedin B
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Best Local Similarity 50.0
Matches 6; Conservative
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33 GKGKNIWDHWYE 44
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'-has 6; Conserve
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83 IRFGRSRNTWEDGY
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January 29, 2002, 11:13:47; Search time 80.65 Seconds (without alignments) 10.002 Million cell updates/sec Run on:

US-09-763-397A-19 131 1 EFTYMINFGRGQNYWEHPYQKS 22 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description							2256			Q42799 glycine max		P22458 oryctolagus	l homo	P08253 homo sapien	ยกร	P50757 oryctolagus		Q90611 gallus gall					Q46631 erwinia amy	P53008 saccharomyc	O55207 rattus norv	041174 p genome po	O88848 mus musculu	P48060 homo sapien	Q11108 caenorhabdi	94	~	9 bomby	Q9y3r5 homo sapien
SUMMARIES	3 ID	L AMA1_PLAF8	L AMA1_PLAFF	AMA1_PLAFG	AMA1_PLAFC	AMA1_PLAFH	l GCS1_SCHPO	L ABNA_ASPNG	RNS1_ARATH	L VTNC_MOUSE	L C932_SOYBN	L VTNC_PIG	L VTNC_RABIT	L VTNC_HUMAN	L MM02_HUMAN	I MM02_MOUSE	L MM02_RABIT	L MM02_RAT	L MM02_CHICK	RS10_AERPE .	L ARL6_HUMAN	L RNS7_NICAL	C931_SOYBN	L AMSA_ERWAM	L CW41_YEAST	l SYJ2_RAT	1 POLG_PEV9U	1 ARL6_MOUSE	1 GLIP_HUMAN	1 YX01_CAEEL	l YM57_YEAST	1 POLN_LORDV	1 VIT_BOMMO	L C215_HUMAN
	Length DB	:		622		622	808	321	230	478	502	459	475	478	999	662	662	662	663													1699	1782	2298
di	Query Match	100.0	100.0	0	96.2	96.2	37.4	S	35.1	35.1	35.1	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.4	•	•	33.6		33.6	•	33.6	33.6	32.8	N	32.8	32.8	32.8	32.8	32.8
	Score	131	131	131	126	126	49	46.5	46	46	46	45	45	45	45	45	45	45	45	44	44	44	44	44	44	44	44	43	43	.43	43	43	43	43
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Gaps

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Query Match
100.0%; Score 131; DB 1; Length 622;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=91101665; PubMed=2270110;
Thomas A.W., Waters A.P., Carr D.;
Thomas A.W., Waters A.P., Carr D.;
"Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum.";
MOI. Biochem. Parasitol. 42.285-287(1990).
-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SIMILARITYS LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITYS: STRONG TO AMA-1 FROM P.CHABADDI AND P.FRAGILE, AND TO PK66 FROM P.KNOWLESI.
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N-LINKED (GLCNAC...) (POTENTIAL).
                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
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01-ocr-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)
                                                                                                                                                         Plasmodium falciparum (isolate FCR-3 / Gambia).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5835;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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Pfam; PF02430; AMA-1; 1.
Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
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1larity 100.0%; Pred. No. 5.9e-12;
Conservative 0; Mismatches 0;
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-!- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK66 FROM P.KNOMLESI.
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MEDLINE=89384584; PubMed=2701947;
Peterson M.G., Marshall V.M., Smythe J.A., Crewther P.E., Lew A., Silva A., Anders R.F., Kemp D.J.;
"Integral membrane protein located in the apical complex of
                                                                                                                                                                                       APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOLTE SURFACE ANTIGEN)
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1 -> N (IN REF. 1; AAA29476).
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H -> N (IN REF. 1; AAA29476).
I -> M (IN REF. 1; AAA29476).
N -> R (IN REF. 1; AAA29476).
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Pred. No. 5.9e-12;
Mismatches 0;
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01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK66 FROM P.KNOWLESI.
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Thomas A.W., Waters A.P., Carr D.; "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."; Mol. Blochem. Parasitol. 42:285-287(1990).
-i- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
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01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=70151;
                                                                                                                                                                                                                                                                                                                                                                                Score 126; DB 1; Length 622;
Pred. No. 3.2e-11;
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N-LINKED (GLCNAC. . ) (PC
N-LINKED (GLCNAC. . ) (PC
                                                                                                                                                                                      EMBL; modulo; manacoloris, moduloris, moduloris, proposition, proposition, proposition, moduloris, Signal; Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                26CE8CF76D07C637 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EFTYMINFGRGQNYWEHPYQKS 22
                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                96.2%;
                                                                                                                                                                                  EMBL; M58545; AAA29718.1; -
                                                                                                                                                                                                                                                                                                                                                71943
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                162
286
371
                                                                                                                                                                                                                                                                                                                                                622 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMA1_PLAFH
                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMA1_PLAFH
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: CLEAVES THE DISTAL ALPHA 1,2-LINKED GLUCOSE RESIDUE FROM THE GLC(3)MAN(9)GLCNAC(2) OLIGOSACCHARIDE PRECURSOR HIGHLY SPECIFICALLY (BY SIMILARITY).
-! CATALYTIC ACTIVITY: EXOHYDROLYSIS OF THE NON-REDUCING TERMINAL GLUCOSE RESIDUE IN THE MANNOSYL-OLIGOSACCHARIDE GLC(3)MAN(9)GLCNAC(2).
-! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC RETICULUM (POTENTIAL).
-: SIMILARITY: BELONGS TO FAMILY 63 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Signal-anchor; Endoplasmic reticulum.

Lotroplasmic (Potential).

TRANSMEM 12 31 SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N.LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROBABLE MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Hydrolase; Glycosidase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                     APICAL MEMBRANE ANTIGEN 1. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1FDFA53593C94CC5 CRC64;
                                                                                                                                                                      Transmembrane; Antigen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 1;
Pred. No. 3.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             808 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
                                                                                                            InterPro; IPR003298; Apmem_Agl. Pfam; PF02430; AMA-1; 1. Malaria; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 EFTYMINFGRGONYWEHPYONS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EFTYMINFGRGONYWEHPYOKS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Μ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROCESSING A-GLUCOSIDASE I). SPAC6G10.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.2%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 298603; CAB11295.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.5°
Matches 21, Conservative
                                                                                 EMBL; M58547; AAA29720.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                   24
622
546
567
622
286
371
421
422
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                            421
422
499
622 AA;
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(POTENTIAL).

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Venter J.C.;
                                     RNS1_ARATH P42813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                       Green P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
   RESULT 8
RNS1_ARATH
                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabinase gene of Aspergillus niger.";
Appl. Microbiol. Biotechnol. 40:318-326(1993).
-!- FUNCTION: ITS PREFERED SUBSTRATE IS LINEAR 1,5-ALPHA-L-ARABINAN.
THE ENZYME ACTIVITY IS PROGRESSIVELY REDUCED AS 1,5-ALPHA-CHAINS
BECOME SHORTER OR MORE HIGHLY SUBSTITUTED.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,5-ALPHA-L-
ARABINOFURANOSIDIC LINKAGES IN 1,5-ARABINAS.
-!- PATHWAY: INVOLVED IN DEGRADATION OF THE PLANT CELL WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning, expression and structure of the endo-1,5-alpha-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARABINAN ENDO-1,5-ALPHA-L-ARABINOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARABINAN ENDO-1,5-ALPHA-L-ARABINOSIDASE A PRECURSOR (EC 3.2.1.99)
                 N-LINKED (GLCNAC. .) (POTENTIAL).
31871729E6F95254 CRC64;
                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46.5; DB 1; Length 321;
Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! SIMILARITY: BELONGS TO FAMILY 43 OF GLYCOSYL HYDROLASES.
                                                                                   DB 1; Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: BY L-ARABAN, ARABINOGALACTAN AND L-ARABITOL
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN+CBS 120.49 / N400;
MEDLINE-94128348; PubMed-7764386;
Flipphi M.J.A., Panneman H., van der Veen P., Visser J.,
de Graaff L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..) (F
3087D7D0592A0B20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 20-32 AND 125-139
LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L23430; AAA32682.1; -.
Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                    321 AA.
                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                (ENDO-1,5-ALPHA-L-ARABINANASE A) (ABN A).
                                                                                  37.4%; Score 49; 53.8%; Pred. No.
                                                                                                                                                                                                                                                                    PRT;
                              92889 MW;
                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYSACCHARIDE L-ARABINAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34454 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 TYYINFG---SFWDDIYQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TYMINFGRGONYWEHPYQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                      : || |:||| |
711 VYFGTGENYWRGP 723
                                                                                                                                                 6 INFGRGQNYWEHP 18
                                                               32 8
39.
808 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295
321 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus niger.
                                                                                                                                                                                                                                                                  ABNA_ASPNG
                 CARBOHYD
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                                SEQUENCE
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FT
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                                                                                              RIBONULEASE 1 FINALONDON 1.16.
RNS1 OR ATSG02990 OR TITMI3.16.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COLUMBIA,
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Vanken S.E., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 23-41.
Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,
                                                                                                                                                                                                                                                                                            Bariola P.A., Howard C.J., Taylor C.B., Verburg M.T., Jaglan V.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: MAY REMOBILIZE PHOSPHATE, PARTICULARLY WHEN CELLS SENESCE OR WHEN PHOSPHATE BECOMES LIMITING.
-i- CATALYTIC ACTIVITY: TWO-STAGE ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONONUCLEOTIDES MITH 2', 3'-CYCLIC PHOSPHATE INTERMEDIATES.
-i- INDUCTION: BY PHOSPHATE STARVATION.
-i- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
                                                                                                                                                                                                                                                                                                                              The Arabidopsis ribonuclease gene RNS1 is tightly controlled in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclease; Endonuclease; Signal; Multigene family.
                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1997) to the SWISS-PROT data bank
                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-04UG-2001 (Rel. 40, Last annotation update)
RIBONUCLEASE 1 PRECURSOR (EC 3.1.27.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONUCLEASE 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 230 AA.
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SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                 response to phosphate limitation."; Plant J. 6:673-685(1994).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF0045; ribonuclease_T2; 1.
PROSITE; PS00530; RNASE_T2_1; 1.
PROSITE; PS00531; RNASE_T2_2; 1.
                                                                                                                                                                                                                                                      STRAIN=CV, COLUMBIA;
MEDLINE=95093473; PubMed=8000425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001568; RNase_T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC004138; AAC32917.1;
HSSP; P08056; 1BOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U05206; AAC48925.1;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
230
126
221
65
119
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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ACT_SITE
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DOMAIN
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                                                                                                                                                                                                                                                                   SITE
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     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mosher D.F. (eds.);
Blology of vitronectins, pp.1-1, Elsevier, Amsterdam (1996).

1- FUNCTION: VITRONECTIN IS A CELL ADHESION AND SPREADING FACTOR
FOUND IN SERUM AND TISSUES. VITRONECTIN INTERACT WITH
CLYCOSAMINOCLYCANS AND PROTEOGLYCANS. IS RECOGNIZED BY CERTAIN
MEMBERS OF THE INVESTRIN FAMILY AND SERVES AS A CELL-TO-SUBSTRATE
ADHESION MOLECULE. INHIBITOR OF THE MEMBRANE-DAMAGING EFFECT OF
THE TERMINAL CYTOLYTIC COMPLEMENT PATHWAY.

1- FUNCTION: SOMATOMEDIN B IS A GROWTH HORMONE-DEPENDENT SERUM FACTOR
MITH PROTESAE-INHIBITING ACTIVITY.

2- SUBCELLULAR LOCATION: EXTRACELLULAR.

2- SUBCELLULAR LOCATION: EXTRACELLULAR.

2- TISSUE SPECIFICITY: PLASMA.

2- TYROSIDE SPECIFICITY: PLASMA.

2- TYROSIDE SPECIFICITY: PLASMA.

2- TYROSIDE SPECIFICITY: PLASMA.

2- SIMILARITY: CONTAINS 2 HEMOPEXIN LIKE DOMAINS.

2- SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C; TISSUE-Liver;
Ehrlich H.J. Richter B., von der Ahe D., Preissner K.T.;
"Primary structure of vitronectins and homology with other proteins.";
(In) Preissner K.T., Rosenblatt S., Kost C., Wegerhoff J.,
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=92052101; PubMed=1719529; Selffert D., Keeton M., Eguchi Y., Sawdey M., Loskutoff D.J.; Detection of vitronectin mRNA in tissues and cells of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 88:9402-9406(1991).
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                           ö
                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN)
                                                               Score 46; DB 1; Length 230;
Pred. No. 7.8;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUE-Liver;
MEDLINE=94085797; PubMed=7505250;
Selffert D., Poenninger J., Binder B.R.;
"Organization of the gene encoding mouse vitronectin.";
Gene 134:303-304(1993).
             G -> GXP (IN REF. 3).
DFD132D39F02505A CRC64;
                                                                                                                                                                                                               478 AA.
  BY SIMILARITY
                                                                                                                                                                                                               PRT;
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(Rel. 34, Last sequ
                          25396 MW;
                                                               35.18;
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                                                                                         6; Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                 9 GRGQNYWEHPYQK 21
                        230 AA;
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
123
39
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                                                                                                                                                                           VINC_MOUSE
ID VINC_MOUSE
AC P29788;
VT 01-1-1
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01-OCT-1996
20-AUG-2001
ACT_SITE
CONFLICT
                          SEQUENCE
                                                                                         Matches
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Glycine max (Soybean).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots. Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Robalea; eurosids I; Fabales; Fabaceae; Papliionoideae; Phaseoleae; Glycine.
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                                                                                                                                                                                                   PROSITE; PS00024; HEMOPEXIN; 2.
PROSITE; PS00524; SOMATOMEDIN_B; 1.
Heparin-binding; Cell adhesion; Glycoprotein; Sulfation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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16;
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EBOC772F8BD6A166 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SULFATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEPARIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                        CELL ATTACHMENT SITE. SULFATION (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                HEMOPEXIN-LIKE 1. HEMOPEXIN-LIKE 2.
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15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 93A2 (EC 1.14.-.-).
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                                    MGD; MGI:98940; Vtn.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001212; Somatomedin_B.
Ffam; PF0103; Somatomedin_B: 1.
Ffam; PF0103; Somatomedin_B: 1.
PRINTS; PR0002; SOMATOMEDINB..
SMART; SM00120; HX; 4.
SMART; SM00201; SO; 1.
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15-DEC-1998 (Rel. 37, Last seq
15-DEC-1998 (Rel. 37, Last ann
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Best Local Similarity
Matches 6; Conserv
PIR; S19894; SGMSV
HSSP; P45452; 1PEX
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278
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Q42799;
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InterPro; IPR000585; Hemopexin

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                         between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1 SUBCHILLULAR LOCATION: EXTRACELLULAR.

-1 TISSUE SPECIFICITY: PLASMA.

-1 TISSUE SPECIFICITY: PLASMA.

-1 TISSUE SPECIFICITY: 2 HEMOPEXIN-LIKE DOMAIN.

-1 SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
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Yoneda A., Kojima K., Matsumoto I., Yamamoto K., Ogawa H.;
Yoneda A., Kojima K., Matsumoto I., Yamamoto K., Ogawa H.;
Porcine vitronectin, the most compact form of single-chain
vitronectin: the smallest molecular mass among vitronectins was
ascribed to deletion and substitution of base pairs, and proteolytic
Lrimming of the peptide. "
J. Blochem. 120:954-960(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Cetartiodactyla; Suina; Suidae; Sus.
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20-AUG-2001 (Rel. 40, Last annotation update)
VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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D85C419D0698C77C CRC64;
                                                                                                                                                                                                                                                                               EMBL; D86351; BAA13076.1; -.
InterPro; IPR001128; Cyt_P450.
Prim; PF00067; P450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme.
BINDING 440 HEME (BY SIMILAR
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4; Mismatches
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Best Local Similarity 50.0
Matches 6; Conservative
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396 GRDPNHWENPFE 407
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SEQUENCE FROM N.A.
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HSSP; P45452; 1PEX. GlycoSuiteDB; P48819; -.

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"Monoclonal antibody EMRIa/212D recognizing site of deposition of extracellular lipid in atheroselerosis. Isolation and corracterization of a cDNa clone for the antigen.";
J. Biol. Chem. 265:21232-21236(1990).
-!- FUNCTION: VITRONECTIN IS A CELL ADHESION AND SPREADING FACTOR FOUND IN SERUM AND TISSUES. VITRONECTIN INTERACT WITH GLYCOSAMINOGINCANS AND PROFEGGLYCANS. IS RECOGNIZED BY CERTAIN MEMBERS OF THE INTEGRIN FAMILY AND SERVES AS A CELL-TO-SUBSTRATE ADHESION MOLECULE. INHIBITOR OF THE MEMBRANE-DAMAGING EFFECT OF THE TERMINAL CYTOLYTIC COMPLEMENT PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                    PRINTS; PRO0022; SOMATOMEDINB.
SMART; SM00120; HX; 4.
SMART; SM00201; SO; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00524; SOVATOMEDIN B; 1.
HEPATIN-binding; Cell adhesion; Glycoprotein; Sulfation; Signal.
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
630E134B0DC706BE CRC64;
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                                                                                                                                                                                                                 CELL ATTACHMENT SITE (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 40, Last annotation update)
VITRONECTIN PRECURSOR (SERUM SPREADING FACTOR) (S-PROTEIN)
(GLYCOPROTEIN 66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: PLASMA.
PUR. SULEATED NO 2 TYROSINE RESIDUES (BY SIMILARITY).
SIMILARITY: CONTAINS 2 HEMOPEXIN-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                  Length 459
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                                                                                                                                                                                       HEMOPEXIN-LIKE 1. HEMOPEXIN-LIKE 2.
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Pred. No. 22;
6; Mismatches
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            IPR001212; Somatomedin_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91065939; PubMed=1701177;
          InterPro; IPR001212; somaromecom-
Pfam; PF00045; hemopexin; 4.
Pfam; PF01033; somaromedin_B; 1.
                                                                                                                                                                                                                                                                                                                                         MM;
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37.5%;
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Best Local Similarity
Matches 6; Conserv
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P22458;
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VTNC_RABIT
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InterPro; IPR000585; Hemopexin.
     Jenne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki S., Oldberg A., Hayman E.G., Pierschbacher M.D., Ruoslahti E.; "Complete amino acid sequence of human vitronectin deduced from cDNA. Similarity of cell attachment sites in vitronectin and fibronectin."; EMBO J. 4:2519-2524(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki S., Oldberg A., Hayman E.G., Pierschbacher M.D., Ruoslahti E.;
Submitted (JUN-1986) to the PIR data bank.
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Last annotation update)
(SERUM SPREADING FACTOR) (S-PROTEIN) [CONTAINS:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 HEMOPEXIN-LIKE 1.
HEMOPEXIN-LIKE 2.
GLYCOSAMINOGLYCAN BINDING REGION.
GLL ATTACHENT SITE.
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
N-LINKED (GLCNAC...) (PROBABLE).
N-LINKED (GLCNAC...) (PROBABLE).
N-LINKED (GLCNAC...) (PROBABLE).
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Pred. No. 22;
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                                                                                                                    HSSP; P45452; 1PEX.
InterPro; IPR000585; Hemopexin.
InterPro; IPR001212; Somatomedin_B.
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PROSITE; PS00524; SOMATOMEDIN_B; 1.
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MEDLINE-86030229; Pubmed-2414098;
                                                                                                                                                                       Pfam; PF00045; hemopexin; 4.
Pfam; PF01033; Somatomedin_B; 1.
PRINTS; PR00022; SOMATOMEDINB.
SWART; SM00120; HX; 4.
SWART; SM00201; SO; 1.
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MEDLINE-86135941; Pubmed-3004934;
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271 VYFFKGDKYWEYQFQQ 286
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Matches 6; Conserv
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SOMATOMEDIN B].
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-78127267; PubMed-631332;
MEDLINE-78127267; PubMed-631332;
Pryklund L., Sievertsson H.;
Primary structure of somatomedin B: a growth hormone-dependent serum
factor with protease inhibiting activity.";
FEBS Lett. 87:55-60(1978).
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88107592; Pubmed-2447940;
Jenne D., Stanley K.K.;
"Nucleotide sequence and organization of the human S-protein gene:
repeating peptide motifs in the 'pexin' family and a model for their evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F., Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R., Appel R.D., Hughes G.J.;
Submitted (JUN-1992) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jenne D., Hille A., Stanley K.K., Huttner W.B.; "Sulfation of two tyrosine-residues in human complement S-protein
                  "Molecular cloning of S.protein, a link between complement, coaqulation and cell-substrate adhesion."; EMBO J. 4:3153-3157(1985).
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-!- TISSUE SPECIFICITY: PLASMA.
-!- PTM: SULFATED ON 2 TYROSINE RESIDUES.
-!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 SOMATOMEDIN-B TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Biochem. 185:391-395(1989).
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MEDLINE-90060125; PubMed-2479556;
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EMBL; X05006; CAA28659.1; ALT_SEO.
PIR; A29744; SGHUIV.
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GlycosuiteDB; P04004; -.
SWISS-2DPAGE; P04004; HUMAN.
Stanley K.K.;
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MEDLINE-88198218; PubMed-2834383;
Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
Seltzer J.L., Kronberger A., He C., Bauer E.A., Goldberg G.I.;
"H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
secrete a single metalloprotease capable of degrading basement
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     Pfam; PF00045; hemopexin; 4.
Pfam; PF01033; Somatomedin_B; 1.
PRINTS; PR00022; SOMATOMEDINB.
SMART; SM00120; HX; 4.
PROSITE; PS00024; HEMOPEXIN; 2.
PROSITE; PS0024; SOMATOMEDINB; 1.
PROSITE; PS0024; SOMATOMEDIN_B; 1.
Heparin-binding; Cell adhesion; Glycoprotein; Sulfation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Last sequence update)
20-A06_2001 (Rel. 40, Last annotation update)
72 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.24) (72 KDA
GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A)
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                                                                                                                                             CLEAVAGE.
SULFATION (PROBABLE).
SULFATION (PROBABLE).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
SULFATION (POTENTIAL).
N-LINKED (GLCNAC...).
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                                                                                                                       HEMOPEXIN-LIKE 1.
HEMOPEXIN-LIKE 2.
CELL ATTACHMENT SITE.
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S -> N (IN REF. 3 A
A -> T (IN REF. 3).
T -> M (IN REF. 3 A
                                                                                        VITRONECTIN (V75).
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                                                                                                               SOMATOMEDIN B.
                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                       SUBUNIT
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Pred. No.
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InterPro; IPR001212; Somatomedin_B.
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J. Biol. Chem. 263:6579-6587(1988)
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271 VYFFKGKQYWEYQFQ 285
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478 AA;
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Best Local Similarity
Matches 6; Conserv
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                                                                       Phosphorylation
SIGNAL
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P08253;
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CARBOHYD
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                                                                                                                                                                                                                                                                            SECUENCE OF 1-51 FROM N.A. MEDLINES-90228972; PubMed=2158484; MEDLINES-90228972; PubMed=2158484; Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B., Tryggvason K.; "Completion of the primary structure of the human type IV collagenase preproenzyme and assignment of the gene (CLG4) to the q21 region of chromosome 16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collier I.E., Bruns G.A.P., Goldberg G.I., Gerhard D.S.; "On the structure and chromosome location of the 72- and 92-kDa human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
MEDLINE-96069777; PubMed=7583664;
Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
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MEDLINE-96140723; PubMed-8549817;
Gohlke U., Gomis-Ruth F.X., Crabbe T., Murphy G., Docherty A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystal structure of the haemopexin-like C-terminal domain of gelatinase \mathbf{A}.\,\mathbf{T};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bode W.; "The C-terminal (haemopexin-like) domain structure of human
                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=90293047; Pubmed=2162831;
Huhtala P., Chow L.T., Trygqvason K.;
"Structure of the human type IV collagenase gene.";
J. Biol. Chem. 265:11077-11082(1990).
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                                                         type IV collagenase genes.";
Genomics 9:429-434(1991).
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PDB; IRTG; 10-JUN-96.
PDB; IGEN; 17-AUG-96.
MEROPS; M10.003; -.
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M55583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lattman E.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M55584;
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CATALYTIC ACTIVITY: CLEAVAGE OF GELATIN TYPE I AND COLLAGEN TYPES IV, V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-ILE-ALA-GLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A42496; A42496
HSSP; P08253; 1RTG.
MEROPS; M10.003; -.
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METAL
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
72 KDA TYPE IV COLLAGENASE.
COLLAGENASE-LIKE.
COLLAGEN-BINDING.
COLLAGEN-BINDING.
COLLAGEN-TUTPE-II 1.
FIBRONECTIN TYPE-II 2.
FIBRONECTIN TYPE-II 2.
FIBRONECTIN TYPE-II 3.
FIBRONECTIN TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium; Collagen degradation; Extracellular matrix; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE-92218452; Pubmed-1373140;
MEDILINE-92218452; Pubmed-1373140;
Reponen P., Sahlberg C., Huhtala P., Hurskainen T., Thesleff I.,
Tryggvason K.;
Tryggvason K.;
Tryggvason R.;
Tryggvason G.;
Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
72 KDA TYPE IV COLLAGENASE PRECURSOR (EC 3.4.24.24) (72 KDA GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1; Length 660;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; BC7147DC8B49F289 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                              InterPro; IFR001818; Martixin.
InterPro; IPR000180; Zn_MTpeptdse.
Ffam: PF00040; fn2; 3.
Ffam: PF00040; hempexin: 4.
Ffam: PF000413; Peptidase_M10; 1.
PRINTS; PR00013; PRTYPEII.
PRINTS; PR00181; MATRIXIN.
ProDom; PD000995; FN_Type_II; 3.
SMART; SM00029; FN_Type_II; 3.
SMART; SM00120; HX; 4.
PROSITE; PS00024; HEMOPEXIN: 1.
PROSITE; PS00024; HEMOPEXIN: 1.
PROSITE; PS00024; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00546; CYSTEINE_SWITCH; 1.
                        InterPro; IPR000562; FN_Type_II. InterPro; IPR000585; Hemopexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 28, Created)
(Rel. 28, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73882
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660 AA;
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Matches 10; Conserv
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30
1110
1110
2222
3397
2284
342
466
466
404
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MM02_MOUSE
ID P33434;
- P33434;
- FEB-199/
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METAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                              Gaps
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COLLAGEN-BINDING.
COLLAGEN-BINDING.
COLLAGEN-BINDING.
FIBRONECTIN TYPE-II 1.
FIBRONECTIN TYPE-II 3.
HEMOPEXIN-LIKE.
CYSTEINE SMITCH (POTENTIAL).
ZINC (CATALLTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALLTIC) (BY SIMILARITY).
ZINC (CATALLTIC) (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠.
-!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
-!- SUBUNIT: LIGAND FOR INTEGRIN ALPHA "V/BETA" 3.
-!- SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIOA (ZINC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 662; 31;
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C630A7DBDB272F02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.4%; Score 45; 58.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩.
                                                                                                                                                                                                                                                                                EMBL; M84324; AAA39338.1; ..
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EADIMINEGR----WEH 178
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662
221
396
467
283
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us-09-763-397a-19.rsp

Search completed: January 29, 2002, 11:13:47 Job time: 823 sec

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090969 plasmodium 090967 plasmodium 090967 plasmodium 090965 plasmodium 090962 plasmodium 090961 plasmodium 090961 plasmodium 090961 plasmodium 090961 plasmodium 090967 plasmodium 090967 plasmodium 090967 plasmodium 090967 clostridium 090995 clostridium 09090855 antirrhinum 090817 trypanosoma 091023 arabidopsis
                                                                                                                                                                                                                                                 Q95ge4 arabidopsis
Q49833 nicotiana a
Q95sx4 torenia hyb
Q2xsg6 lycium ande
Q9vpt6 drosophila
        plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kocken C.H.M., Narum D.L., Massoughodji A., Ayivi B., Dubbeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (ANA-1), comparison with p. falciparum ANA-1, and antibody-mediated inhibition of red cell invasion."
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL, AJ71168; CAB97180.1;
InterPro; IPR003298; Apmem_Agl.
Pfam; PP02430; ANA-1; 1.
PRINTS; PR01361; MEROZOITESA.
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            936u60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0UT-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 131; DB 5;
100.0%; Pred. No. 1.2e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                               526 AA
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         0909F6
0909E9
0909E9
0909E6
0909E6
0909E1
0909E1
0909E1
0909F4
0909F6
                                                                                                                                                                                                                                                  09SGE4
049833
09SSX4
09ZSG6
09VPI6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-44-2;
MEDLINE-20416492; PubMed=10960173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTYMINEGRGONYWEHPYOKS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EFTYMINFGRGONYWEHPYOKS 22
                                               Ouery Match
Best Local Similarity 100.
Matches 22; Conservative
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526 AA;
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NON_TER
SEQUENCE
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Q9N9G1;
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Q9N9G1
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Q9N9F8
(without alignments)
11.277 Million cell updates/sec
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plasmodium
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plasmodium
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Q9n9f8 plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                January 29, 2002, 11:12:14; Search time 285.36 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09n9f7 | 09n9f5 | 09n9f5 | 09n9f2 | 09n9f2 | 09n9e4 | 09n9e4 | 025745 | 025745 | 025745 | 0099vb7 | 000784 | 000784 | 000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 | 0000784 |
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Q99205
Q25750
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09n9g0
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                           131
1 EFTYMINFGRGONYWEHPYQKS 22
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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0909F7
0909F5
0909F3
0909E4
0909E3
0909E0
025745
025745
025749
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Q9GZ05
Q25750
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Q9N9G0
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sp_bacteria:*
sp_fungl:*
sp_fungl:*
sp_human:*
sp_nvertebrate:*
sp_mammal:*
sp_mhc:*
sp_organele:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_unclassified:*
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sp_virus:*
sp_vertebrate:*
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Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL: AJZ71171; CAB97183.1; -.
InterPro: IPR003299; Apmem_A91.
Pfam: PF02430; AMA-1; 1.
PRINTS: PR01361; MEROZOITESA.
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"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P, falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";

MOL Biochem. Parasitol. 109:147-156(2000).

EMBL; AJ71172; CAB97184.1;

PINTEPRO13298; Apmem_A91.

PRO1351; MERCZOITESA.
                                                                                                                                                                    Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.; "Molecular characterisation of Plasmodium reichenowi apical membrane
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                              Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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 526 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last ann
                        Created)
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APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
                       01-OCT-2000 (TrEMBLrel. 15, Last seq
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01-UNY-2001 (TrEMBLrel. 17, Last ann
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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MEDLINE=20416492; PubMed=10960173;
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01-JUN-2001 (TrEMBLrel.
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Best Local Similarity
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Kocken C.H.M., Narum D.L., Massoughodji A., Ayivi B., Dubbeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.; van der Wel A., Conway D.J., Sanni A., Thomas A.W.; "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AWA-1), comparison with P. falciparum AMA-1, and antibodymediated inhibition of red cell invasion."; Mol. Blochem. Parasitol. 109:147-156(2000).

EMBL, AJZ71174; CAB97186.1; -InterPro; IPR03298; Apmem_Ag1.
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"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P., falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL, AJ211176; CAB97188.1;
PinterPro; IPR0023298; Apmem_Agl.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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17, Last annotation update)
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MEDLINE=20416492; PubMed=10960173;
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MEDLINE-20416492; PubMed-10960173;
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EFTYMINFGRGONYWEHPYQKS 22
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Mol. Biochem. Parasitol. 109:147-156(2000).
                PRINTS; PR01361; MEROZOITESA
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"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P, falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";
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"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-I (AMA-I), comparison with P. falciparum AMA-I, and antibodymediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL; AJ271177; CAB97189.1;
InterPro; IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-I: 1.
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NCBI_TaxID=5833;
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NCBL_TaxID=5833;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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                                                           Score 131; DB 5;
Pred. No. 1.2e-11;
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100.0%; Pred. No. 1.2e-11;
Live 0; Mismatches 0;
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01-UN-2001 (TrEMBLrel. 17, Last and
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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MEDLINE=20416492; PubMed=10960173;
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MEDLINE-20416492; PubMed-10960173;
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1 Similarity 100.0%; P
22; Conservative 0;
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Matches 22; Conserv
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"Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P, falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL, AJZ71186; CAB97198-1;
InterPro; IPR003298; Apmem_Ag1.
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                                                                                                 Length 526;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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526 526
526 AA; 60917 MW; C6522FB072078D2D CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2011 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN 1 (FRAGMENT).
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100.0%; Pred. No. 1.2e-11;
tive 0; Mismatches 0;
                                                                                              Score 131; DB 5;
Pred. No. 1.2e-11;
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MEDLINE=20416492; Pubmed=10960173;
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Best Local Similarity 100.0%; P
Matches 22; Conservative 0;
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Query Match
Best Local Similarity 100.
Matches 22; Conservative
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592 AA;
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Best Local Similarity
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01-MAR-2001 (
01-JUN-2001 (
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Q9GVB7
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"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
Mol. Blochem. Parasitol. 77:109-113(1996).
EMBL; U33275; AAC47105.1; -.
InterPro; IPR003298; Apmem_Ag1.
Pfam: PF02430; AMA-1: 1.
                  Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A., van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
"Molecular coharacterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibodymediated inhibition of red cell invasion.";
Mol. Biochem. Parasitol. 109:147-156(2000).
EMBL, AJ271189; CAB972011.;
InterPro; IPR003298; Apmem_Ag1.
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Chung Kuo Chi Sheng Chung Hsueh Yu Chi Sheng Chung 13:203-208(1995).
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                                                                                                                                                                                Length 526;
                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                 934A9EFD7B93DF91 CRC64;
                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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100.0%; Pred. No. 1.4e-11;
Live 0; Mismatches 0;
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Pred. No. 1.2e-11;
Mismatches 0;
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STRAIN=25-6.1;
MEDLINE=20416492; PubMed=10960173;
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                                                                                                                  PRINTS; PR01361; MEROZOITESA.
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Best Local Similarity 100.
Matches 22; Conservative
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22; Conservative
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SEQUENCE FROM N.A.
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Best Local Simi
Matches 22;
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"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 77:109-113(1996).
EMBL; U33276; AAC47106.11, ...
InterPro; IPR003298; Apmem_A91.
Pfam; PF02430; AMA-1; 1.
NON_TER 604
E04 AA; 69892 MW; CB83EE928376BFFB CRC64;
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"Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
MOL. Biochem. Parasitol. 77:109-113(1996).
EMBL; U33279; AAC47109-11.
InterPro: IPR003298; Apmem_Agl.
Pfam; PF02430; AMA-1; 1.
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                                                                                              Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5839;
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NCBI_TaxID=5847;
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Last sequence update)
Last annotation update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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MEDLINE=96379227; PubMed=8784778;
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        AMA-1.
Plasmodium falciparum.
Bukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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NCBI_TaxID=57269;
                                                                                                                                                                                                                           Length 605;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        605 AA; 69897 MW; F6D89F02F7690C19 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
APICAL MEMBRANE ANTIGEN-1 (FRAGMENT).
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100.0%; Pred. No. 1.4e-11;
tive 0; Mismatches 0;
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nilarity 100.0%; Pred. No. 1.4e-11;
Conservative 0; Mismatches 0;
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APICAL MEMBRANE ANTIGEN 1 (FRAGMENT)
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Matches 22; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           Query Match
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AC Q9TY48;
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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96
1 NEREDERTLTKEYEDIVLK 19
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Plasmodium falcipa	Recombinant vaccin	P. falciparum SABP	Silaic acid bindin	P. falciparum SABP	TNF-R-EBA 175 fusi	CD4-EBA175 fusion	Immunogenic agent	Erythrocyte bondin	N.meningitidis BZ8	TbpB sequence from
	ID	AAY70296	AAY70278	AAR70232	AAW22477	AAY77900	AAR70105	AAR41043	AAW35466	AAW35507	AAR88656	AAY01524
	90	21	21	16	18	21	16	14	18	18	17	20
	Query Match Length DB	19	350	1435	1435	1435	1604	1786	21	21	587	619
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	61.5	56.2	50.0	50.0
	Score	96	96	96	96	96	96	96	59	54	48	48
	Result No.	-	7	e	4	s	9	7	80	0	10	11

, 685 20 AAY01525 0 689 17 AAR88648 0 689 20 AAY01523	45.0 199 17 ANALOGE Nomentials 45.0 245.0	46.9 245 22 AAM13856 46.9 245 22 AAM26263	5 46.9 245 22 AAM01599 5 46.9 645 22 AAGR2945	46.9 1501 22 AAG82878	4 45.8 51/ 18 AAW30519 3 44.8 211 22 AAG91906	3 44.8 234 21 AAG04280	3 44.8 494 21 AAG36673	3 44.8 521 21 AAG36672	3 44.8 520 21 AAG355/1 3 44.8 693 22 AAM40118	3 44.8 1316 21 AAB30505	3 44.8 133/ 21 AAB3U3U4 / 3 44.8 2573 21 AAB18234 /	2 43.8 265 22 AAGB2827	2 43.8 /66 22 AAG82/42 1 42.7 52 21 AAB11628	1 42.7 259 21 AAB54134	1 42.7 270 19 AAW70602 1 42.7 270 19 AAW76770	1 42.7 270 21 AAB11583	1 42.7 285 21 AAG56678	1 42.7 28/ 21 AABILDIB 1 42.7 309 22 AABB7763	1 42.7 312 19 AAW70601	1 42.7 312 19 AAW76769	42.7 312 21 AAB11582 42.7 371 21 AAG56677	ALIGNMENTS)296 standard; peptide; 19 AA.	1296;	, 6 ; 20 +	ON-2000 (IIISL entry)	nodium falciparum EBA-175 antigenic epitope, P546.	nbinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;		<pre>umsporozoite protein; CSP; sporozoite surface protein-2; SSP-2;</pre>	175	EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.	nodium falciparum.	0011179-A1.	JG-1999; 99WO-US18869.		-) NAT INST IMMUNOLOGY.) US DEPT
50.	4.0	46.	5 46.	5 46.	3 44.	3 44.	3 44.	3 44.	3 44	3 44.	3 44.	2 43.	43.	1 42.	1 42.	1 42.	1 42.	1 42.	1 42.	1 42.	1 42. 1 42.			AAY70296;		18.ITT) 0007-NOC-	asmodium falcipar	mbinant protein	ll epitope; tet	umsporozoite pr	al membrane ant	175; rhoptry as 7; antiparasiti	smodium falcipar		:666	-1998;	NAIM-) NAT INST IM USSH) US DEPT HEA	

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Key
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                                                                                 The present sequence is the antigenic epitope P546, derived from crythrocyte binding antigen-175 (EBA-175) of the asexual blood stage of plasmodium fatchparum. It is used in the construction of recombinant protein CDC/MIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (H18) fatg, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 contigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/MIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/MIIMALVAC-1 antibodies can be used for catecting P. falciparum in biological samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein. CSP; sporozoite surface protein.2; SSP-2; liver stage antigen.1; LSA-1; merozoite surface protein.1, MSP-2; apical membrane antigen.1; LSA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein.1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
          Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
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                                                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 96; DB 21;
100.0%; Pred. No. 3.6e-08;
Live 0; Mismatches 0;
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/label= Melittin_siqnal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Derived from Honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278 standard; Protein; 350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                               Claim 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US18869
                                                                                                                                                                                                                                                                                                                                                                                      1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                     98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200011179-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70278;
                                                                                                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70278
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                 Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; binding domain; merozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 21; 100.0%; Pred. No. 1.1e-06;
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(NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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/label= Binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peterson DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70232 standard; Protein; 1435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers

    P. falciparum in biological samples

                                                                                                                                                                                                                                                                                                                               Claim 3; Page 43-44; 52pp; English.
                                                                               Shi YP, Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US10230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SABP; sialic acid binding malaria; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum.
                                                                                                                                    WPI; 2000-237654/20.
N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. falciparum SABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1994;
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Wellems TE;
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used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducting a protective immune response in a mammal to Plasmodium merozoites (especially Plasmodium falciparum or Plasmodium vivax).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DBL gene family; SABP; sialic acid binding protein; merozoite; malaria; Duffy antigen binding protein; DABP; erythrocyte; var-1; var-2; var-3; var-7; vaccine; therapy; immune response; Plasmodium.
                                                                                                                                                                                                                                                          Sequences from the SABP gene (given in AA083525) were PCR amplified, expressed on the surface of COS cells and tested for erythrocyte binding to identify the binding domain polypeptide. A prefd. SABP binding domain comprises residues I to about 616 of the SABP protein (AAR70232). Recombinant binding domain was expressed in B. coli, yeast, mammalian, insect, and in vaccinia virus and adenovirus-infected cells. It provides protection against P. falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New malaria vaccines - contains cysteine-rich DBL family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding domains homologous domains of the Duffy and sialic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                      New erythrocyte binding domain polypeptide(s) - isolated from Plasmodium binding proteins, used in diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 16; 100.0%; Pred. No. 5.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                           Disclosure; Page 39-41; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 37-40; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22477 standard; Protein; 1435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silaic acid binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miller LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum.
                                                                                                                                                     prevention of malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-052231/05.
     WPI; 1995-123427/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT72888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding proteins
                                   N-PSDB; AAQ83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9640766-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996
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Wellems TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Duffy-binding like) gene family. The ebl-1 proteins are substantially identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid Binding Protein (DABP) and Sialic Acid Binding Protein (SABP), which are soluble proteins that appear in the culture supernatant after erythrocytes infected with malaria release merozoites. Immunochemical studies indicate that DABP and SABP are the respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy and sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be used to vaccinate against malaria, especially caused by P. falciparum. Immunization with the polypeptide provides effective protection against malaria. The present sequence represents the SABP binding domain
                                                                                                                                                                                                                                                                                                                                                          ne; Duffy-binding like gene; ebl-1; Duffy Antigen Binding Protein; Sialic Acid Binding Protein; SABP; malaria; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to ebl-1 polypeptides that are encoded by the DBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated protein binding domains from Plasmodium vivax and Plasmodium falciparum erythrocyte binding proteins useful for vaccinating against
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller LH;
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                                               Length 1435;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wellems TE,
                                           Score 96; DB 18;
Pred. No. 5.5e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                             P. falciparum SABP binding domain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Su X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Columns 45-52; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                         AAY77900 standard; Protein; 1435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peterson DS,
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0
                                               100.0%;
100.0%;
                                                                                                                              1069 neredertltkeyedivlk 1087
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                                                                                                               1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0119677
                                                                                                                                                                                                                                                                                           (first entry)
                                               Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sim KL, Chitnis C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-194198/17
1435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ98282
                                                                                                                                                                                                                                                                                                                                                                                            protozoacide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1993;
                                                                                                                                                                                                                                                                                          13-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5993827-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                               DBL gene;
 Sequence
                                                                                                                                                                                                                                                           AAY77900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Merozoite; Erythrocyte Binding Antigen 175; malaria; HIV; env; human immunodeficiency virus; envelope glycoprotein; hybrid protein; red blood cell; erythrocyte; AIDS; molecular machine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-viral fusion peptide(s) - comprise viral-binding and malaria merozoite red cell binding component, for e.g. HIV, and hepatitis
                                                                                                                                                                                      AAR41043 standard; protein; 1786 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric Homo sapiens.
                                                1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                              CD4-EBA175 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-303474/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prendergast KF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1992;
08-JUL-1992;
24-JUL-1992;
                                                                                                                                                                                                                                                                                22-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1992
03-MAR-1993
                                                                                                                                                                                                                                  AAR41043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                             AAR41043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding to a red blood cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples of these hybrid peptides. AAR70105 a fusion of tumour necrosis factor receptor (in accordance with H Lootscher et al Cell, Vol. 61, 351-359) and erythrocyte binding antigen (EBA)(175 kDa). The use of cytokine receptors not normally found on RBCs means that the cytokine can bind harmlessly to the RBC without deleterious effect. The RBC protects the hybrid peptides from excretion from the kidney, and due to steric hindrance prevents the cytokines binding to a receptor in another cell. Glycophorin binding peptide (GBP) 130 or GBPH (GBP homologue) are the prefid. malaria parasite peptides used, others include EBA 175. PWMSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by plasmodium viaxa). These peptides bind to pref. glycophorin A, B and C, sialo glycoproteins, cond on the surface of RBCs. The hybrid peptides are thus used to lower a surface are surface pathological
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein; red blood cell; cytokine receptor; glycophorin binding peptide 130; GBPH; glycophorin binding peptide homologue; glycophorin A.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and a receptor peptide.
                                                                    ;
0
                        Length 1435;
                                                                 Indels
                   Score 96; DB 21;
Pred. No. 5.5e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example A; Page 48-51; 93pp; English.
                                                                                                                                                                                                                                                                           AAR70105 standard; Protein; 1604 AA.
                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Homo sapiens.
Chimeric Plasmodium falciparum.
                   100.0%;
100.0%;
                                                                                                                                        1069 neredertltkeyedivlk 1087
                                                                                                                                                                                                                                                                                                                                                                                                                     TNF-R-EBA 175 fusion protein
                                                                                                               1 NEREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93GB-0018350.
94GB-0017021.
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                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1995 (first entry)
Ouery Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PREN/) PRENDERGAST K F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-115452/15.
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23-AUG-1994;
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                                                                                                                                                                                                                                                                                                                         AAR70105;
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92GB-0005276. 92GB-0014481. 92GB-0015829. 92GB-0019562.

93WO-GB00505

/note= "residues 20-1435 of EBA-175"

1..371 /note= "residues 1-371 of CD4" 372..1786

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                 The hybrid protein NH2-CD4(1-371)-EBA175(20-1435)-COOH is a specifically claimed example of a fusion protein of the invention; it comprises at least part of the CD4 molecule fused to a peptide from a malarial parasite merozoite protein with affinity for red blood cells. The fusion protein can bind free HIV in the blood to red blood cells and consequently reduce viral titre, prevent transmission of the virus and improve safety of blood transfusions.
                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                             Length 1786;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 14;
100.0%; Pred. No. 7.1e-06;
ive 0; Mismatches 0;
Claim 9; Page 44-47; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1420 neredertltkeyedivlk 1438
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                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                 1786
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Gaps

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Indels

100.0%; Score 96; DB 16; ilarity 100.0%; Pred. No. 6.3e-06; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 19; Conserv

Length 1604;

component treating

Mon Feb

AAW35507;

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                                                                                                                                                                                                                                                                                                                                                                                                                              through a linker to a solid phase, forming a complex of (A)-solid phase.

through a linker to a solid phase, forming a complex of (A)-solid phase.

Where (A) comprises 10-50 amino acids cappable of forming a secondary

structure in a benign buffer after liberation from the solid phase, and

further the (A)-solid phase complex comprises an immunogenic substance

and/or an immune mediator coupled on (A). The present sequence

confidence as specifically claimed immunogenic agent peptide from the

invention. An (A)-solid phase complex can be used as a scaffold for the

traching molecules at attachment points. Alternatively (A) is used as

a scaffold-peptide for the incorporation into an Immunostimulating

complex (Iscom) resulting an (A)-Iscom complex which is used for the

complex (Iscom) resulting an (A)-Iscom complex which is used for the

conjugation. (A) derivatised with one or more peptides having

conjugation. (A) derivatised with one or more peptides having

conjugation healing. Also a derivatised (A) can be used for the selection

of wound healing. Also a derivatised (A) can be used for the selection

of specifically-binding aptemers or as a diagnostic agent. Such

of specifically-binding aptemers or as a diagnostic agent. Such

or indicative of pregnancy or of a disease, such as an infectious,

autoimmune or cancerous disease.
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                                                                                                                  T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                         Non-dendritic peptide carrier linked to a solid phase - useful as a diagnostic agent and as a scaffold for production of chemical derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 59; DB 18; Length 21; 100.0%; Pred. No. 0.016; 1ve 0; Mismatches 0; Indels
                                                                                              Immunogenic agent peptide EBA 175-peptide.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 105; Page 209; 262pp; English.
                   AAW35466 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW35507 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                          96DK-0000398
                                                                                                                                                                                                                                 97WO-DE00146
                                                                                                                                                                                                                                                                                                           Heegaard PMH, Jakobsen PH;
                                                                   22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.5
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                    (PEPR-) PEPRESEARCH AS
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                                                                                                                                                                                                                                                                                                                                 WPI; 1997-512645/47.
                                                                                                                                                         Unidentified
                                                                                                                                                                                WO9738011-A1
                                                                                                                                                                                                                                 03-APR-1997;
                                                                                                                                                                                                                                                          03-APR-1996;
                                                                                                                                                                                                          16-0CT-1997.
                                           AAW35466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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through a linker to a solid phase, forming a complex of (A)-solid phase.

Where (A) comprises 10-50 amino acids capable of forming a secondary structure in a benign buffer after liberation from the solid phase.

Where (A) comprises 10-50 amino acids capable of forming a secondary structure in a benign buffer after liberation from the solid phase.

C tructure the (A)-solid phase complex comprises an immunogenic substance and/or and/or an immune mediator coupled on (A). The present sequence represents a peptide used in an example from the present invention. An (A)-solid phase complex can be used as a scaffold for the production of chemical derivatives, characterised by covalently attaching molecules at attachment points. Alternatively (A) is used as a scaffold peptide for the incorporation into an Immunostimulating Complex (Iscom) resulting an (A)-scom complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. (A) derivatised with one or more peptides having fibronectin. laminin or vitronectin-like binding activities can be used for the promotion of cell-attachment to plastic surfaces, in particular to inhibit tumour growth and metastasis, and for promotion of specifically pinding aptemers or as a diagnostic agent. Such diagnostic (A) molecules cond a disease, such as an entire of presented and promotion of presented and promotion of presented and an entire agent molecules could be used to detect molecules and a disease, such as an entire condition of presented and an entire condition of presented and an entire condition of a disease, such as an entire condition of presented and an entire condition of a disease, such as an entire condition of presented and an entire condition of presented and an entire condition of presented and an entire condition of a disease, such as an entire condition of a disease, such as an entire condition of a disease.
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                                                                                                                                                                                                    T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-dendritic peptide carrier linked to a solid phase - useful as a diagnostic agent and as a scaffold for production of chemical derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious, autoimmune or cancerous disease.
                                                                                                    Erythrocyte bonding antigen-175 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 20; Page 124; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88656 standard; Protein; 587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96DK-0000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heegaard PMH, Jakobsen PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1996 (first entry)
22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEPR-) PEPRESEARCH AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TLTKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-512645/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA;
                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9738011-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR88656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88656
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immunotherapy; domain 2.

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Deletion mutants derived from the N.meningitidis strain IM2169 transferrin Tbp2 subunit are claimed in which at least one of the first domains is partially or totally deleted, provided that the first and second domains are not simultaneously partially or totally deleted. Derivatives of IM2169-related strains are also claimed and for these polypeptides the positions of the 3 domains are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides of the invention can generate an immune response against Numeningitidis. The present sequence is that of a preferred mutant BZ83 have been deleted (see features table).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oeptide(s) for vaccination against Neisseria meningitidis group comprising deletion mutants of transferrin receptor Tbp2
                                                                                                                                             /note- "mature Tbp2 sequence of 669 amino acids
from which residues 339-356, 395-421,
443-458 and 477-497 have been deleted"
                                      Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
                                                                                                                                                                                                                                                                                                                                  339..376
/note= "residues 357-394 of wild-type Tbp2"
377..397
                                                                                                                                                                                                                                                                                                                                                                    /note= "residues 422-442 of wild-type Tbp2"
398..415
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residues 498-669 of wild-type Tbp2"
                                                                                                                                                                                                                                                                                                                    /note= "residues 1-338 of wild-type Tbp2"
                                                                                                                                                                                                                                         /label= Domain_2_(partially_deleted)
/note= "partially deleted hinge domain"
                                                                                                                                                                                               /label- Domain_1
/note- "complete N-terminal domain"
            N.meningitidis BZ83 Tbp2 domain 2 deletion mutant.
                                                                                                                                                                                                                                                                                             /note= "complete C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INMR ) PASTEUR MERIEUX SERUMS & VACCINS (TRGE ) TRANSGENE SA.
                                                                               Neisseria meningitidis (strain BZ83)
                                                                                                                      Location/Qualifiers
1..587
                                                                                                                                                                                                                                                                     440..587
/label= Domain_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 24; Page -; 114pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-FR00701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94FR-0006594
                                                                                                                                                                                                                                                                                                                                                                                                                416..587
                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Legrain M,
                                                      passive immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-030562/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide(s) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9533049-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC:1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Millet MBJ;
                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunit
                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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Lissolo L;

Mazarin V,

Length 587;

17;

DB 7

Score 48; Pred. No.

50.0%;

Query Match Best Local Similarity

"residues 459-476 of wild-type Tbp2"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low molecular weight subunit; TbpB; human transferrin receptor; hTR; Neisseria meningitidis; vaccine; meningococcal infection; meningitis.
 Gaps
                                                                                                                                                                                                                          Low molecular weight subunit; TbpB; human transferrin receptor; hTR; Neisseria meningitidis; vaccine; meningococcal infection; meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine containing small subunit of human transferrin receptor from Neisseria meningitidis – for treatment and prevention of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TbpB) of the human transferrin receptor (hTR) from a specific strain of Neisseria meningitidis that contains TbpB-encoding DNA. Compositions containing TbpB are used as vaccines for treatment or prevention of meningococcal infections, particularly meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the low molecular weight subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
  Indels
                                                                                                                                                                                                  TbpB sequence from Neisseria meningitidis strain M982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TbpB sequence from Neisseria meningitidis strain 8680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ů,
 5;
                                                                                                                                                                                                                                                                                                                                                                                              (INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 41;
4; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 38-40; 73pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY01525 standard; Protein; 685 AA.
                                                                                                                     AAY01524 standard; Protein; 679
  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                             98WO-FR01730
                                                                                                                                                                                                                                                                                                                                                                     97FR-0010301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||: || :||:
516 ertdekeipkeqqdivyr 533
                                       || || : || :|| :
424 ertdekeipkeggdivyr 441
                                                                                                                                                                                                                                                                                                                                                                                                                          B, Quentin-Millet M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EREDERTLTKEYEDIVLK 19
                           EREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
  Conservative
                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-190036/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX26576
                                                                                                                                                                                                                                                                                         WO9907741-A1.
                                                                                                                                                                        14-JUN-1999
                                                                                                                                                                                                                                                                                                                                             03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                     07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1999
                                                                                                                                                                                                                                                                                                                    18-FEB-1999.
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                                                                                                                                                AAY01524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          Rokbi
                                                                                           11
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  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY01525
                                                                                                          AAY01524
                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                            Qγ
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Low molecular weight subunit; TbpB; human transferrin receptor; hTR; Neisseria meningitidis; vaccine; meningococcal infection; meningitis.
                                                                                                                                                                                                             Polypeptide(s) for vaccination against Neisseria meningitidis group B\, - comprising deletion mutants of transferrin receptor Tbp2 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine containing small subunit of human transferrin receptor from
                                                                                                                                                                                                                                                                                                            The present sequence is that of the N.meningitidis strain B283 transferrin Tbp2 subunit. The Tbp2 polypeptide has three domains (see features table); deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in B283 are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides of the invention can generate an immune response against N.meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 17; Length 689;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TbpB sequence from Neisseria meningitidis strain BZ83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                         Lissolo L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 42;
4; Mismatches
                                                                             (INMR ) PASTEUR MERIEUX SERUMS & VACCINS
                                                                                                                                                                                                                                                                                  Disclosure; Page 76-81; 114pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY01523 standard; Protein; 689 AA.
                                                                                                                         Mazarin V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0010301.
              95WO-FR00701
                                             94FR-0006594
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526 ertdekeipkeggdivyr 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EREDERTLTKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quentin-Millet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                           Legrain M,
                                                                                          ) TRANSGENE SA
                                                                                                                                                                       WPI; 1996-030562/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-190036/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           689 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX26575.
                                                                                                                                                                                       N-PSDB; AAT11243
              30-MAY-1995;
                                             31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9907741-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-1997;
                                                                                                                         E, L
MBJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY01523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rokbi B,
                                                                                                                           Jacobs
                                                                                          (TRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01523
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                                                                                                                                                                                                                                                            Vaccine containing small subunit of human transferrin receptor from Neisseria meningitidis - for treatment and prevention of meningitis
                                                                                                                                                                                                                                                                                                                                           The present sequence encodes the low molecular weight subunit (TDpB) of the human transferrin receptor (MTR) from a specific strain of Neisseria meningitidis that contains TDpB-encoding DNA. Compositions containing TDpB are used as vaccines for treatment or prevention of meningococcal infections, particularly meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis BZ83 transferrin receptor Tbp2 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine; passive immunisation; immunotherapy; IM2169; IM2394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
42;
                                                                                                                                                     (INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542..689
/label- Domain_3
/note- "C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note- "N-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label- signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343..341
/label- Domain_2
/note- "hinge domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis (strain BZ83).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label- Tbp2_subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                               Claim 10; Page 43-46; 73pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88648 standard; Protein; 689 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21..342
/label- Domain_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                                                                        98WO-FR01730
                                                                                                                       97FR-0010301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || : : || :|| :
522 ertdekeipkeqqdivyr 539
                                                                                                                                                                                    Quentin-Millet M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EREDERTLTKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541
Neisseria meningitidis
                                                                                                                                                                                                                   WPI; 1999-190036/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           685 AA
                                                                                                                                                                                                                                    N-PSDB; AAX26577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-SEP-1996
                                                                                          03-AUG-1998;
                                                                                                                       07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9533049-A2
                           WO9907741-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1995
                                                           18-FEB-1999
                                                                                                                                                                                    Rokbi B,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дома1n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
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completed: January 29, 2002, 10:21:51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deletion mutants derived from the N.meningitidis strain IM2169 transferin TbD2 subunit are claimed in which at least one of the three domains is partially or totally deleted, provided that the first and second domains are not simultaneously partially or totally deleted. Derivatives of IM2169 related strains are also claimed and for these polypeptides the positions of the 3 domains are defined by alignment with the IM2169 sequence. The deletion mutant polypeptides
                                                                                                                                                                                                               Gaps
- for treatment and prevention of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide(s) for vaccination against Neisseria meningitidis group B \, -comprising deletion mutants of transferrin receptor Tbp2 \,
                                                    The present sequence represents the low molecular weight subunit (TDpB) of the human transferrin receptor (hTR) from a specific strain of Neisseria meningitidis that contains TbpB-encoding DNA. Compositions containing TbpB are used as vaccines for treatment or prevention of meningococcal infections, particularly meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..199
/label= Domain_2
/note= "complete hinge domain; the entire domain 1
and domain 3 sequences have been deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                             N.meningitidis BZ83 Tbp2 domain 1 and domain 3 deletion mutant.
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
                                                                                                                                                                                 DB 20; Length 689; 42;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      passive immunisation; immunotherapy; domain 2.
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                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INMR ) PASTEUR MERIEUX SERUMS & VACCINS
                                                                                                                                                                                 Score 48;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (strain BZ83)
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         AAR88661 standard; Protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mazarin V,
                          Claim 4; Page 32-34; 73pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page -; 114pp; French.
                                                                                                                                                                                 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94FR-0006594
                                                                                                                                                                                                                                                         || || : || :|| : || 526 ertdekeipkeggdivyr 543
                                                                                                                                                                                                                                        2 EREDERTLIKEYEDIVLK 19
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                               Local Similarity 50.0 es 9; Conservative
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Legrain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TRGE ) TRANSGENE SA
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                                                                                                                                        689 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacobs E, L
'Millet MBJ;
                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1995
                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                     AAR88661;
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit
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Matches
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of the invention can generate an immune response against N.meningitLidis. The present sequence is that of a preferred mutant in which domains 1 and 3 of the IM2169-related strain B283 have been deleted in their entirety, i.e. it is the sequence of domain 2 of
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                   ;
0
                                                                                                                                                             Length 199;
                                                                                                                                                                                                   Indels
                                                                                                                                                             DB 17;
                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                  Pred. No. 14;
                                                                                                                                                               Score 47;
                                                                                                                                                               49.0%;
56.2%;
                                                                                                                                            Ouery Match
Best Local Similarity 56.2.
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184 ertdekeipkeggdiv 199
                                                                                                                                                                                                                                     2 EREDERTLIKEYEDIV 17
                                                                         the BZ83 Tbp2 subunit.
                                                                                                            199 AA;
                                                                                                            Sequence
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Plasmodium falciparum
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REFERENCE/DOCKET NUMBER: NIHII
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1435 amino acids
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  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-568-459A-4
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US-08-568-459A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
  Sequence 145, Appliageduence 2, Appliageduence 2, Appliageduence 33, Appliageduence 33, Appliageduence 33, Appliageduence 18, Appliageduence 18, Appliageduence 9, Appliagedue
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Sequence 7, Appli
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3.210 Million cell updates/sec
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                                                                                                                                                                                  ; Search time 133.18 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Sequence 33, Sequence 33, Sequence 33, Sequence 18, Sequence 18, Sequence 18, Sequence 9, 
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pCTUS_COMB.pep:*
                                                  Compugen Ltd.
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US-09-065-474-170
US-08-031-485-7
US-08-031-485-7
US-09-065-474-145
US-09-065-474-1
US-09-065-474-2
US-09-065-474-2
US-09-065-474-2
US-09-065-474-2
US-09-065-474-3
US-09-065-474-3
US-09-065-474-3
US-09-065-474-18
US-08-149-106-18
US-08-149-106-18
US-08-1298-021-18
US-08-1298-021-18
US-08-125-343A-9
US-08-125-343A-9
US-08-155-343A-9
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US-08-643-563A-9
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US-08-445-468A-9
US-08-461-397A-9
                         GenCore version 4.5 Copyright (c) 1993 - 2000 Com
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               January 29, 2002, 10:24:10
                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                              1 NEREDERTLIKEYEDIVLK 19
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Gapop 10.0 , Gapext 0.5
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96
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Maximum DB seq length: 200000000
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Match Length
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NIH121,001CP1

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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING PRACIPARUM ERYTHROCYTE BINDING PROTEINS
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: California
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Sequence 23, A
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Sequence 7, App
Sequence 156, Sequence 
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                      Sequence
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US-08-478-097A-10

US-08-445-467-9

US-08-480-215A-9

US-08-218-23

US-08-214-56A-9

US-09-054-55A-9

US-09-054-55A-9

US-08-211-55A-7

US-08-211-55A-9

US-08-211-39-156

US-08-210-22-01968-9

PCT-US93-07190-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08142-9

PCT-US93-08188-9
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APPLICATION NUMBER: US/08/568,459A
FILLING DATE: 07-DEC-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08568459A Patent No. 5849306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
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GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
WIMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                        Blehm, E. Scot
JENTION: DIROCHLARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
FENTION: USES THEREOF
                                                                                                                                                                                                                                                                    COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC Compatible
OPERATIOR SYSTEM: Windows 95
SOFTWARE: WORDPERFECT for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION NUMBER: US/09/065,474
FILING APPLICATION NUMBER: 37,459
REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: HW-5-C1
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                 NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 3
Pred. No. 6.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                      ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09031485 Patent No. 5824306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 970/493-727.
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 61.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: Protein
      APPLICANT: Tang, Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 EERTITTYEDDV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 DERTLTKEYEDIV 17
                          APPLICANT: Blehm, E
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
GY: linear
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                                                                                                                                                                                                                                                          ZIP: 80525
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US-09-031-485-7
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                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-Zihaun
APPLICANT: Su, Xin-Zihaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
CORRESPONDENCE ADDRESS:
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  Length 1435;
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
100.0%; Score 96; DB 2; 100.0%; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96; DB 2;
Pred. No. 7.1e-07;
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Knobbe Martens Olson & Bear
                                        Mismatches
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PILIOR DATE: 10-SEP-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Israelsen, wed
REGISTRATION UNMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CH
TELECHOUNE: (619) 235-8550
TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-065-474-170
Sequence 170, Application US/09065474
; Patent No. 6063599
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Plasmodium falciparum
US-08-487-8268-4
                                                                                                                                                                                                           Sequence 4, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:
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100.0%;
                                                                                                   1069 NEREDERTLIKEYEDIVLK 1087
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                                                                                                                                                                                                                                                                        Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                             1 NEREDERTLIKEYEDIVLK 19
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Best Local Similarity 100.
Matches 19; Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                         US-08-487-826B-4
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Gaps

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Length 52; 3; Indels

DB 3;

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Gaps

APPLICATION NUMBER: US/09/031,485

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Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
                                                                                                                                                                                                                                                      Sequence 7, Application US/09065474
Patent No. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blahm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                 Score 41; DB 2; Length 270;
Pred. No. 40;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 3; Length 270;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALP: 803.2.
CALP: 803.2.
CALP: 803.2.
MEDIUM TYPE: Floppy disk
COMPUTER: Elbopy disk
COMPUTER: Elb PC compatible
OPERATIOS SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02.09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION NUMBER: 37.459
REGFERNCE/DOCKET NUMBER: 37.459
REFERENCE/DOCKET NUMBER: 37.459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 970/484-950.2
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.78;
61.58;
                    42.7%;
ilarity 61.5%;
Conservative
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970/484-9505
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Best Local Similarity 61.5
Matches 8; Conservative
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MOLECULE TYPE: protein
US-09-065-474-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
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132 EERTITTYEDDV 144
                                                                                                                               5 DERTLTKEYEDIV 17
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                    Query Match
Best Local Similarity
Matches 8; Conserva
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Patent No. 5827692
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/847,429A

FILING DATE: 24-APR-1997

CLASSIFICATION: 435
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Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-ARR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                         NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/449-7572
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37 459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.7%;
                                                                                                                                                                                                                                                                                                        : 270 amino acids amino acid
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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FILING DATE:
CLASSIFICATION: 530
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429A
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INCEMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
PURPER PROCKET NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2;
Pred. No. 48;
2; Mismatches 3
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Pred. No. 48;
  APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08847429A Patent No. 5827692
                                                                                                        REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
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61.5%;
                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERITICS:
                                                                                                                                                                                                                                                                                                                                                                                          42.7%;
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                        LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.7
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-031-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-847-429A-2
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Best Local Similarity
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US-08-847-429A-2
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APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
APPLICANT: Blahm, E. Scot
TITLE OF INVENTION: DIRFILLARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DIRFILLARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DIRFILLARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STREET: Clorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 3; Length 287;
Pred. No. 43;
2; Mismatches 3; Indels
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IEM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
                                                           ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELEPOMNUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPAX: 970/484-9505
TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09031485 Patent No. 5824306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Protein US-09-065-474-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||:| ||| |
149 EERTITTYEDDV 161
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                                                                                                                                                                                              80525
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                                                                                                                                                                          COUNTRY:
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US-09-031-485-2
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US-08-847-429A-33
Sequence 33, Application US/08847429A
Patent No. 5827692
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E Scot
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
TID: OACE OF COLORADO
STATE: Colorado
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Pred. No. 3.2e+02;
2; Mismatches 3; Indels
                                                                                                                                       COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPUTER: BIM PC compatible
COMPUTER: BIM PC compatible
COMPUTER: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATFORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,459
REFERENCE/POCKET UNMBER: 37,459
REFERENCE/POCKET UNMBER: 37,459
RELEPANICATION NUMBER: 37,459
REQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
LENGTH: 1745 Amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/847,429A FILING DATE: 24-APR-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
               STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
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  Heska Corporation
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Best Local Similarity 61.5
Matches 8; Conservative
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1607 EERTITTYEDDV 1619
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  ADDRESSEE:
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US-09-065-474-2

Sequence 2, Application US/09065474

Sequence 2, Application US/09065474

Sequence 2, Application US/09065474

Sequence 2, Application US/09065474

GENERAL INFORMATION:

APPLICANT: Tang, Liang

APPLICANT: Blehm, E. Scot

TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: DROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TUMBER OF SEQUENCES: 171

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-031-485-33

Sequence 33, Application US/09031485

Patent No. 5824306

GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 3; Length 312;
Pred. No. 48;
2; Mismatches 3; Indels
  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carol Talkington Verser, Ph.D.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELEPHONE: 970/493-7272
TELEPHONE: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
5;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 anino acids
TYPE: amino acid
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8; Conservative
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                                                                           :|||:| ||| |
297 EERTITTYEDDV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||:| ||| |
297 EERTITTYEDDV 309
                                                 5 DERTLIKEYEDIV 17
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Best Local Similarity
Matches 8; Conserv
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Matches
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1607 EERTITTTYEDDV 1619

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DB 1; Length 25;
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APPLICATION NUMBER: US/07/718,274A
FILING DATE: 19910620
CLASSITCATION: 435
PROR APPLICATION NUMBER: US 07/415,555
FILING DATE: 04-OCT-1989
PROR REPLICATION NUMBER: US 07/256,034
PRICH REPLICATION NUMBER: US 07/256,034
                                                                                                                                                                                                                               APPLICANT: Trinna, Lynn
APPLICANT: Parsons, Thomas F.
APPLICANT: Theofan, Georgia
TITLE OF INVENTION: Osteogenic Factor
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSE: ABISHAIL, O'TOOLE, GERSTEIN, MURTAY & ADDRESSEE: Bickhell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB Pred. No. 4.1; 7; Mismatches
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Sequence 18, Application US/08149106
Sequence 18, Application US/08149106
Sequence 18, Application US/08149106
Sequence 18, Application Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                Sequence 18, Application US/07718274A Patent No. 5284756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 2712;
TELECHONE: (312) 346-5750
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
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; MOLECULE TYPE: protein
US-07-718-274A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 25 am-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
                                                                                RESULT 14
US-07-718-274A-18
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US-09-065-474-33

Sequence 33, Application US/09065474

Fatent No. 6063599

Patent No. 6063599

GENERAL INFORMATION:
APPLICANT: Blehm, E. Scot

TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 171

CORRESPONDENCES: 171

CORRESPONDENCES: 174

ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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42.7%; Score 41; DB 3; Length 1745;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 2; Length 1745;
Pred. No. 3.2e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT TRORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37.459
REPERBING-COCKET WUMBER: HW-5-C1
TELECHMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHAX: 970/484-9555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACIERISTICS:
LENGTH: 1745 amino acids
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW
TELECOMUNICATION INFORMATION:
TELEPHONE: 970/483-7272
TELEFRAX: 970/484-9505
                                                                                                                                                  TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
ERNGTH: 1745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-09-065-474-33
                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-847-429A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DERTLIKEYEDIV 17
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                                                                                                                                                                                                                                                                                              amino acid
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Gaps

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Pred. No. 4.1;
7; Mismatches 3; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER: TDAM PC.COS/MS-DOS
COMPUTER: TDAM PC.COS/MS-DOS
COMPUTER: PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PAPELCATION DATA:
MEDIUM TYPE: Ploppy disk
COMPUTER: PAPELCATION NUMBER: US 07/415,555
FILING DATE: 04-0CT-1989
PRIOR APPLICATION NUMBER: US 07/256,034
FILING DATE: 11-0CT-1989
PRIOR APPLICATION NUMBER: 31879
FILING DATE: 11-0CT-1989
ATTORNEY/AGENT INFORMATION:
MESTISTATION NUMBER: 31879
FILING DATE: 11-0CT-1989
ATTORNEY/AGENT INFORMATION:
MESTISTATION NUMBER: 27129/9430
FILING DATE: 1346-5750
FILING DATE: 1346-5750
TELECOMMUNICATION NOR SED ID NO: 18:
TELERAX: 25-3856
INFORMATION POR SED ID NO: 18:
SEQUENCE CHARACTERISTICS:
LEUGHTH: 25-3866
INFORMATION POR SED ID NO: SEDUENCE LINEAR
TYPE: ADDRESSED SED NO: SED ID NO: SEDUENCE TYPE: PROCEDING
TYPE: PROCEDING TYPE: PROCEDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
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Search completed: January 29, 2002, 10:24:11 Job time: 517 sec

|:|::| |:|:: 5 ENEKVVLKNYQDMVVE 20

q

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 29, 2002, 10:26:46; Search time 144.96 Seconds (without alignments) 9.984 Million cell updates/sec

US-09-763-397A-20 96 1 NEREDERTLTKEYEDIVLK 19 Perfect score: Sequence:

Scoring table:

219241 segs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OUT O CLOUD

		•			SUMMARIES	
Result		Ollery				
S S	Score	Match	Length	DB	Π	Description
-	96	100.0	1435	7	A37793	erythrocyte-bindin
2	20	52.1	368	7	~	hypothetical prote
3	49	51.0	442	~	A36469	•
4	49	51.0	598	7	T38241	probable U3 small
S	48	50.0	217	7	S61546	transferrin bindin
9	48	50.0	689	~	S70661	transferrin-bindin
7	46		213	-	QQV215	D9R protein - vacc
80	46	۲.	213	Н	F36847	
თ	46	٠	213	7	H42515	
10	46	7	213	~	A72163	F9R protein - vari
11	46	47.9	213	~	T28537	hypothetical prote
12	46	•	213	7	Т37382	25K mutT-like prot
13	46	47.9		7	D84509	hypothetical prote
14	46	47.9			T37768	probable vacuolar
15	46	47.9			T31307	type I fatty acid
16	45	46.9			839969	tubulin alpha chai
17	45	46.9			S39691	UTPhexose-1-phos
18	45	46.9			T30577	DNA topoisomerase
19	44.5	46.4	361		C71242	hypothetical prote
20	44	45.8			A38094	D-lactate dehydrog
21	44	45.8			H81311	transcription-repa
22	44	45.8			S59330	Na+/H+-exchanging
23	43.5	45.3			S29870	DNA-binding protei
24	43	44.8			D81069	glutathione synthe
25	43	44.8	342	7	H81404	S-adenosylmethioni
56	43	4	943	7	S59317	DIP2 protein - yea
27	43	44.8	1829	7	T24583	1 pr
28	43	44.8	2573	7	D71614	_
59	42.5	44.3	604	~	T15514	_

ribosomal protein fumarate reductase	hypothetical prote	nyporneticai proce 5-aminolevulinate	hypothetical prote	hypothetical prote	ORF MSV156 hypothe	protein P120 - Myc	hypothetical prote	protein F12A21.23	hypothetical prote	hypothetical prote	protein calE - Esc	hypothetical prote	annexin P35 - maiz
R5YM4C C44954	T19330	TZU39Z SYCHAL	T29523	S20531	T28317	T18352	H70926	669965	T19843	T19573	C64724	T15274	T02975
	~	7 ~	7	~	~	7	~	~	~	7	7	7	7
208	274	635	647	876	1127	1078	101	110	188	191	203	204	314
43.8	43.8	4.3.0	43.8	43.8	43.8	43.2	42.7	42.7	42.7	42.7	42.7	42.7	42.7
4 4 2 2	4.	4 4	42	42	42	41.5	41	41	41	41	41	41	41
30	35	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Asylysa Asylysa Region of the Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: 30.Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jun-2000
C;Accession: A37793; Sil561
R;Sim, B.K.L.; Orlandi, P.A.; Haynes, J.D.; Klotz, F.W.; Carter, J.M.; Camus, D.; Zeg
J. Cell Biol. 111, 1877-1884, 1990
A;Title: Primary structure of the 175K Plasmodium falciparum erythrocyte binding anti
A;Reference number: A37793
A;Accession: A37793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1435 <SIN>A;Cim, B.K.L.
Mol. Biochem. Parasitol. 41, 293-295, 1990
A;Title: Sequence conservation of a functional domain of erythrocyte binding antigen
A;Reference number: S11561; MuID:90377299
A;Residues: 995-1158
A;Residues: 995-1158
A;Cross-references: EMBL:X52524

Gaps ö Length 1435; Indels ö Query Match 100.0%; Score 96; DB 2; Best Local Similarity 100.0%; Pred. No. 2e-06; Matches 19; Conservative 0; Mismatches 0;

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1 NEREDERTLTKEYEDIVLK 19 δy

1069 NEREDERTLIKEYEDIVLK 1087 g

hypothetical protein At2g27780 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C; Accession: H84676
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A; Recession: H84676
A; Accession: H84676
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: AE002093; NID: 93860254; PIDN: AAC73022.1; GSPDB: GN00139
C; Genetics:

RESULT A36469

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R;Wilton, J.; Ala'Aldeen, D.; Palmer, H.M.; Borriello, S.P.
FEMS Microbiol. Lett. 107, 59-66, 1993
A;Title: Cloning and partial sequence of transferrin-binding protein 2 of Neisseria m
A;Reference number: S37625; MUID:93224009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X75167; NID:9405780; PIDN:CAA53009.1; PID:9405781
A; Experimental source: strain B15P1.16
R; Legrain, M.; Findell, A.; Villeval, D.; Quentin-Millet, M.J.; Jacobs, E. Mol. Microbiol. 19, 159-169, 1996
A; Title: Molecular characterization of hybrid Tbp2 proteins from Neisseria meningitid A; Reference number: S70659; MUID:96419172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent recepto C;Keywords: membrane protein 
C;Keywords: membrane protein 
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-689/Product: transferrin-binding protein 2 #status predicted <MAT>
                                                                                                                                    Cyccession: S61546
R; Rokbi, B.; Maitre-Wilmotte, G.; Mazarin, V.; Fourrichon, L.; Lissolo, L.; Quentin-M Aritle: Variable sequences in a mosaic-like domain of meningococcal tbp2 encode immu A; Reference number: S61544; MUID:96039602
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-217 - RROK>
A; Cross-references: EMBL:X88867; NID:g1070368; PIDN:CAA61337.1; PID:g1070369
A; Cross-references: EMBL:X88867; NID:g1070368; PIDN:CAA61337.1; PID:g1070369
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent recepto C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-689 <LEG>
A;Cross-references: EMBL:250732; NID:91177570; PIDN:CAA90599.1; PID:91177571
                                      transferrin binding protein 2 - Neisseria meningitidis (fragment)
C.Species: Neisseria meningitidis
A.Variety: strain 2996
C.Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transferrin-binding protein 2 precursor - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S70661; S37626; S70659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 2;
Pred. No. 5.2;
4; Mismatches
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19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S70661; S37626; S70659
R;Legrain, M.
submitted to the EMBL Data Library, August 1995
A;Reference number: S70661
A;Accession: S70661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 21-245,'D',247-260,'D',262-689
A; Cross-references: EMBL:250732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
50.0%;
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183 ERTDEKEIPKEQQDIVYR 200
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 25-65 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S37626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable U3 small nucleolar ribonucleoprotein component - fission yeast (Schizosaccharom C; Species: Schizosaccharomyces pombe
C; Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
R; Schossion: T38241
R; Brown, D; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1995
A; Reference number: Z21781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rimckearin, D.M.; Spradling, A.C.
Genes Dev. 4, 2242-2251, 1990
Ayfitle: bag-of-marbles: a Drosophila gene required to initiate both male and female gam
A;Reference number: A36469; MUID:91122627
A;Accession: A36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-598 <BRO>
A;Cross-references: EMBL:298559; PIDN:CAB11156.1; GSPDB:GN00066; SPDB:SPAC23C11.03
A;Experimental source: strain 972h-; cosmid c23C11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                       bam protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                        A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g32820
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                                                                                                                            Length 368
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A Molecule type: DNA
A; Residues: 1-442 <MCK>
A; Cross-references: GB:X56202; NID:g2558529; PID:g7639
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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Pred. No. 11;
; Mismatches
                                                                                                                               5;
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Pred. No. 8.1;
0; Mismatches
                                                                                                                            Score 50; DB 2
Pred. No. 4.7;
5; Mismatches
                                                                                                                            DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: FlyBase:bam
A;Cross-references: FlyBase:FBgn0000158
C;Superfamily: fruit fly bam protein
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47.4%;
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66.7%;
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                                                                                                                            Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                       170 NKKEDQRSLTRETEKI 185
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Best Local Similarity
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A; Gene: SPDB:SPAC23C11.03
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Best Local Similarity
Matches 10; Conserv
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A; Gene: At2g27780
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Matches

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Gaps

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C; Species: variola minor virus
C; Species: variola minor virus
C; Date: 24 Nov-1999 #sequence_revision 24 Nov-1999 #text_change 20-Jun-2000
C; Date: 24 Nov-1999 #sequence_revision 24 Nov-1999 #sequence_revision 24 Nov-1999 #sequence_revision 24 Nov-1999 #sequence_revision 24 Nov-1999 #sequence of Date: Massung, R.F.; Losubmitted to GenBank, March 1998
A; Description: Analysis of the complete coding sequence of DNA of alastrim variola minimate and A; Reference number: A72150
A; Reference number: A72151
A; Reference number: A72153
A; Residues: 1-213 <SHC>
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R; Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au Nature 366, 748-751, 1993
A; Title: Potential virulence determinants in terminal regions of variola smallpox vir A; Reference number: 220488; MUID:9408B747
A; Accession: T28537
A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                    C; Species: vaccinia virus
A; Note: host Homo saptens (man)
C; Accession: H42515
R; Johnson, G.P.
Submitted to GenBank, June 1990
A; Reference number: A33172
A; Rccession: H42515
A; Status: preliminary
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C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54699.1; PID:95830660 A;Experimental source: strain Garcia-1966 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: DNA
A.Residues: 1-213 <MAS>
A.Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60847.1; PID:g439017
A.Experimental source: strain Bangladesh-1975
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A;Residues: 1-213 <JOH
C;Superfamily: vaccinia virus D9R protein; mutr domain homology
F;106-140/Pomain: mutr domain homology <MUTr>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: vaccinia virus D9R protein; mutT domain homology
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Pred. No. 10;
4; Mismatches
                                                   D9R protein - vaccinia virus (strain Copenhagen)
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4; Mismatches
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44.48;
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Best Local Similarity 44...
Best B; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
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                                                                                                                                                                                                                                                       C; Species: vaccinia virus
C; Species: vaccinia virus
C; Date: Od-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jul-1999
C; Accession: A03885
R; Niles, E.G.; Condit, R.C.; Caro, P.; Davidson, K.; Matusick, L.; Seto, J.
R; Niles, E.G.; Condit, R.C.; Caro, P.; Davidson, K.; Matusick, L.; Seto, J.
R; Nicology 153, 96-112, 1986
A; Title: Nuclectide sequence and genetic map of the 16-kb vaccinia virus HindIII D fragm
A; Reference number: A01146; MUID:86291159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: GB:x69198; NID:g456758; PIDN:CAA49040.1; PID:g297279
KShchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.;
dzhaparidze, O.G.; Sandakhchiev, L.S.
Virus Res. 27, 25-35, 1993
A;Title: Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments.
A;Reference number: S33069; MUID:93190624
A;Accession: S33113
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A;Residuas: 1-213 <SHC>
A;Residuas: 1-213 <SHC>
A;Cross-references: EMBL:X67119; NID:g62330; PIDN:CAA47598.1; PID:g62375
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
C;Superfamily: vaccinia virus D9F protein; mutT domain homology
F;106-140/Domain: mutT domain homology <MUTT>
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N'Alternate names: D9R protein
C;Species: variola virus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: F36847; S33113
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Gaps
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Pred. No. 10;
4; Mismatches 6; Indels
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Indels
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5.
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Mismatches
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D9R protein - vaccinia virus (strain WR)
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submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: F36847
A;Status: preliminary
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526 ERTDEKEIPKEQQDIVYR 543
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                                                EREDERTLIKEYEDIVLK 19
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Best Local Similarity 44.4
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-213 <BLI>
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A: Molecule type: DNA
A: Residues: 1-213 <NIL>
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Matches
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A Note: FAS1

(S. Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate--CoA lig
C. Superfamily: 3-oxoacyl-[acyl-carrier-protein]
F;100-714/Domain: acetate--CoA ligase homology <ACL>-
F;710-861/Domain: acyl carrier protein homology <ACPI>-
F;905-1308/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>-
F;305-23463/Domain: acyl carrier protein homology <ACPI>-
F;515-5227/Domain: acyl carrier protein homology <ACPI>-
F;515-5227/Domain: acyl carrier protein homology <ACPI>-
F;515-45689/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>-
F;517-45689/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASI>-
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submitted to the EMBL Data Library, August 1998
A;Description: Characterization of a type I FAS gene in the parasitic protozoon Crypt
A;Reference number: 220993
A;Accession: T31307
                                                                                                                                                                                                                                                                                                                                  probable vacuolar biogenesis protein - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Species: Schizosaccharomyces pombe C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Species: Cryptosporidium parvum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000
C;Accession: T31307
R;Zhu, G.; Marchewka M T
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pred. No. 6.2e+02;
5; Mismatches 5; Indels
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                                                                                                                                                                                                                         R;Murphy, L.; Harris, D.; Wood, V.; Barrell, I submitted to the EMBL Data Library, June 1997 A;Reference number: 221738 A;Accession: T37768
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1889 NIKEDPKIMYEEYEEIGLK 1907
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57.1%;
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Matches 9; Conserve
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Best Local Similarity
'-hos 8; Conserve
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A; Introns: 40/3; 100/3
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C; Accession: D84509
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. Buss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R: Antoine...; Sobieflinger, F.; Falkner, F.G.; Dorner, F. submitted to the EMBL Data Library, March 1997
A; Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strainerence number: 220877
A; Reference number: 220877
A; A; Accession: T3382
A; A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Species: vaccinia virus
A; Variaty: strain Ankara
C; Date: 21.Jan-2000 #sequence_revision 21.Jan-2000 #text_change 04-Mar-2000
C; Accession: T37382
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Pred. No. 20;
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A; Cross-references: EMBL:U94848; PIDN:AAB96517.1
A; Experimental source: strain Ankara
C; Genetics:
A; Note: MVA106R
C; Superfamily: vaccinia virus D9R protein; mutT domain homology
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Best Local Similarity 57.1%;
Matches 8; Conservative
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